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(54) Title: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY		
(57) Abstract <p>The present invention relates to mammalian mahogany genes, including the human mahogany gene, which are novel genes involved in the control of mammalian body weight. The invention encompasses nucleotide sequences of the mahogany gene, host cell expression systems of the mahogany gene, and hosts which have been transformed by these expression systems, including transgenic animals. The invention also encompasses novel mahogany gene products, including mahogany proteins, polypeptides and peptides containing amino acid sequences mahogany proteins, fusion proteins of mahogany proteins polypeptides and peptides, and antibodies directed against such mahogany gene products. The present invention also relates to methods and compositions for the diagnosis and treatment of mammalian body weight disorders, including obesity, cachexia, and anorexia, and for the identification of subjects susceptible to such disorders. Further, the invention relates to methods of using the mahogany gene and gene products of the invention for the identification of compounds which modulate the expression of the mahogany gene and/or the activity of the mahogany gene product. Such compounds can be useful as therapeutic agents in the treatment of mammalian body weight disorders, including obesity, cachexia, and anorexia.</p>		

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METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

Priority of provisional application no. 60/093,630 filed
5 on July 21, 1998 and of provisional application no.
60/104,978 filed on October 20, 1998, each of which is
incorporated herein by reference in its entirety, is claimed
under 35 U.S.C. § 119(e) (1).

10 1.

INTRODUCTION

The present invention relates to mammalian mahogany
genes, including the human mahogany gene, which are novel
genes involved in the control of mammalian body weight. The
invention encompasses nucleotide sequences of the mahogany
gene, host cell expression systems of the mahogany gene, and
15 hosts which have been transformed by these expression
systems, including transgenic animals. The invention also
encompasses novel mahogany gene products, including mahogany
proteins, polypeptides and peptides containing amino acid
sequences mahogany proteins, fusion proteins of mahogany
20 proteins polypeptides and peptides, and antibodies directed
against such mahogany gene products.

The present invention also relates to methods and
compositions for the diagnosis and treatment of mammalian
body weight disorders, including obesity, cachexia, and
25 anorexia, and for the identification of subjects susceptible
to such disorders. Further, the invention relates to methods
of using the mahogany gene and gene products of the invention
for the identification of compounds which modulate the
expression of the mahogany gene and/or the activity of the
mahogany gene product. Such compounds can be useful as
30 therapeutic agents in the treatment of mammalian body weight
disorders, including obesity, cachexia, and anorexia.

2. BACKGROUND OF THE INVENTION

Obesity represents the most prevalent of body weight disorders, and it is the most important nutritional disorder in the western world, with estimates of its prevalence ranging from 30% to 50% within the middle-aged population. Other body weight disorders, such as anorexia nervosa and bulimia nervosa, which together affect approximately 0.2% of the female population of the western world, also pose serious health threats. Further, such disorders as anorexia and cachexia (wasting) are also prominent features of other diseases such as cancer, cystic fibrosis, and AIDS.

Obesity, defined as an excess of body fat relative to lean body mass, also contributes to other diseases. For example, this disorder is responsible for increased incidence of diseases such as coronary artery disease, hypertension, stroke, diabetes, hyperlipidemia, and some cancers (See, e.g., Nishina, P.M. et al., 1994, Metab. 43: 554-558; Grundy, S.M. & Barnett, J.P., 1990, Dis. Mon. 36: 641-731). Obesity is not merely a behavioral problem, i.e., the result of voluntary hyperphagia. Rather, the differential body composition observed between obese and normal subjects results from differences in both metabolism and neurologic/metabolic interactions. These differences seem to be, to some extent, due to differences in gene expression, and/or level of gene products or activity (Friedman, J.M. et al., 1991, Mammalian Gene 1: 130-144).

The epidemiology of obesity strongly shows that the disorder exhibits inherited characteristics (Stunkard, 1990, N. Eng. J. Med. 322: 1438). Moll et al. have reported that, in many populations, obesity seems to be controlled by a few genetic loci (Moll et al., 1991, Am. J. Hum. Gen. 49: 1243). In addition, human twin studies strongly suggest a substantial genetic basis in the control of body weight, with estimates of heritability of 80-90% (Simopoulos, A.P. &

Childs, E., eds., 1989, in "Genetic Variation and Nutrition in Obesity", World Review of Nutrition and Diabetes 63, S. Karger, Basel, Switzerland; Bjorjeson, M., 1976, Acta. Paediatr. Scand. 65: 279-287).

5 In other studies, non-obese persons who deliberately attempted to gain weight by systematically over-eating were found to be more resistant to such weight gain and able to maintain an elevated weight only by very high caloric intake. In contrast, spontaneously obese individuals are able to
10 maintain their status with normal or only moderately elevated caloric intake. In addition, it is a commonplace experience in animal husbandry that different strains of swine, cattle, etc., have different predispositions to obesity. Studies of the genetics of human obesity, and of animal models of obesity demonstrate that obesity results from complex
15 defective regulation of both food intake, food induced energy expenditure, and of the balance between lipid and lean body anabolism.

There are a number of genetic diseases in man and other species which feature obesity among their more prominent
20 symptoms, along with, frequently, dysmorphic features and mental retardation. For example, Prader-Willi syndrome (PWS; reviewed in Knoll, J.H. et al., 1993, Am. J. Med. Genet. 46: 2-6) affects approximately 1 in 20,000 live births, and involves poor neonatal muscle tone, facial and genital deformities, and generally obesity.

25 In addition to PWS, many other pleiotropic syndromes have been characterized which include obesity as a symptom. These syndromes are genetically straightforward, and appear to involve autosomal recessive alleles. Such diseases include, among others, Ahlstrom, Carpenter, Bardet-Biedl,
30 Cohen, and Morgagni-Stewart-Monell Syndromes.

A number of models exists for the study of obesity (see, e.g., Bray, G. A., 1992, Prog. Brain Res. 93: 333-341; and

Bray, G.A., 1989, Amer. J. Clin. Nutr. 5: 891-902). For example, animals having mutations which lead to syndromes that include obesity symptoms have also been identified. Attempts have been made to utilize such animals as models for the study of obesity, and the best studied animal models to date for genetic obesity are mice. For reviews, see, e.g., Friedman, J.M. et al., 1991, Mamm. Gen. 1: 130-144; Friedman, J.M. and Liebel, R.L., 1992, Cell 69: 217-220.

Studies utilizing mice have confirmed that obesity is a very complex trait with a high degree of heritability. Mutations at a number of loci have been identified which lead to obese phenotypes. These include the autosomal recessive mutations obese (*ob*), diabetes (*db*), fat (*fat*), and tubby (*tub*).

The dominant Yellow mutation (*Ay*) at the agouti locus causes a pleiotropic syndrome which causes moderate adult onset obesity, a yellow coat color, and a high incidence of tumor formation (Herberg, L. and Coleman, D.L., 1977, Metabolism 26:59), and an abnormal anatomic distribution of body fat (Coleman, D.L., 1978, Diabetologia 14:141-148). The mutation causes the widespread expression of a protein which is normally seen only in neonatal skin (Michaud, E. J. et al., 1994, Genes Devel. 8:1463-1472). The agouti protein has been reported to be a competitive antagonist of α -MSH binding to the melanocortin receptors MC1-R and MC4-R *in vitro* (Lu et al., 1996, Nature 371:799-802), and the authors speculated that de-regulated ubiquitous expression of agouti may lead to obesity by antagonism of melanocortin receptors expressed outside the hair follicles.

Mahogany (*mg*) and mahoganoid (*md*) are mutations that suppress the phenotypic effects of agouti protein *in vivo* (Lane and Green, 1960, J. Hered. 51: 228-230). The mahogany and mahoganoid mutation have been mapped to mouse chromosomes 2 and 16, respectively (Green, 1989, "Catalog of mutant genes

and polymorphic loci", pp. 12-403 in Genetic Variants and Strains of the Laboratory Mouse, Lyon, M. F. and Searle, A.G., eds., Oxford University Press, Oxford). Mutations of both *mg* and *md* have been shown to suppress the effects of agouti on obesity as well as on coat color (Miller et al., 1997, *Genetics* 146: 1407-1415).

In summary, therefore, obesity, which poses a major, worldwide health problem, represents a complex, highly heritable trait. Given the severity, prevalence, and potential heterogeneity of such disorders, there exists a great need for the identification of those genes that participate in the control of body weight.

3. SUMMARY OF THE INVENTION

The present invention relates to the identification of novel nucleic acid molecules and proteins encoded by such nucleic acid molecules that are involved in the control of mammalian body weight, and which, further, are associated with mammalian body weight disorders such as obesity, cachexia, and anorexia. The nucleic acid molecules of the present invention represent the genes corresponding to the mammalian mahogany gene, including the human mahogany gene.

In particular, the compositions of the present invention include nucleic acid molecules which comprise the following sequences: (a) nucleotide sequences of the mahogany gene, including, e.g., murine mahogany sequences as shown in FIGS. 2A, 3B-D, 6A-B, 8A, and 9A, as well as allelic variants and homologs thereof, and human mahogany sequences, as shown, e.g., in FIGS. 10A, 18A, 19A and 20A, as well as allelic variants and homologs thereof; (b) nucleotide sequences that encode the mahogany gene product amino acid sequences, as shown, e.g., in FIGS. 2B, 8B, 9B, 10B, 17, 18B, 19B and 20B; (c) nucleotide sequences that encode portions of the mahogany gene product corresponding to its functional domains

and individual exons; (d) nucleotide sequences comprising the novel mahogany gene sequences disclosed herein that encode mutants of the mahogany gene product in which all or a part of one or more of the domains is deleted or altered, as shown, e.g., in FIG. 6; (e) nucleotide sequences that encode fusion proteins comprising the mahogany gene product, or one or more of its domains fused to a heterologous polypeptide; (f) nucleotide sequences within the mahogany gene, as well as chromosome sequences flanking the mahogany gene, see, e.g., FIG. 3, which can be utilized as part of the methods of the present invention for the diagnosis of mammalian body weight disorders, including obesity, cachexia, and anorexia, which are mediated by the mahogany gene, as well as for the identification of subjects susceptible to such disorders; (g) nucleic acid sequences that hybridize to the above described sequences under stringent or moderately stringent conditions, particularly human mg homologs. The nucleic acid molecules of the invention include, but are not limited to, cDNA and genomic DNA sequences of the mahogany gene.

The present invention also encompasses expression products of the nucleic acid molecules listed above; i.e., proteins and/or polypeptides that are encoded by the above mahogany nucleic acid molecules.

Agonists and antagonists of the mahogany gene and/or gene product are also included in the present invention. Such agonists and antagonists will include, for example, small molecules, large molecules, and antibodies directed against the mahogany gene product. Agonists and antagonists of the invention also include nucleotide sequences, such as antisense and ribozyme molecules, and gene or regulatory sequence replacement constructs, that can be used to inhibit or enhance expression of the mahogany gene.

The present invention further encompasses cloning vectors, including expression vectors, that contain the

nucleic acid molecules of the invention and can be used to express those nucleic acid molecules in host organisms. The present invention also relates to host cells engineered to contain and/or express the nucleic acid molecules of the invention. Further, host organisms which have been transformed with these nucleic acid molecules are also encompassed in the present invention. Host organisms of the invention include organisms transformed with the cloning vectors described above, e.g., transgenic animals, particularly non-human transgenic animals, and particularly transgenic non-human mammals.

The transgenic animals of the invention include animals that express a mutant variant or polymorphism of a mahogany gene, particularly a mutant variant or polymorphism of a mahogany gene that is associated with a weight disorder such as obesity, cachexia, or anorexia. The transgenic animals of the invention further include those that express a mahogany transgene at higher or lower levels than normal. The transgenic animals of the invention further include those which express the mahogany gene in all their cells, "mosaic" animals which express the mahogany gene in only some of their cells, and those in which the mahogany gene is selectively introduced into and expressed in a specific cell type(s). The transgenic animals of the invention also include "knock-out" animals. Knock-out animals comprise animals which have been engineered to no longer express the mahogany gene.

The present invention also relates to methods and compositions for the diagnosis of mammalian body weight disorders, including obesity, cachexia, and anorexia, as well as for the identification of subjects susceptible to such disorders. Such methods comprise, for example, measuring expression of the mahogany gene in a patient sample, or detecting a mutation in the mahogany gene in the genome of a mammal, including a human, suspected of exhibiting such a

weight disorder. The nucleic acid molecules of the invention can also be used as diagnostic hybridization probes, or as primers for diagnostic PCR analysis to identify of mahogany gene mutations, allelic variations, or regulatory defects, such as defects in the expression of the mahogany gene. Such diagnostic PCR analyses can be used to diagnose individuals with a body weight disorder associated with a particular mahogany gene mutation, allelic variation, or regulatory defect. Such diagnostic PCR analyses can also be used to identify individuals susceptible to such body weight disorders and hyperphagia.

Methods and compositions, including pharmaceutical compositions, for the treatment of body weight disorders such as obesity, cachexia, and anorexia are also included in the invention. Such methods and compositions are capable of modulating the level of mahogany gene expression and/or the level of activity of the mahogany gene product. Such methods include, for example, modulating the expression of the mahogany gene and/or the activity of the mahogany gene product for the treatment of a body weight disorder which is mediated by some other gene, for example by the agouti gene.

The invention still further relates to methods for identifying compounds which modulate the expression of the mammalian mahogany gene and/or the synthesis or activity of mammalian mahogany gene products. Such compounds include therapeutic compounds which can be used as pharmaceutical compositions to reduce or eliminate the symptoms of mammalian body weight disorders such as obesity, cachexia, and anorexia. Cellular and non-cellular assays are described that can be used to identify compounds that interact with the mahogany gene and/or gene product, e.g., modulate the activity of the mahogany gene and/or bind to the mahogany gene product. Such cell-based assays of the invention

utilize cells, cell lines, or engineered cells or cell lines that express the mahogany gene product.

In one embodiment, such methods comprise contacting a compound to a cell that expresses a mahogany gene, measuring
5 the level of mahogany gene expression, gene product expression, or gene product activity, and comparing this level to the level of mahogany gene expression, gene product expression, or gene product activity produced by the cell in the absence of the compound, such that if the level obtained
10 in the presence of the compound differs from that obtained in its absence, a compound that modulates the expression of the mammalian mahogany gene and/or the synthesis or activity of mammalian mahogany gene products has been identified.

In an alternative embodiment, such methods comprise administering a compound to a host, e.g., a transgenic animal
15 that expresses a mahogany transgene or a mutant mahogany transgene, and measuring the level of mahogany gene expression, gene product expression, or gene product activity. The measured level is compared to the level of mahogany gene expression, gene product expression, or gene
20 product activity in a host that is not exposed to the compound, such that if the level obtained when the host is exposed to the compound differs from that obtained when the host is not exposed to the compound, a compound that modulates the expression of the mammalian mahogany gene
25 and/or the synthesis or activity of mammalian mahogany gene products, and/or the symptoms of a mammalian body weight disorder, such as obesity, cachexia, or anorexia, has been identified.

The Example presented in Section 6, below, describes the genetic and physical mapping of the mahogany gene to a
30 specific 700 kb interval of mouse chromosome 2. The example presented in Section 7, below, describes the identification of a transcription unit within this chromosome interval,

referred to herein as the MG gene, which represents the mahogany gene. The expression and sequence analysis of this candidate mahogany gene is described in the example presented in Section 8, below. These experiments prove that the candidate gene MG is indeed the mahogany gene. The example presented in Section 9, below, presents data demonstrating that the mechanism of mahogany action is specific for diet-induced obesity, therefore supporting the use of mahogany antagonists as a specific therapeutic for treatment of diet-induced body weight disorders. The example presented in Section 10, below, presents the identification and characterization of the human mg gene, variants thereof and polypeptides encoded by the human mahogany sequences.

DEFINITIONS

As used herein, the following terms shall have the abbreviations indicated.

BAC, bacterial artificial chromosomes
bp, base pair(s)
EST, expressed sequence tag
mg, mahogany gene
RFLP, restriction fragment length polymorphism
RT-PCR, reverse transcriptase PCR
SSCP, single-stranded conformational polymorphism
SSLP, simple sequence length polymorphisms
STS, short tag sequence
YAC, yeast artificial chromosome

4. BRIEF DESCRIPTION OF THE FIGURES

FIG. 1. Physical map of the mahogany interval of mouse chromosome 2.

FIG. 2. Panel A(1)-A(3): cDNA nucleotide sequence of the wild-type (C57BL/6J) murine mahogany gene (SEQ ID NO: 1),

including the 5' and 3' untranslated regions, and Panel B: the derived amino acid sequence (SEQ ID NO: 2) of the mahogany gene product.

5 FIG. 3. Genomic structure and nucleotide sequences derived from the wild-type (C57BL/6J) mouse genomic regions containing the mg gene. Panel A, genomic structure; Panel B(1)-B(9), genomic sequence c56 (SEQ ID NO: 3); Panel C(1)-C(4), genomic sequence c96 (SEQ ID NO: 4); Panel D(1)-D(37),
10 genomic sequence of c110/111 (SEQ ID NO: 5).

FIG. 4. Structural depiction of MG cDNA without introns. CUB=CUB domain, metal=metallothionin domain; T-transmembrane domain.

15 FIG. 5(1)-5(4). Nucleotide sequence of primers used to amplify each of the exons in the mg gene.

FIG. 6. Nucleotide sequence of the wild-type (SEQ ID NO: 6) and mahogany mutant (SEQ ID NO: 7) sequences in exon
20 15 of the MG gene. Bases shown in bold are deleted in Mg3J mutant mg.

FIG. 7. Differential 5' start sequences in the murine mahogany gene showing splice forms akml003 and akml004.

25 FIG. 8. Panel A, cDNA sequence (SEQ ID NO: 8) from one form of the differential 5' start site found in the murine (akml003), Panel B, amino acid sequence (SEQ ID NO: 9) encoded by the cDNA of Panel A; Panel C, hydropathy plot of
30 the akml003 amino acid sequence.

FIG. 9. Panel A, cDNA sequence (SEQ ID NO: 10) from one form of the differential 5' start site found in the

murine (akml004); Panel B, amino acid sequence (SEQ ID NO: 11) encoded by the cDNA of Panel A; Panel C, hydropathy plot of the akml004 amino acid sequence.

5 FIG. 10. Nucleotide sequence (SEQ ID NO: 12) of a contig containing a portion of the human MG cDNA, panel A(1)-A(3) and the translated amino acid sequence (SEQ ID NO: 13), panel E.

10 FIG. 11. Effect of *mg* on *MC4r* $-/-$ induced weight gain in females (FIG. 11A) and males (FIG. 11B); values depicted are the mean \pm SD within a designated time interval.

15 FIG. 12. Effect of *mg* on monogenic obese mutants *Lepr^{db}* (FIG. 12A), *tub* (FIG. 12B), *Cpe^{fat}* (FIG. 12C), and on high fat diet induced obesity (FIG. 12D); the values indicated are the mean \pm SD of the weight length ratio for each animal.

20 FIG. 13. Genetic and physical map of the region surrounding the *mg* locus; all MIT markers are presented with shortened names, e.g., D2MIT77 is indicated as D2M77; locations of loci which also mapped on the human cytogenetic map are indicated in parentheses after the gene symbol.

25 FIG. 13A. The genetic map of the *mg* gene region on the Millennium BSB mapping panel (Misumi, D.J. et al., 1997, *Science* 278:135-138);

FIG. 13B. The genetic map obtained from crosses segregating *mg* mutant alleles;

30 FIG. 13C. The \sim 1 Mb BAC contig across the *mg* gene region of mouse Chromosome 2;

FIG. 13D. The transcriptional units identified in the *mg* region; the filled box indicates the *mg* gene,

whereas the hatched box is a member of the High Mobility Group (HMG) gene family which sits between coding exons 21 and 22 of the *mg* gene.

5 FIG. 14. Northern blot analysis with C3H/HeJ (lane 1), and three mutant alleles of *mg*: C3HeB/FeJ-*mg*^{3J} (Lane 2), LDJ/Le-*mg* (Lane 3), and C3H/HeJ-*mg*⁻ (Lane 4); the size marker is shown on the left, and hybridization with actin is shown below for loading comparisons.

10 FIG. 15. In situ hybridization data: FIG. 15A demonstrates widespread expression of *mg* throughout the mouse brain is seen in an antisense autoradiographic image of a C3H/HeJ brain at the level of the 3rd ventricle; decreased expression in *mg* mutants is documented in selected antisense
15 darkfield images of 10 μ m whole mount cross sections of the ventromedial hypothalamic nucleic (VMH) of C3H/HeJ (FIG. 15B), LDJ/Le-*mg* (FIG. 15C), and C3HeB/FeJ-*mg*^{3J} (FIG. 15D).

20 FIG. 16. Alignment of the MG protein sequence with its family members showing the transmembrane region (indicated in brackets) and cytoplasmic tail (FIG. 16A); and a schematic of the molecular modular architecture of MG (FIG 16B).

25 FIG. 17A-C. Sequence alignment of the predicted MG protein sequence (top) with the Attractin protein sequence. Characteristic MG domains are as indicated. See Section 10.2 for details.

30 FIG. 18A-B. Panel A: cDNA nucleotide sequence (SEQ ID NO: 14) of the long splice variant of the human ortholog of the mahogany gene, and Panel B: the derived amino acid sequence (SEQ ID NO: 15) of the mahogany gene product which it encodes.

FIG. 19A-B. Panel A: cDNA nucleotide sequence (SEQ ID NO: 16) of a shorter splice variant of the human ortholog of the mahogany gene, and Panel B: the derived amino acid sequence (SEQ ID NO: 17) of the mahogany gene product which it encodes.

FIG. 20A-B. Panel A: cDNA nucleotide sequence (SEQ ID NO: 18) of a second shorter splice variant of the human ortholog of the mahogany gene, and Panel B: the derived amino acid sequence (SEQ ID NO: 19) of the mahogany gene product which it encodes.

5. DETAILED DESCRIPTION OF THE INVENTION

Described herein is the identification of the novel mammalian mahogany (*mg*) gene, including the human mahogany gene, which is involved in the control of mammalian body weight. Also described are recombinant mammalian, including human mahogany DNA molecules, cloned genes, and degenerate variants thereof. The compositions of the present invention further include *mg* gene products (e.g., proteins) that are encoded by the *mg* DNA molecules of the invention, and the modulation of *mg* gene expression and/or *mg* gene product activity in the treatment of mammalian body weight disorders, including obesity, cachexia, and anorexia. Also described herein are antibodies against *mg* gene products (e.g., proteins), or conserved variants or fragments thereof, and nucleic acid probes useful for the identification of *mg* gene mutations, and the use of such nucleic acid probes in diagnosing mammalian body weight disorders, including obesity, cachexia, and anorexia. Further described are methods for the use of the *mg* gene and/or *mg* gene products in the identification of compounds which modulate the activity of the *mg* gene product.

5.1.

THE MAHOGANY GENE

The mahogany genes are novel mammalian genes involved in the control of body weight. The nucleic acid sequences of the mahogany genes, including the murine mahogany gene
5 sequences shown in FIGS. 2A, 3B-D, 6A-B, 8A, and 9A, as well as allelic variants and homologs thereof, and human mahogany sequences, as shown, e.g., in FIGS. 10A, 18A, 19A and 20A, as well as allelic variants and homologs thereof. The genomic sequence and structure, i.e., the intron/exon structure, of
10 the mahogany genes have also been elucidated, FIG. 3.

The mahogany gene nucleic acid molecules of the present invention comprise: (a) the DNA sequence shown in FIGS. 2A, 3, 6A-B, 8A, 9A, 10A, 18A, 19A or 20A, or any DNA sequence that encodes the amino acid sequence of the mahogany gene product shown in FIGS. 2B, 8B, 9B, 10B, 17, 18B, 19B or 20B;
15 (b) nucleotide sequences comprising the novel mahogany sequences disclosed herein that encode mutants of the mahogany gene product in which all or a part of one or more of the domains is deleted or altered, as shown, e.g., FIG. 6; (c) nucleotide sequences that encode fusion proteins
20 comprising a mahogany gene product, or one of its domains fused to a heterologous polypeptide; and (d) nucleotide sequences within a mahogany gene, nucleotide sequences on the chromosome flanking the mahogany gene, see, e.g., FIG. 3 and human genomic sequences syntenic to the sequences depicted in
25 FIG. 3, which can be utilized as part of the methods of the invention for identifying and diagnosing individuals who exhibit or are susceptible to weight disorders, including obesity, cachexia, and anorexia.

The mahogany nucleotide sequences of the invention further comprise: (a) any nucleotide sequence that
30 hybridizes to the complement of a nucleic acid molecule that encodes a mahogany gene product under highly stringent conditions, e.g., hybridization to filter-bound DNA in 0.5 M

NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1xSSC/0.1% SDS at 68°C (Ausubel F.M. et al., eds., 1989, Current Protocols in Molecular Biology, Vol. 1, Green Publishing Associates, Inc., and John Wiley & Sons, Inc., New York, at p. 2.10.3) particularly human *mc* sequences, FIG. 10; and (b) any nucleotide sequence that hybridizes to the complement of a nucleic acid molecule that encodes a mahogany gene product under less stringent conditions, such as moderately stringent conditions, e.g., washing in 0.2xSSC/0.1% SDS at 42 °C (Ausubel et al., 1989, *supra*), yet which still encodes a functionally equivalent mahogany gene product.

"Functionally equivalent", as utilized herein, refers to a gene product (e.g., a protein) capable of exhibiting a substantially similar *in vivo* activity as the endogenous *mc* gene products encoded by the *mc* gene sequences described above. The *in vivo* activity of the *mc* gene product, as used herein, refers to the ability of the *mc* gene product, when present in an appropriate cell type, to ameliorate, prevent, or delay the appearance of the mahogany phenotype relative to its appearance when that cell type lacks a functional mahogany gene product.

The invention also includes nucleic acid molecules, preferably DNA molecules, that are the complements of the nucleotide sequences described above. Among the nucleic acid molecules of the invention are deoxyoligonucleotides ("oligos") which hybridize under highly stringent or moderately stringent conditions to the mahogany nucleic acid molecules described above. Exemplary highly stringent conditions may refer, e.g., to washing in 6xSSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligos), 48°C (for 17-base oligos), 55°C (for 20-base oligos), and 60°C (for 23-base oligos). These nucleic acid molecules may encode or act as antisense molecules, useful, for example, in mahogany gene

regulation, and/or as antisense primers in amplification reactions of mahogany gene nucleic acid sequences. With respect to mahogany gene regulation, such techniques can be used to regulate, for example, weight disorders such as obesity, cachexia, or anorexia. Such sequences may also be used as part of ribozyme and/or triple helix sequences, which are also useful for mahogany gene regulation. Still further, such molecules may be used as components of diagnostic methods whereby, for example, the presence of a particular mahogany allele associated with a weight disorder, such as obesity, cachexia, or anorexia, may be detected. Among the molecules which can be used for diagnostic methods, such as those which involve amplification of genomic mahogany sequences, are primers or probes that can routinely be obtained using the genomic and cDNA sequences disclosed herein.

In one embodiment, the nucleic acid molecules of the invention do not include nucleic acid molecules that consist solely of the nucleotide sequence that encodes the attractin protein sequence depicted in FIG. 17A-C.

The mahogany nucleic acid sequences of the invention further include fragments of the nucleic acid sequences described above. For example, mahogany nucleic acid fragments can include fragments of at least 10, 12, 15, 20, 30, 40, 50, 100, 150, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000 or more nucleotides.

The nucleotide sequences of the present invention also include (a) DNA vectors that contain any of the foregoing mahogany coding sequences and/or their complements; (b) DNA expression vectors that contain any of the foregoing mahogany coding sequences operatively associated with a regulatory element that directs the expression of the coding sequences; and (c) genetically engineered host cells and organisms that

contain any of the foregoing mahogany coding sequences operatively associated with a regulatory element that directs the expression of the coding sequence in the host cell. As used herein, regulatory elements include, but are not limited to inducible and non-inducible promoters, enhancers, operators, and other elements known to those skilled in the art that drive and regulate gene expression. Such regulatory elements include, but are not limited to, the cytomegalovirus hCMV immediate early gene, the early or late promoters of SV40 adenovirus, the lac system, the trp system, the TAC system, the TRC system, the major operator and promoter regions of phage A, the control regions of fd coat protein, the promoter for 3'-phosphoglycerate kinase, the promoters of acid phosphatase, and the promoters of the yeast alpha-mating factors.

In addition to the mahogany gene sequences described above, homologs of such sequences, exhibiting extensive homology to one or more domains of the mahogany gene product can be present in other species. In a preferred embodiment, the mahogany gene homologue maps to a chromosomal region that is syntenic to the chromosomal region of the mahogany gene. In a particularly preferred embodiment, a human mahogany gene homologue sequence maps to a human chromosome region that is syntenic to the region of mouse chromosome 2 to which the murine mahogany gene maps, namely 20p15, and comprises the contiged human MG cDNA provided herein. Further, there can also exist homologue genes at other genetic loci within the genome of the same species which encode proteins having extensive homology to one or more domains of the mahogany gene product. Such mahogany homologs can include, for example, secreted forms of the mahogany sequences, see, e.g., Duke-Cohan, J.S. et al. (1998, *Proc. Natl. Acad. Sci. U.S.A.* 95:11336-11341). Such sequences, can be used, for example, in the screening assays, described in Section 5.4.2 below,

for compounds that interact with the mahogany gene and/or its gene product and that may therefore be useful in treating and ameliorating body weight disorders.

Other mahogany homologs can be identified and readily
5 isolated, without undue experimentation, by molecular
biological techniques well known in the art, and are
therefore within the scope of the present invention. As an
example, in order to clone a human mahogany gene homologue
using isolated murine mahogany gene sequences, such murine
mahogany gene sequences may be labeled and used to screen a
10 cDNA library constructed from mRNA obtained from appropriate
cells or tissues derived from the organism (in this case,
human) of interest. With respect to the cloning of such a
human mahogany homologue, a human cDNA library may, for
example be used for screening, such as a cDNA library
15 obtained from mRNA isolated from brain tissues, particularly
containing hypothalamic regions.

The hybridization washing conditions used should be of a
lower stringency when the cDNA library is derived from an
organism different from the type of organism from which the
20 labeled sequence was derived. With respect to the cloning of
a human mahogany homologue, for example, hybridization can be
performed for 4 hours at 65°C using Amersham Rapid Hyb™
buffer (Cat. #RPN1639) according to manufacturer's protocol,
followed by washing, with a final washing stringency of
1.0xSSC/0.1% SDS at 50°C for 20 minutes being preferred.

25 Low stringency conditions are well known to those of
skill in the art, and will vary predictably depending on the
specific organisms from which the library and the labeled
sequences are derived. For guidance regarding such
conditions see, for example, Sambrook et al., 1989, Molecular
30 Cloning, A Laboratory Manual, Cold Springs Harbor Press,
N.Y.; and Ausubel et al., 1989, Current Protocols in

Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y.

Alternatively, the labeled fragment may be used to screen a genomic library derived from the organism of interest, again, using appropriately stringent conditions.

Further, a mahogany gene homologue may be isolated from nucleic acid of the organism of interest by performing PCR using two degenerate oligonucleotide primer pools designed on the basis of amino acid sequences within the mahogany gene product disclosed herein. The template for the reaction may be cDNA obtained by reverse transcription of mRNA prepared from, for example, human or non-human cell lines or tissue known or suspected to express a mahogany gene allele.

The PCR product may be subcloned and sequenced to ensure that the amplified sequences represent the sequences of a mahogany gene nucleic acid sequence. The PCR fragment may then be used to isolate a full length cDNA clone by a variety of methods. For example, the amplified fragment may be labeled and used to screen a cDNA library, such as a bacteriophage cDNA library. Alternatively, the labeled fragment may be used to isolate genomic clones via the screening of a genomic library. This method has been used to isolate sequences encoding each of the murine MG gene exons as well as to isolate contigs containing the human MG sequences provided herein, FIG. 10.

PCR technology may also be utilized to isolate full length cDNA sequences. For example, RNA may be isolated, following standard procedures, from an appropriate cellular or tissue source (i.e., one known, or suspected, to express the mahogany gene). A reverse transcription reaction may be performed on the RNA using an oligonucleotide primer specific for the most 5' end of the amplified fragment for the priming of the first strand synthesis. The resulting RNA/DNA hybrid may then be "tailed" with guanines using a standard terminal

transferase reaction, they hybrid may be digested with RNAase H, and second strand synthesis may then be primed with a poly-C primer. Thus, cDNA sequences upstream of the amplified fragment may easily be isolated. For a review of cloning strategies which may be used, see e.g., Sambrook et al., 1989 *supra*.

10 Mahogany gene sequences may additionally be used to isolate mutant mahogany alleles. Such mutant alleles may be isolated from individuals either known or proposed to have a phenotype which contributes to the symptoms of body weight disorders such as obesity, cachexia, or anorexia or disorders associated with hyperphagia. Mutant alleles and mutant allele products may then be utilized in the therapeutic and diagnostic systems described below. Additionally, such mahogany gene sequences can be used to detect mahogany gene
15 regulatory (e.g. promoter) defects which can affect body weight.

A cDNA of a mutant mahogany gene may be isolated, for example, by using PCR, a technique which is well known to those of skill in the art. In this case, the first cDNA
20 strand may be synthesized by hybridizing an oligo-dT oligonucleotide to mRNA isolated from tissue known or suspected to be expressed in an individual putatively carrying the mutant mahogany allele, and by extending the new strand with reverse transcriptase. The second strand of the cDNA is then synthesized using an oligonucleotide that
25 hybridizes specifically to the 5' end of the normal gene. Using these two primers, the product is then amplified via PCR, cloned into a suitable vector, and subjected to DNA sequence analysis through methods well known to those of skill in the art. By comparing the DNA sequence of the
30 mutant mahogany allele to that of the normal mahogany allele, the mutation(s) responsible for the loss of alteration of

activity of the mutant mahogany gene product can be ascertained.

Alternatively, a genomic library can be constructed using DNA obtained from an individual suspected of or known to carry the mutant mahogany allele, or a cDNA library can be constructed using RNA from a tissue known, or suspected to express the mutant mahogany allele. The normal mahogany gene or any suitable fragment thereof may then be labeled and used as a probe to identify the corresponding mutant mahogany allele in such libraries. Clones containing the mutant mahogany gene sequences may then be purified and subjected to sequence analysis according to methods well known to those of skill in the art.

Additionally, an expression library can be constructed utilizing cDNA synthesized from, for example, RNA isolated from a tissue known, or suspected to express a mutant mahogany allele in an individual suspected of or known to carry such a mutant allele. In this manner, gene products made by the putatively mutant tissue may be expressed and screened using standard antibody screening techniques in conjunction with antibodies raised against the normal mahogany gene product as described, below, in Section 5.3. For screening techniques, see, for example, Harlow, E. and Lane, eds., 1988, "Antibodies: A Laboratory Manual", Cold Spring Harbor Press, Cold Spring Harbor. In cases where a mahogany mutation results in an expressed gene product with altered function (e.g., as a result of a missense or a frameshift mutation) a polyclonal set of anti-mahogany gene product antibodies are likely to cross-react with the mutant mahogany gene product. Library clones detected via their reaction with such labeled antibodies can be purified and subjected to sequence analysis according to methods well known to those of skill in the art.

5.2. PROTEIN PRODUCTS OF THE MAHOGANY GENE

Mahogany gene products (e.g., proteins), polypeptides and peptide fragments, mutant, truncated, or deleted forms of the mahogany gene product, and/or fusion proteins of the mahogany gene product can be prepared for a variety of uses. For example, such gene products, or peptide fragments thereof, can be used for the generation of antibodies in diagnostic assays, or for the identification of other cellular or extracellular products involved in the regulation of mammalian body weight.

10 Mahogany gene products, also referred to herein as mahogany proteins, of the present invention include those gene products encoded by the mahogany gene sequences described in Section 5.1, above. For example, FIG. 2E, 8E and 9E depict murine mahogany amino acid sequences. Mahogany
15 gene products also include human mahogany gene products as shown, e.g., in FIGS. 10E, 17E, 18E, 19E, and 20E.

In addition, mahogany gene products may include proteins that represent functionally equivalent gene products. Such an equivalent mahogany gene product may contain deletions, including internal deletions, additions, including additions yielding fusion proteins, or substitutions of amino acid residues within and/or adjacent to the amino acid sequence encoded by the mahogany gene sequences described, in Section 5.1, above, but that result in a "silent" change, in that the change produces a functionally equivalent mahogany gene
25 product. Such amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine,
30 isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and

glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid.

"Functionally equivalent", as utilized herein, refers to a gene product (e.g., a protein) capable of exhibiting a substantially similar *in vivo* activity as the endogenous *mg* gene products encoded by the *mg* gene sequences described in Section 5.1, above. The *in vivo* activity of the *mg* gene product, as used herein, refers to the ability of the *mg* gene product, when present in an appropriate cell type, to ameliorate, prevent, or delay the appearance of the mahogany phenotype relative to its appearance when that cell type lacks a functional mahogany gene product.

Alternatively, where alteration of function is desired, deletion or non-conservative alterations can produce altered, including reduced-activity, mahogany gene products. Such alterations can, for example, alter one or more of the biological functions of the mahogany gene product. Further, such alterations can be selected so as to generate mahogany gene products that are better suited for expression, scale up, etc. in the host cells chosen. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

As another example, altered mahogany gene products can be engineered that correspond to mutants or variants of the mahogany gene product associated with mammalian weight disorders, such as obesity, cachexia, or anorexia. Altered mahogany gene products can also be engineered that correspond to mutants or variants of the mahogany gene product known to neutralize or ameliorate the symptoms of body weight disorders, such as obesity, cachexia, or anorexia, which are mediated by some other gene, including, but not limited to, body weight disorders mediated by the *agouti* gene.

Also within the scope of the present invention are peptides and/or proteins corresponding to one or more domains of the mahogany protein or any one of the individual exon encoded regions of the MG protein, as well as fusion proteins
5 in which the full length mahogany protein, a mahogany peptide, or a truncated mahogany protein or peptide is fused to an unrelated heterologous protein. Such proteins and peptides can be designed on the basis of the mahogany nucleotide sequence disclosed in Section 5.1, above, and/or
10 on the basis of the mahogany amino acid sequence disclosed in the Section.

The mahogany gene products of the invention further include fragments of the gene products described herein. For example, mahogany gene product fragments can include fragments of at least 10, 12, 15, 20, 30, 40, 50, 100, 150,
15 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300 or more amino acids in length.

In one embodiment, it is understood that the gene products of the present invention do not include a gene product that consists solely of the amino acid sequence of
20 the attractin polypeptide depicted in FIG. 17.

Fusion proteins of the invention include, but are not limited to, IgFc fusions which stabilize the mahogany protein or peptide and prolong half life *in vivo*; or fusions to any amino acid sequence that allows the fusion protein to be
25 anchored to the cell membrane; or fusions to an enzyme, fluorescent protein, or luminescent protein which provides a marker function.

The mahogany gene products, peptide fragments thereof and fusion proteins thereof, may be produced by recombinant DNA technology using techniques well known in the art. Thus,
30 methods for preparing the mahogany gene products, polypeptides, peptides, fusion peptide and fusion polypeptides of the invention by expressing nucleic acid

containing mahogany gene sequences are described herein. Methods that are well known to those skilled in the art can be used to construct expression vectors containing mahogany gene product coding sequences and appropriate transcriptional
5 and translational control signals. These methods include, for example, *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. See, for example, the techniques described in Sambrook, et al., 1989, *supra*, and Ausubel, et al., 1989, *supra*. Alternatively, RNA
10 capable of encoding mahogany gene product sequences may be chemically synthesized using, for example, synthesizers. See, for example, the techniques described in "Oligonucleotide Synthesis", 1984, Gait, ed., IRL Press, Oxford.

A variety of host-expression vector systems may be
15 utilized to express the mahogany gene product coding sequences of the invention. Such host-expression systems represent vehicles by which the coding sequences of interest may be produced and subsequently purified, but also represent cells that may, when transformed or transfected with the
20 appropriate nucleotide coding sequences, exhibit the mahogany gene product of the invention *in situ*. These include but are not limited to microorganisms such as bacteria (e.g., *E. coli*, *B. subtilis*) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing
25 mahogany gene product coding sequences; yeast (e.g., *Saccharomyces*, *Pichia*) transformed with recombinant yeast expression vectors containing the mahogany gene product coding sequences; insect cell systems infected with recombinant virus expression vectors (e.g., baculovirus)
30 containing the mahogany gene product coding sequences; plant cell systems infected with recombinant virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expres-

sion vectors (e.g., Ti plasmid) containing mahogany gene product coding sequences; or mammalian cell systems (e.g., COS, CHO, BHK, 293, 3T3) harboring recombinant expression constructs containing promoters derived from the genome of 5 mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter).

In bacterial systems, a number of expression vectors may be advantageously selected depending upon the use intended for the mahogany gene product being expressed. For example, 10 when a large quantity of such a protein is to be produced, for the generation of pharmaceutical compositions of mahogany gene product or for raising antibodies to mahogany gene product, for example, vectors that direct the expression of high levels of fusion protein products that are readily 15 purified may be desirable. Such vectors include, but are not limited, to the *E. coli* expression vector pUR278 (Ruther et al., 1983, EMBO J. 2, 1791), in which the mahogany gene product coding sequence may be ligated individually into the vector in frame with the *lac Z* coding region so that a fusion 20 protein is produced; pIN vectors (Inouye and Inouye, 1985, Nucleic Acids Res. 13, 3101-3109; Van Heeke and Schuster, 1989, J. Biol. Chem. 264, 5503-5509); and the like. pGEX vectors may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In 25 general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. The pGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned target gene product can be released from the GST 30 moiety.

In an insect system, *Autographa californica*, nuclear polyhydrosis virus (AcNPV) is used as a vector to express

foreign genes. The virus grows in *Spodoptera frugiperda* cells. The mahogany gene product coding sequence may be cloned individually into non-essential regions (for example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the polyhedrin promoter). Successful insertion of mahogany gene product coding sequence will result in inactivation of the polyhedrin gene and production of non-occluded recombinant virus (i.e., virus lacking the proteinaceous coat coded for by the polyhedrin gene). These recombinant viruses are then used to infect *Spodoptera frugiperda* cells in which the inserted gene is expressed. (e.g., see Smith, et al., 1983, J. Virol. 46, 584; Smith, U.S. Patent No. 4,215,051).

In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, the mahogany gene product coding sequence of interest may be ligated to an adenovirus transcription/translation control complex, e.g., the late promoter and tripartite leader sequence. This chimeric gene may then be inserted in the adenovirus genome by *in vitro* or *in vivo* recombination. Insertion in a non-essential region of the viral genome (e.g., region E1 or E3) will result in a recombinant virus that is viable and capable of expressing mahogany gene product in infected hosts. (e.g., See Logan and Shenk, 1984, Proc. Natl. Acad. Sci. USA 81, 3655-3659). Specific initiation signals may also be required for efficient translation of inserted mahogany gene product coding sequences. These signals include the ATG initiation codon and adjacent sequences. In cases where an entire mahogany gene, including its own initiation codon and adjacent sequences, is inserted into the appropriate expression vector, no additional translational control signals may be needed. However, in cases where only a portion of the mahogany gene coding sequence is inserted,

exogenous translational control signals, including, perhaps, the ATG initiation codon, must be provided. Furthermore, the initiation codon must be in phase with the reading frame of the desired coding sequence to ensure translation of the entire insert. These exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements, transcription terminators, etc. (see Bittner, et al., 1987, Methods in Enzymol. 153, 516-544).

In addition, a host cell strain may be chosen that modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Such modifications (e.g., glycosylation) and processing (e.g., cleavage) of protein products may be important for the function of the protein. Different host cells have characteristic and specific mechanisms for the post-translational processing and modification of proteins and gene products. Appropriate cell lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed. To this end, eukaryotic host cells that possess the cellular machinery for proper processing of the primary transcript, glycosylation, and phosphorylation of the gene product may be used. Such mammalian host cells include but are not limited to CHO, VERO, BHK, HeLa, COS, MDCK, 293, 3T3, and WI38.

For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines that stably express the mahogany gene product may be engineered. Rather than using expression vectors that contain viral origins of replication, host cells can be transformed with DNA controlled by appropriate expression control elements (e.g., promoter, enhancer, sequences, transcription terminators, polyadenylation sites, etc.), and

a selectable marker. Following the introduction of the foreign DNA, engineered cells may be allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci that in turn can be cloned and expanded into cell lines. This method may advantageously be used to engineer cell lines that express the mahogany gene product. Such engineered cell lines may be particularly useful in screening and evaluation of compounds that affect the endogenous activity of the mahogany gene product.

A number of selection systems may be used, including but not limited to the herpes simplex virus thymidine kinase (Wigler, et al., 1977, Cell 11, 223), hypoxanthine-guanine phosphoribosyltransferase (Szybalska and Szybalski, 1962, Proc. Natl. Acad. Sci. USA 48, 2026), and adenine phosphoribosyltransferase (Lowy, et al., 1980, Cell 22, 817) genes can be employed in tk⁻, hgp^rt⁻ or ap^rt⁻ cells, respectively. Also, antimetabolite resistance can be used as the basis of selection for the following genes: dhfr, which confers resistance to methotrexate (Wigler, et al., 1980, Natl. Acad. Sci. USA 77, 3567; O'Hare, et al., 1981, Proc. Natl. Acad. Sci. USA 78, 1527); gpt, which confers resistance to mycophenolic acid (Mulligan and Berg, 1981, Proc. Natl. Acad. Sci. USA 78, 2072); neo, which confers resistance to the aminoglycoside G-418 (Colberre-Garapin, et al., 1981, J. Mol. Biol. 150, 1); and hyg^r, which confers resistance to hygromycin (Santerre, et al., 1984, Gene 30, 147).

Alternatively, the expression characteristic of an endogenous mahogany gene within a cell line or microorganism may be modified by inserting a heterologous DNA regulatory element into the genome of a stable cell line or cloned microorganism such that the inserted regulatory element is

operatively linked with the endogenous mahogany gene. For example, an endogenous mahogany gene which is normally "transcriptionally silent", i.e., a mahogany gene which is normally not expressed, or is expressed only a very low levels in a cell line or microorganism, may be activated by inserting a regulatory element which is capable of promoting the expression of a normally expressed gene product in that cell line or microorganism. Alternatively, a transcriptionally silent, endogenous mahogany gene may be activated by insertion of a promiscuous regulatory element that works across cell types.

A heterologous regulatory element may be inserted into a stable cell line or cloned microorganism, such that it is operatively linked with an endogenous mahogany gene, using techniques, such as targeted homologous recombination, which are well known to those of skill in the art, and described e.g., in Chappel, U.S. Patent No. 4,215,051; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

Alternatively, any fusion protein may be readily purified by utilizing an antibody specific for the fusion protein being expressed. For example, a system described by Janknecht, et al. allows for the ready purification of non-denatured fusion proteins expressed in human cell lines (Janknecht, et al., 1991, Proc. Natl. Acad. Sci. USA 88, 8972-8976). In this system, the gene of interest is subcloned into a vaccinia recombination plasmid such that the gene's open reading frame is translationally fused to an amino-terminal tag consisting of six histidine residues. Extracts from cells infected with recombinant vaccinia virus are loaded onto Ni^{2+} -nitriloacetic acid-agarose columns and

histidine-tagged proteins are selectively eluted with imidazole-containing buffers.

The mahogany gene products can also be expressed in transgenic animals. Animals of any species, including, but not limited to, mice, rats, rabbits, guinea pigs, pigs, micro-pigs, goats, sheep, and non-human primates, e.g., baboons, monkeys, and chimpanzees may be used to generate mahogany transgenic animals. The term "transgenic," as used herein, refers to animals expressing mahogany gene sequences from a different species (e.g., mice expressing human mahogany gene sequences), as well as animals that have been genetically engineered to over express endogenous (i.e., same species) mahogany sequences or animals that have been genetically engineered to no longer express endogenous mahogany gene sequences (i.e., "knock-out" animals), and their progeny.

Any technique known in the art may be used to introduce a mahogany gene transgene into animals to produce the founder lines of transgenic animals. Such techniques include, but are not limited to pronuclear microinjection (Hoppe and Wagner, 1989, U.S. Pat. No. 4,873,191); retrovirus mediated gene transfer into germ lines (Van der Putten, et al., 1985, Proc. Natl. Acad. Sci., USA 82, 6148-6152); gene targeting in embryonic stem cells (Thompson, et al., 1989, Cell 56, 313-321); electroporation of embryos (Lo, 1983, Mol. Cell. Biol. 3, 1803-1814); and sperm-mediated gene transfer (Lavitrano et al., 1989, Cell 57, 717-723) (For a review of such techniques, see Gordon, 1989, Transgenic Animals, Intl. Rev. Cytol. 115, 171-229)

Any technique known in the art may be used to produce transgenic animal clones containing a mahogany transgene, for example, nuclear transfer into enucleated oocytes of nuclei from cultured embryonic, fetal or adult cells induced to

quiescence (Campbell, et al., 1996, Nature 380, 64-66; Wilmut, et al., Nature 385, 810-813).

The present invention provides for transgenic animals that carry a mahogany transgene in all their cells, as well as animals that carry the transgene in some, but not all their cells, i.e., mosaic animals. The transgene may be integrated as a single transgene or in concatamers, e.g., head-to-head tandems or head-to-tail tandems. The transgene may also be selectively introduced into and activated in a particular cell type by following, for example, the teaching of Lasko et al. (Lasko, et al., 1992, Proc. Natl. Acad. Sci. USA 89, 6232-6236). The regulatory sequences required for such a cell-type specific activation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art. When it is desired that the mahogany transgene be integrated into the chromosomal site of the endogenous mahogany gene, gene targeting is preferred. Briefly, when such a technique is to be utilized, vectors containing some nucleotide sequences homologous to the endogenous mahogany gene are designed for the purpose of integrating, via homologous recombination with chromosomal sequences, into and disrupting the function of the nucleotide sequence of the endogenous mahogany gene. The transgene may also be selectively introduced into a particular cell type, thus inactivating the endogenous mahogany gene in only that cell type, by following, for example, the teaching of Gu, et al. (Gu, et al., 1994, Science 265, 103-106). The regulatory sequences required for such a cell-type specific inactivation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art.

Once transgenic animals have been generated, the expression of the recombinant mahogany gene may be assayed utilizing standard techniques. Initial screening may be accomplished by Southern blot analysis or PCR techniques to

analyze animal tissues to assay whether integration of the transgene has taken place. The level of mRNA expression of the transgene in the tissues of the transgenic animals may also be assessed using techniques that include but are not limited to Northern blot analysis of tissue samples obtained from the animal, in situ hybridization analysis, and RT-PCR (reverse transcriptase PCR). Samples of mahogany gene-expressing tissue, may also be evaluated immunocytochemically using antibodies specific for the mahogany transgene product.

5.3. ANTIBODIES TO MAHOGANY GENE PRODUCTS

Described herein are methods for the production of antibodies capable of specifically recognizing one or more *mg* gene product epitopes, or epitopes of conserved variants, or peptide fragments of the *mg* gene products. Further, antibodies that specifically recognize mutant forms of *mg* gene products, are encompassed by the invention.

Such antibodies may include, but are not limited to, polyclonal antibodies, monoclonal antibodies (mAbs), humanized or chimeric antibodies, single chain antibodies, Fab fragments, F(ab')₂ fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies, and epitope-binding fragments of any of the above. Such antibodies may be used, for example, in the detection of a *mg* gene product in an biological sample and may, therefore, be utilized as part of a diagnostic or prognostic technique whereby patients may be tested for abnormal levels of *mg* gene products, and/or for the presence of abnormal forms of such gene products. Such antibodies may also be utilized in conjunction with, for example, compound screening schemes, as described, below, in Section 5.4.2, for the evaluation of the effect of test compounds on *mg* gene product levels and/or activity. Additionally, such antibodies can be used in conjunction with the gene therapy techniques described,

below, in Section 5.4.3.2, to, for example, evaluate the normal and/or engineered mahogany-expressing cells prior to their introduction into the patient.

Anti-*mg* gene product antibodies may additionally be used in methods for inhibiting abnormal *mg* gene product activity. Thus, such antibodies may, therefore, be utilized as part of weight disorder treatment methods.

For the production of antibodies against a *mg* gene product, various host animals may be immunized by injection with a *mg* gene product, or a portion thereof. Such host animals may include, but are not limited to rabbits, mice, and rats, to name but a few. Various adjuvants may be used to increase the immunological response, depending on the host species, including but not limited to Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and *Corynebacterium parvum*.

Polyclonal antibodies are heterogeneous populations of antibody molecules derived from the sera of animals immunized with an antigen, such as a *mg* gene product, or an antigenic functional derivative thereof. For the production of polyclonal antibodies, host animals such as those described above, may be immunized by injection with *mg* gene product supplemented with adjuvants as also described above.

Monoclonal antibodies, which are homogeneous populations of antibodies to a particular antigen, may be obtained by any technique that provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique of Kohler and Milstein, (1975, Nature 256, 495-497; and U.S. Patent No. 4,376,110), the human B-cell hybridoma technique

(Kosbor et al., 1983, Immunology Today 4, 72; Cole et al., 1983, Proc. Natl. Acad. Sci. USA 80, 2026-2030), and the EBV-hybridoma technique (Cole et al., 1985, Monoclonal Antibodies And Cancer Therapy, Alan R. Liss, Inc., pp. 77-96). Such antibodies may be of any immunoglobulin class including IgG, IgM, IgE, IgA, IgD and any subclass thereof. The hybridoma producing the mAb of this invention may be cultivated in vitro or in vivo. Production of high titers of mAbs in vivo makes this the presently preferred method of production.

10 In addition, techniques developed for the production of "chimeric antibodies" (Morrison, et al., 1984, Proc. Natl. Acad. Sci., 81, 6851-6855; Neuberger, et al., 1984, Nature 312, 604-608; Takeda, et al., 1985, Nature, 314, 452-454) by splicing the genes from a mouse antibody molecule of appropriate antigen specificity together with genes from a human antibody molecule of appropriate biological activity
15 can be used. A chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region. (See, e.g.,
20 Cabilly et al., U.S. Patent No. 4,816,567; and Boss et al., U.S. Patent No. 4,816,397, which are incorporated herein by reference in their entirety.)

In addition, techniques have been developed for the production of humanized antibodies. (See, e.g., Queen, U.S. Patent No. 5,585,089, which is incorporated herein by
25 reference in its entirety.) An immunoglobulin light or heavy chain variable region consists of a "framework" region interrupted by three hypervariable regions, referred to as complementarily determining regions (CDRs). The extent of the framework region and CDRs have been precisely defined
30 (see, "Sequences of Proteins of Immunological Interest", Kabat, E. et al., U.S. Department of Health and Human Services (1983). Briefly, humanized antibodies are antibody

molecules from non-human species having one or more CDRs from the non-human species and a framework region from a human immunoglobulin molecule.

Alternatively, techniques described for the production of single chain antibodies (U.S. Patent 4,946,778; Bird, 1988, Science 242, 423-426; Huston, et al., 1988, Proc. Natl. Acad. Sci. USA 85, 5879-5883; and Ward, et al., 1989, Nature 334, 544-546) can be adapted to produce single chain antibodies against mahogany gene products. Single chain antibodies are formed by linking the heavy and light chain fragments of the Fv region via an amino acid bridge, resulting in a single chain polypeptide.

Antibody fragments that recognize specific epitopes may be generated by known techniques. For example, such fragments include but are not limited to: the F(ab')₂ fragments, which can be produced by pepsin digestion of the antibody molecule and the Fab fragments, which can be generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed (Huse, et al., 1989, Science, 246, 1275-1281) to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity.

5.4. USES OF THE MAHOGANY GENES, GENE PRODUCTS, AND ANTIBODIES

Described herein are various applications of the mahogany genes, of the mahogany gene products, including peptide fragments thereof, and of antibodies directed against mahogany gene products and peptide fragments thereof. Such applications include, for example, prognostic and diagnostic evaluation of body weight disorders and the identification of subjects with a predisposition to such disorders, as described below, in Section 5.4.1. Additionally, such applications include methods for the treatment of body weight

and body weight disorders, as described below, in Section 5.4.2, and for the identification of compounds which modulate the expression of the mahogany gene and/or the activity of the mahogany gene product, as described in Section 5.4.3, below. Such compounds can include, for example, other cellular products which are involved in body weight regulation. These compounds can be used, for example, in the amelioration of body weight disorders, including obesity, cachexia, and anorexia.

While, for clarity, the uses described in this section are primarily uses related to body weight disorder abnormalities, it is to be noted that each of the diagnostic and therapeutic treatments described herein can additionally be utilized in connection with other defects associated with the mahogany gene, such as hyperpigmentation, hyperphagia and other disorders resulting in increased metabolic rates.

5.4.1. DIAGNOSIS OF BODY WEIGHT DISORDER ABNORMALITIES

A variety of methods can be employed for the diagnostic and prognostic evaluation of body weight disorders, including obesity, cachexia, and anorexia, and for the identification of subjects having a predisposition to such disorders.

Such methods may, for example, utilize reagents such as the mahogany gene nucleotide sequences described in Section 5.1, and antibodies directed against mahogany gene products, including peptide fragments thereof, as described, above, in Section 5.3. Specifically, such reagents may be used, for example, for:

- (1) the detection of the presence of mahogany gene mutations, or the detection of either over- or under-expression of mahogany gene relative to levels of mahogany expression in a wild-type, non-body weight disorder state

which correlates with certain body weight disorders or susceptibility toward such body weight disorders;

(2) the detection of over- or under-abundance of mahogany gene product relative to the abundance of mahogany gene product in a wild-type non-body weight disorder state which correlates with certain body weight disorders or susceptibility toward such body weight disorders; and

(3) the detection of an aberrant level of mahogany gene product activity relative to mahogany gene product activity levels in a wild-type, non-body weight disorder state which correlates with certain body weight disorders or susceptibility toward such body weight disorders.

Mahogany gene nucleotide sequences can, for example, be used to diagnose a body weight disorder using, for example, the techniques for detecting mutations in the mahogany gene described above in Section 5.1, above.

The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one specific mahogany gene nucleic acid or anti-mahogany gene product antibody reagent described herein, which may be conveniently used, e.g., in clinical settings, to screen and diagnose patients exhibiting body weight disorder abnormalities, and to screen those individuals exhibiting a predisposition to developing a body weight disorder abnormality.

For the detection of mahogany gene mutations, any nucleated cell can be used as a starting source for genomic nucleic acid. For the detection of mahogany gene expression or mahogany gene products, any cell type or tissue in which the mahogany gene is expressed may be utilized, such as, for example, tissues or cells shown herein to express the MG gene.

5 5.4.1.1. DETECTION OF MAHOGANY GENE NUCLEIC
ACID MOLECULES

Genomic DNA may be used in hybridization or amplification assays of biological samples to detect abnormalities involving mahogany gene structure, including point mutations, insertions, deletions and chromosomal rearrangements. Such assays may include, but are not limited to, Southern analyses, single stranded conformation polymorphism analyses (SSCP), and PCR analyses.

After incubation, all non-annealed nucleic acids are removed from the nucleic acid:mahogany molecule hybrid. The presence of nucleic acids that have hybridized, if any such

molecules exist, is then detected. Using such a detection scheme, the nucleic acid from the cell type or tissue of interest can be immobilized, for example, to a solid support such as a membrane, or a plastic surface such as that on a microtiter plate or polystyrene beads. In this case, after incubation, non-annealed, labeled nucleic acid reagents of the type described in Section 5.1 are easily removed. Detection of the remaining, annealed, labeled mahogany nucleic acid reagents is accomplished using standard techniques well-known to those in the art. The mahogany gene sequences to which the nucleic acid reagents have annealed can be compared to the annealing pattern expected from a normal mahogany gene sequence in order to determine whether a mahogany gene mutation is present.

In a preferred embodiment, mahogany gene mutations or polymorphisms can be detected by using a microassay of mahogany nucleic acid sequences immobilized to a substrate or "gene chip" (see, e.g. Cronin, et al., 1996, Human Mutation 7:244-255).

Alternative diagnostic methods for the detection of mahogany gene specific nucleic acid molecules, in patient samples or other appropriate cell sources, may involve their amplification, e.g., by PCR (the experimental embodiment set forth in Mullis, 1987, U.S. Patent No. 4,683,202), followed by the analysis of the amplified molecules using techniques well known to those of skill in the art, such as, for example, those listed above. The resulting amplified sequences can be compared to those that would be expected if the nucleic acid being amplified contained only normal copies of the mahogany gene in order to determine whether a mahogany gene mutation exists.

Among those mahogany nucleic acid sequences which are preferred for such amplification-related diagnostic screening analyses are oligonucleotide primers which amplify mahogany

exon sequences. The sequences of such oligonucleotide primers are, therefore, preferably derived from mahogany intron sequences so that the entire exon, or coding region, can be analyzed as discussed below. Primer pairs useful for 5 amplification of mahogany exons are preferably derived from adjacent introns. Appropriate primer pairs can be chosen such that each of the 25 mahogany exons are amplified. Primers for the amplification of mahogany exons can be routinely designed by one of ordinary skill in the art by utilizing the exon and intron sequences of mahogany shown in 10 Figures, particularly FIGS. 3 and 5.

Additional mahogany nucleic acid sequences which are preferred for such amplification-related analyses are those which will detect the presence of a mahogany polymorphism which differs from the consensus mahogany sequence depicted 15 in Figures, particularly those that detect the polymorphism identified in exon 15 (Figure 7). Such polymorphisms include ones which represent mutations associated with body weight disorders such as obesity, cachexia, or anorexia.

Further, well-known genotyping techniques can be 20 performed to type polymorphisms that are in close proximity to mutations in the mahogany gene itself, including mutations associated with weight disorders such as obesity, cachexia, or anorexia. Such polymorphisms can be used to identify individuals in families likely to carry mutations in the mahogany gene. If a polymorphism exhibits linkage 25 disequilibrium with mutations in the mahogany gene, the polymorphism can also be used to identify individuals in the general population who are likely to carry such mutations. Polymorphisms that can be used in this way include restriction fragment length polymorphisms (RFLPs), which 30 involve sequence variations in restriction enzyme target sequences, single-base polymorphisms, and simple sequence length polymorphisms (SSLPs).

For example, Weber (U.S. Pat. No. 5,075,217) describes a DNA marker based on length polymorphisms in blocks of (dC-dA)_n-(dG-dT)_n short tandem repeats. The average separation of (dC-dA)_n-(dG-dT)_n blocks is estimated to be 30,000-60,000
5 bp. Markers that are so closely spaced exhibit a high frequency co-inheritance, and are extremely useful in the identification of genetic mutations, such as, for example, mutations within the mahogany gene, and the diagnosis of diseases and disorders related to mutations in the mahogany gene.

10 Also, Caskey et al. (U.S. Pat.No. 5,364,759) describe a DNA profiling assay for detecting short tri and tetra nucleotide repeat sequences. The process includes extracting the DNA of interest, such as the mahogany gene, amplifying the extracted DNA, and labelling the repeat sequences to form
15 a genotypic map of the individual's DNA.

A mahogany probe could additionally be used to directly identify RFLPs. Further, a mahogany probe or primers derived from the mahogany sequence could be used to isolate genomic clones such as YACs, BACs, PACs, cosmids, phage, or plasmids.
20 The DNA contained in these clones can be screened for single-base polymorphisms or SSLPs using standard hybridization or sequencing procedures.

The level of mahogany gene expression can also be assayed. For example, RNA from a cell type or tissue known, or suspected, to express the mahogany gene, such as muscle,
25 brain, kidney, testes, heart, liver, lung, skin, hypothalamus, spleen, and adipose tissue may be isolated and tested utilizing hybridization or PCR techniques such as are described, above. The isolated cells can be derived from cell culture or from a patient. The analysis of cells taken
30 from culture may be a necessary step in the assessment of cells to be used as part of a cell-based gene therapy technique or, alternatively, to test the effect of compounds

on the expression of the mahogany gene. Such analyses may reveal both quantitative and qualitative aspects of the expression pattern of the mahogany gene, including activation or inactivation of mahogany gene expression.

5 In one embodiment of such a detection scheme, a cDNA molecule is synthesized from an RNA molecule of interest (e.g., by reverse transcription of the RNA molecule into cDNA). All or part of the resulting cDNA is then used as the template for a nucleic acid amplification reaction, such as a
10 PCR amplification reaction, or the like. The nucleic acid reagents used as synthesis initiation reagents (e.g., primers) in the reverse transcription and nucleic acid amplification steps of this method are chosen from among the mahogany gene nucleic acid reagents described in Section 5.1. The preferred lengths of such nucleic acid reagents are at
15 least 9-30 nucleotides.

For detection of the amplified product, the nucleic acid amplification may be performed using radioactively or non-radioactively labeled nucleotides. Alternatively, enough amplified product may be made such that the product may be
20 visualized by standard ethidium bromide staining or by utilizing any other suitable nucleic acid staining method.

As an alternative to amplification techniques, standard Northern analyses can be performed to determine the level of mRNA expression of the mahogany gene, if a sufficient
25 quantity of the appropriate cells can be obtained.

Additionally, it is possible to perform such mahogany gene expression assays "in situ", i.e., directly upon tissue sections (fixed and/or frozen) of patient tissue obtained from biopsies or resections, such that no nucleic acid purification is necessary. Nucleic acid reagents such as
30 those described in Section 5.1 may be used as probes and/or primers for such in situ procedures (see, for example, Nuovo,

G.J., 1992, "PCR In Situ Hybridization: Protocols And Applications", Raven Press, NY).

5

5.4.1.2. DETECTION OF MAHOGANY GENE PRODUCTS

Mahogany gene products, including both wild-type and mutant mahogany gene products, conserved variants, and polypeptide fragments thereof, which are discussed above, in Section 5.2, may be detected using antibodies which are
10 directed against such mahogany gene products. Such antibodies, which are discussed in Section 5.3, below, may thereby be used as diagnostics and prognostics for a body weight disorder. Such methods may be used to detect abnormalities in the level of mahogany gene expression or of
15 mahogany gene product synthesis, or abnormalities in the structure, temporal expression, and/or physical location of mahogany gene product. The antibodies and immunoassay methods described herein have, for example, important in vitro applications in assessing the efficacy of treatments
20 for body weight disorders such as obesity, cachexia, and anorexia. Antibodies, or fragments of antibodies, such as those described below, may be used to screen potentially therapeutic compounds in vitro to determine their effects on mahogany gene expression and mahogany gene product
25 production. The compounds that have beneficial effects on body weight disorders, such as obesity, cachexia, and anorexia, can thereby be identified, and a therapeutically effective dose determined.

In vitro immunoassays may also be used, for example, to assess the efficacy of cell-based gene therapy for a body
30 weight disorders, including obesity, cachexia, and anorexia. Antibodies directed against mahogany gene products may be used in vitro to determine, for example, the level of

mahogany gene expression achieved in cells genetically engineered to produce mahogany gene product. In the case of intracellular mahogany gene products, such an assessment is done, preferably, using cell lysates or extracts. Such analysis will allow for a determination of the number of transformed cells necessary to achieve therapeutic efficacy *in vivo*, as well as optimization of the gene replacement protocol.

10 The tissue or cell type to be analyzed will generally include those that are known, or suspected, to express the mahogany gene. The protein isolation methods employed herein may, for example, be such as those described in Harlow and Lane (1988, "Antibodies: A Laboratory Manual", Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York). The isolated cells can be derived from cell culture or from a
15 patient. The analysis of cells taken from culture may be a necessary step in the assessment of cells to be used as part of a cell-based gene therapy technique or, alternatively, to test the effect of compounds on the expression of the mahogany gene.

20 Preferred diagnostic methods for the detection of mahogany gene products, conserved variants or peptide fragments thereof, may involve, for example, immunoassays wherein the mahogany gene products or conserved variants or peptide fragments are detected by their interaction with an
25 anti-mahogany gene product-specific antibody.

For example, antibodies, or fragments of antibodies, such as those described, above, in Section 5.3, may be used to quantitatively or qualitatively detect the presence of mahogany gene products or conserved variants or peptide fragments thereof. This can be accomplished, for example, by
30 immunofluorescence techniques employing a fluorescently labeled antibody (see below, this Section) coupled with light microscopic, flow cytometric, or fluorimetric detection.

Such techniques are especially preferred for mahogany gene products that are expressed on the cell surface.

The antibodies (or fragments thereof) useful in the present invention may, additionally, be employed
5 histologically, as in immunofluorescence or immunoelectron microscopy, for *in situ* detection of mahogany gene products, conserved variants or peptide fragments thereof. *In situ* detection may be accomplished by removing a histological specimen from a patient, and applying thereto a labeled
10 antibody that binds to a mahogany polypeptide. The antibody (or fragment) is preferably applied by overlaying the labeled antibody (or fragment) onto a biological sample. Through the use of such a procedure, it is possible to determine not only the presence of the mahogany gene product, conserved variants or peptide fragments, but also its distribution in the
15 examined tissue. Using the present invention, those of ordinary skill will readily recognize that any of a wide variety of histological methods (such as staining procedures) can be modified in order to achieve *in situ* detection of a mahogany gene product.

20 Immunoassays for mahogany gene products, conserved variants, or peptide fragments thereof will typically comprise: (1) incubating a sample, such as a biological fluid, a tissue extract, freshly harvested cells, or lysates of cells in the presence of a detectably labeled antibody
25 capable of identifying mahogany gene products, conserved variants or peptide fragments thereof; and (2) detecting the bound antibody by any of a number of techniques well-known in the art.

The biological sample may be brought in contact with and immobilized onto a solid phase support or carrier, such as
30 nitrocellulose, that is capable of immobilizing cells, cell particles or soluble proteins. The support may then be washed with suitable buffers followed by treatment with the

detectably labeled mahogany gene product specific antibody. The solid phase support may then be washed with the buffer a second time to remove unbound antibody. The amount of bound label on the solid support may then be detected by conventional means.

By "solid phase support or carrier" is intended any support capable of binding an antigen or an antibody. Well-known supports or carriers include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite. The nature of the carrier can be either soluble to some extent or insoluble for the purposes of the present invention. The support material may have virtually any possible structural configuration so long as the coupled molecule is capable of binding to an antigen or antibody. Thus, the support configuration may be spherical, as in a bead, or cylindrical, as in the inside surface of a test tube, or the external surface of a rod. Alternatively, the surface may be flat such as a sheet, test strip, etc. Preferred supports include polystyrene beads. Those skilled in the art will know many other suitable carriers for binding antibody or antigen, or will be able to ascertain the same by use of routine experimentation.

One of the ways in which the mahogany gene product-specific antibody can be detectably labeled is by linking the same to an enzyme, such as for use in an enzyme immunoassay (EIA) (Voller, A., "The Enzyme Linked Immunosorbent Assay (ELISA)", 1978, Diagnostic Horizons 2, 1-7, Microbiological Associates Quarterly Publication, Walkersville, MD); Voller, A. et al., 1978, J. Clin. Pathol. 31, 507-520; Butler, J.E., 1981, Meth. Enzymol. 73, 482-523; Maggio, E. (ed.), 1980, Enzyme Immunoassay, CRC Press, Boca Raton, FL.; Ishikawa, E. et al., (eds.), 1981, Enzyme Immunoassay, Kigaku Shoin, Tokyo). The enzyme which is bound to the antibody will react

with an appropriate substrate, preferably a chromogenic substrate, in such a manner as to produce a chemical moiety that can be detected, for example, by spectrophotometric, fluorimetric or by visual means. Enzymes that can be used to
5 detectably label the antibody include, but are not limited to, malate dehydrogenase, staphylococcal nuclease, delta-5-steroid isomerase, yeast alcohol dehydrogenase, o-glycerophosphate dehydrogenase, triose phosphate isomerase, horseradish peroxidase, alkaline phosphatase, asparaginase,
10 glucose oxidase, β -galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase and acetylcholinesterase. The detection can be accomplished by colorimetric methods that employ a chromogenic substrate for the enzyme. Detection may also be accomplished by visual
15 comparison of the extent of enzymatic reaction of a substrate in comparison with similarly prepared standards.

Detection may also be accomplished using any of a variety of other immunoassays. For example, by radioactively labeling the antibodies or antibody fragments, it is possible to detect mahogany gene products through the use of a
20 radioimmunoassay (RIA) (see, for example, Weintraub, B., Principles of Radioimmunoassays, Seventh Training Course on Radioligand Assay Techniques, The Endocrine Society, March, 1986). The radioactive isotope can be detected by such means as the use of a gamma counter or a scintillation counter or
25 by autoradiography.

It is also possible to label the antibody with a fluorescent compound. When the fluorescently labeled antibody is exposed to light of the proper wave length, its presence can then be detected due to fluorescence. Among the most commonly used fluorescent labeling compounds are
30 fluorescein isothiocyanate, rhodamine, phycoerythrin, phycocyanin, allophycocyanin, o-phthaldehyde and fluorescamine.

The antibody can also be detectably labeled using fluorescence emitting metals such as ^{152}Eu , or others of the lanthanide series. These metals can be attached to the antibody using such metal chelating groups as diethylenetriaminepentacetic acid (DTPA) or ethylenediaminetetraacetic acid (EDTA).

The antibody also can be detectably labeled by coupling it to a chemiluminescent compound. The presence of the chemiluminescent-tagged antibody is then determined by detecting the presence of luminescence that arises during the course of a chemical reaction. Examples of particularly useful chemiluminescent labeling compounds are luminol, isoluminol, theromatic acridinium ester, imidazole, acridinium salt and oxalate ester.

Likewise, a bioluminescent compound may be used to label the antibody of the present invention. Bioluminescence is a type of chemiluminescence found in biological systems in which a catalytic protein increases the efficiency of the chemiluminescent reaction. The presence of a bioluminescent protein is determined by detecting the presence of luminescence. Important bioluminescent compounds for purposes of labeling are luciferin, luciferase and aequorin.

5.4.2.SCREENING ASSAYS FOR COMPOUNDS THAT INTERACT WITH THE MAHOGANY GENE OR GENE PRODUCT

The following assays are designed to identify compounds that bind to a mahogany gene product, compounds that bind to proteins, or portions of proteins that interact with a mahogany gene product, compounds that interfere with the interaction of a mahogany gene product with proteins and compounds that modulate the activity of the mahogany gene (i.e., modulate the level of mahogany gene expression and/or modulate the level of mahogany gene product activity). Assays may additionally be utilized that identify compounds

that bind to mahogany gene regulatory sequences (e.g., promoter sequences; see e.g., Platt, 1994, J. Biol. Chem. 269, 28558-28562), which is incorporated herein by reference in its entirety, and that can modulate the level of mahogany gene expression. Such compounds may include, but are not limited to, small organic molecules, such as ones that are able to cross the blood-brain barrier, gain to and/or entry into an appropriate cell and affect expression of the mahogany gene or some other gene involved in the body weight regulatory pathway, or intracellular proteins.

Methods for the identification of such proteins are described, below, in Section 5.4.2.2. Such proteins may be involved in the control and/or regulation of body weight. Further, among these compounds are compounds that affect the level of mahogany gene expression and/or mahogany gene product activity and that can be used in the therapeutic treatment of body weight disorders, including obesity, cachexia, and anorexia, as described, below, in Section 5.9.

Compounds may include, but are not limited to, peptides such as, for example, soluble peptides, including but not limited to, Ig-tailed fusion peptides, and members of random peptide libraries; (see, e.g., Lam, et al., 1991, Nature 354, 82-84; Houghten, et al., 1991, Nature 354, 84-86), and combinatorial chemistry-derived molecular library made of D- and/or L- configuration amino acids, phosphopeptides (including, but not limited to members of random or partially degenerate, directed phosphopeptide libraries; see, e.g., Songyang, et al., 1993, Cell 72, 767-778), antibodies (including, but not limited to, polyclonal, monoclonal, humanized, anti-idiotypic, chimeric or single chain antibodies, and FAb, F(ab'), and FAb expression library fragments, and epitope-binding fragments thereof), and small organic or inorganic molecules.

Compounds identified via assays such as those described herein may be useful, for example, in elaborating the biological function of the mahogany gene product and for ameliorating body weight disorders, such as obesity, cachexia, or anorexia. Assays for testing the effectiveness of compounds identified by, for example, techniques such as those described in Sections 5.4.2.1-5.4.2.3, are discussed, below, in Section 5.4.2.4.

10

5.4.2.1. IN VITRO SCREENING ASSAYS FOR COMPOUNDS THAT BIND TO THE MAHOGANY GENE PRODUCT

In vitro systems may be designed to identify compounds capable of binding the mahogany gene products of the invention. Compounds identified may be useful, for example, in modulating the activity of unimpaired and/or mutant mahogany gene products, may be useful in elaborating the biological function of the mahogany gene product, may be utilized in screens for identifying compounds that disrupt normal mahogany gene product interactions, or may in themselves disrupt such interactions.

The principle of the assays used to identify compounds that bind to the mahogany gene product involves preparing a reaction mixture of the mahogany gene product and the test compound under conditions and for a time sufficient to allow the two components to interact and bind, thus forming a complex that can be removed and/or detected in the reaction mixture. These assays can be conducted in a variety of ways. For example, one method to conduct such an assay involves anchoring a mahogany gene product or a test substance onto a solid support and detecting mahogany gene product/test compound complexes formed on the solid support at the end of the reaction. In one embodiment of such a method, the mahogany gene product may be anchored onto a solid support,

and the test compound, which is not anchored, may be labeled, either directly or indirectly.

In practice, microtiter plates are conveniently utilized as the solid support. The anchored component may be
5 immobilized by non-covalent or covalent attachments. Non-covalent attachment may be accomplished by simply coating the solid surface with a solution of the protein and drying. Alternatively, an immobilized antibody, preferably a monoclonal antibody, specific for the protein to be
10 immobilized may be used to anchor the protein to the solid surface. The surfaces may be prepared in advance and stored.

In order to conduct the assay, the non-immobilized component is added to the coated surface containing the anchored component. After the reaction is complete, unreacted components are removed (e.g., by washing) under
15 conditions such that any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the previously non-immobilized component is pre-labeled, the detection of label immobilized on the
20 surface indicates that complexes were formed. Where the previously non-immobilized component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the previously non-immobilized component (the antibody, in turn, may be directly labeled or indirectly labeled with a labeled
25 anti-Ig antibody).

Alternatively, a reaction can be conducted in a liquid phase, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for mahogany gene product or
30 the test compound to anchor any complexes formed in solution, and a labeled antibody specific for the other component of the possible complex to detect anchored complexes.

5.4.2.2. ASSAYS FOR PROTEINS THAT INTERACT WITH THE MAHOGANY GENE PRODUCT

Any method suitable for detecting protein-protein interactions may be employed for identifying mahogany gene product-protein interactions.

Among the traditional methods that may be employed are co-immunoprecipitation, cross-linking and co-purification through gradients or chromatographic columns. Utilizing procedures such as these allows for the identification of proteins that interact with mahogany gene products. Such proteins can include, but are not limited, the mahoganoid gene product.

Once isolated, such a protein can be identified and can be used in conjunction with standard techniques, to identify proteins it interacts with. For example, at least a portion of the amino acid sequence of a protein that interacts with the mahogany gene product can be ascertained using techniques well known to those of skill in the art, such as via the Edman degradation technique (see, e.g., Creighton, 1983, "Proteins: Structures and Molecular Principles," W.H. Freeman & Co., N.Y., pp.34-49). The amino acid sequence obtained may be used as a guide for the generation of oligonucleotide mixtures that can be used to screen for gene sequences encoding such proteins. Screening may be accomplished, for example, by standard hybridization or PCR techniques. Techniques for the generation of oligonucleotide mixtures and the screening are well-known. (See, e.g., Ausubel, *supra*, and 1990, "PCR Protocols: A Guide to Methods and Applications," Innis, et al., eds. Academic Press, Inc., New York).

Additionally, methods may be employed that result in the simultaneous identification of genes that encode a protein which interacts with a mahogany gene product. These methods include, for example, probing expression libraries with

labeled mahogany gene product, using mahogany gene product in a manner similar to the well known technique of antibody probing of Agt11 libraries.

One method that detects protein interactions in vivo, the two-hybrid system, is described in detail for illustration only and not by way of limitation. One version of this system has been described (Chien, et al., 1991, Proc. Natl. Acad. Sci. USA, 88, 9578-9582) and is commercially available from Clontech (Palo Alto, CA).

Briefly, utilizing such a system, plasmids are constructed that encode two hybrid proteins: one consists of the DNA-binding domain of a transcription activator protein fused to the mahogany gene product and the other consists of the transcription activator protein's activation domain fused to an unknown protein that is encoded by a cDNA that has been recombined into this plasmid as part of a cDNA library. The DNA-binding domain fusion plasmid and the cDNA library are transformed into a strain of the yeast *Saccharomyces cerevisiae* that contains a reporter gene (e.g., HBS or lacZ) whose regulatory region contains the transcription activator's binding site. Either hybrid protein alone cannot activate transcription of the reporter gene: the DNA-binding domain hybrid cannot because it does not provide activation function and the activation domain hybrid cannot because it cannot localize to the activator's binding sites. Interaction of the two hybrid proteins reconstitutes the functional activator protein and results in expression of the reporter gene, which is detected by an assay for the reporter gene product.

The two-hybrid system or related methodologies may be used to screen activation domain libraries for proteins that interact with the "bait" gene product. By way of example, and not by way of limitation, mahogany gene products may be used as the bait gene product. Total genomic or cDNA

sequences are fused to the DNA encoding an activation domain. This library and a plasmid encoding a hybrid of a bait mahogany gene product fused to the DNA-binding domain are co-transformed into a yeast reporter strain, and the resulting
5 transformants are screened for those that express the reporter gene. For example, a bait mahogany gene sequence, such as the open reading frame of the mahogany gene, can be cloned into a vector such that it is translationally fused to the DNA encoding the DNA-binding domain of the GAL4 protein. These colonies are purified and the library plasmids
10 responsible for reporter gene expression are isolated. DNA sequencing is then used to identify the proteins encoded by the library plasmids.

A cDNA library of the cell line from which proteins that interact with bait mahogany gene product are to be detected
15 can be made using methods routinely practiced in the art. According to the particular system described herein, for example, the cDNA fragments can be inserted into a vector such that they are translationally fused to the transcriptional activation domain of GAL4. Such a library
20 can be co-transformed along with the bait mahogany gene-GAL4 fusion plasmid into a yeast strain that contains a lacZ gene driven by a promoter that contains GAL4 activation sequence. A cDNA encoded protein, fused to a GAL4 transcriptional activation domain that interacts with bait mahogany gene
25 product will reconstitute an active GAL4 protein and thereby drive expression of the HIS3 gene. Colonies that express HIS3 can be detected by their growth on petri dishes containing semi-solid agar based media lacking histidine. The cDNA can then be purified from these strains, and used to
30 produce and isolate the bait mahogany gene product-interacting protein using techniques routinely practiced in the art.

5.4.2.3. ASSAYS FOR COMPOUNDS THAT INTERFERE WITH MAHOGANY GENE PRODUCT MACROMOLECULE INTERACTION

The mahogany gene products may, *in vivo*, interact with
5 one or more macromolecules, such as proteins. For example,
the mahogany gene products may, *in vivo*, interact with the
mahoganoid gene products. Other macromolecules which
interact with the mahogany gene products may include, but are
not limited to, nucleic acid molecules and those proteins
10 identified via methods such as those described, above, in
Sections 5.4.2.1 - 5.4.2.2. For purposes of this discussion,
the macromolecules are referred to herein as "binding
partners". Compounds that disrupt mahogany gene product
binding to a binding partner may be useful in regulating the
activity of the mahogany gene product, especially mutant
15 mahogany gene products. Such compounds may include, but are
not limited to molecules such as peptides, and the like, as
described, for example, in Section 5.4.2.1 above.

The basic principle of an assay system used to identify
compounds that interfere with the interaction between the
20 mahogany gene product and a binding partner or partners
involves preparing a reaction mixture containing the mahogany
gene product and the binding partner under conditions and for
a time sufficient to allow the two to interact and bind, thus
forming a complex. In order to test a compound for
25 inhibitory activity, the reaction mixture is prepared in the
presence and absence of the test compound. The test compound
may be initially included in the reaction mixture, or may be
added at a time subsequent to the addition of mahogany gene
product and its binding partner. Control reaction mixtures
are incubated without the test compound or with a compound
30 which is known not to block complex formation. The formation
of any complexes between the mahogany gene product and the
binding partner is then detected. The formation of a complex

in the control reaction, but not in the reaction mixture containing the test compound, indicates that the compound interferes with the interaction of the mahogany gene product and the binding partner. Additionally, complex formation within reaction mixtures containing the test compound and normal mahogany gene product may also be compared to complex formation within reaction mixtures containing the test compound and a mutant mahogany gene product. This comparison may be important in those cases wherein it is desirable to identify compounds that disrupt interactions of mutant but not normal mahogany gene product.

The assay for compounds that interfere with the interaction of the mahogany gene products and binding partners can be conducted in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring either the mahogany gene product or the binding partner onto a solid support and detecting complexes formed on the solid support at the end of the reaction. In homogeneous assays, the entire reaction is carried out in a liquid phase. In either approach, the order of addition of reactants can be varied to obtain different information about the compounds being tested. For example, test compounds that interfere with the interaction between the mahogany gene products and the binding partners, e.g., by competition, can be identified by conducting the reaction in the presence of the test substance; i.e., by adding the test substance to the reaction mixture prior to or simultaneously with the mahogany gene product and interactive intracellular binding partner. Alternatively, test compounds that disrupt preformed complexes, e.g., compounds with higher binding constants that displace one of the components from the complex, can be tested by adding the test compound to the reaction mixture after complexes have been formed. The various formats are described briefly below.

In a heterogeneous assay system, either the mahogany gene product or the interactive binding partner, is anchored onto a solid surface, while the non-anchored species is labeled, either directly or indirectly. In practice, microtiter plates are conveniently utilized. The anchored species may be immobilized by non-covalent or covalent attachments. Non-covalent attachment may be accomplished simply by coating the solid surface with a solution of the mahogany gene product or binding partner and drying. Alternatively, an immobilized antibody specific for the species to be anchored may be used to anchor the species to the solid surface. The surfaces may be prepared in advance and stored.

In order to conduct the assay, the partner of the immobilized species is exposed to the coated surface with or without the test compound. After the reaction is complete, unreacted components are removed (e.g., by washing) and any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the non-immobilized species is pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the non-immobilized species is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the initially non-immobilized species (the antibody, in turn, may be directly labeled or indirectly labeled with a labeled anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds that inhibit complex formation or that disrupt preformed complexes can be detected.

Alternatively, the reaction can be conducted in a liquid phase in the presence or absence of the test compound, the reaction products separated from unreacted components, and

complexes detected; e.g., using an immobilized antibody specific for one of the binding components to anchor any complexes formed in solution, and a labeled antibody specific for the other partner to detect anchored complexes. Again, depending upon the order of addition of reactants to the liquid phase, test compounds that inhibit complex formation or that disrupt preformed complexes can be identified.

In an alternate embodiment of the invention, a homogeneous assay can be used. In this approach, a preformed complex of the mahogany gene product and the interactive binding partner is prepared in which either the mahogany gene product or its binding partners is labeled, but the signal generated by the label is quenched due to complex formation (see, e.g., U.S. Patent No. 4,109,496 by Rubenstein which utilizes this approach for immunoassays). The addition of a test substance that competes with and displaces one of the species from the preformed complex will result in the generation of a signal above background. In this way, test substances that disrupt mahogany gene product/binding partner interaction can be identified.

In another embodiment of the invention, these same techniques can be employed using peptide fragments that correspond to the binding domains of the mahogany gene product and/or the binding partner (in cases where the binding partner is a protein), in place of one or both of the full length proteins. Any number of methods routinely practiced in the art can be used to identify and isolate the binding sites. These methods include, but are not limited to, mutagenesis of the gene encoding one of the proteins and screening for disruption of binding in a co-immunoprecipitation assay. Compensating mutations in the gene encoding the second species in the complex can then be selected. Sequence analysis of the genes encoding the respective proteins will reveal the mutations that correspond

to the region of the protein involved in interactive binding. Alternatively, one protein can be anchored to a solid surface using methods described in this Section above, and allowed to interact with and bind to its labeled binding partner, which
5 has been treated with a proteolytic enzyme, such as trypsin. After washing, a short, labeled peptide comprising the binding domain may remain associated with the solid material, which can be isolated and identified by amino acid sequencing. Also, once the gene coding for the segments is engineered to express peptide fragments of the protein, it
10 can then be tested for binding activity and purified or synthesized.

For example, and not by way of limitation, a mahogany gene product can be anchored to a solid material as described, above, in this Section by making a GST-1 fusion
15 protein and allowing it to bind to glutathione agarose beads. The binding partner can be labeled with a radioactive isotope, such as ^{35}S , and cleaved with a proteolytic enzyme such as trypsin. Cleavage products can then be added to the anchored GST-1 fusion protein and allowed to bind. After
20 washing away unbound peptides, labeled bound material, representing the binding partner binding domain, can be eluted, purified, and analyzed for amino acid sequence by well-known methods. Peptides so identified can be produced synthetically or produced using recombinant DNA technology.

25

5.4.2.4. ASSAYS FOR THE IDENTIFICATION OF COMPOUNDS THAT AMELIORATE BODY WEIGHT DISORDERS

Compounds, including but not limited to binding
compounds identified via assay techniques such as those
30 described, above, in Sections 5.4.2.1 - 5.4.2.3, can be tested for the ability to ameliorate body weight disorder symptoms, including obesity, cachexia, and anorexia. It

should be noted that the assays described herein can identify compounds that affect mahogany activity by either affecting mahogany gene expression or by affecting the level of mahogany gene product activity. For example, compounds may be identified that are involved in another step in the pathway in which the mahogany gene and/or mahogany gene product is involved, such as, for example, a step which is either "upfield" or "downfield" of the step in the pathway mediated by the mahogany gene. Such compounds may, by affecting this same pathway, modulate the effect of mahogany on the development of body weight disorders. Such compounds can be used as part of a therapeutic method for the treatment of the disorder.

Described below are cell-based and animal model-based assays for the identification of compounds exhibiting such an ability to ameliorate body weight disorder symptoms.

First, cell-based systems can be used to identify compounds that may act to ameliorate body weight disorder symptoms. Such cell systems can include, for example, recombinant or non-recombinant cell, such as cell lines, that express the mahogany gene.

In utilizing such cell systems, cells that express mahogany may be exposed to a compound suspected of exhibiting an ability to ameliorate body weight disorder symptoms, at a sufficient concentration and for a sufficient time to elicit such an amelioration of such symptoms in the exposed cells. After exposure, the cells can be assayed to measure alterations in the expression of the mahogany gene, e.g., by assaying cell lysates for mahogany mRNA transcripts (e.g., by Northern analysis) or for mahogany gene products expressed by the cell; compounds that modulate expression of the mahogany gene are good candidates as therapeutics.

In addition, animal-based systems or models for a mammalian body weight disorder, for example, transgenic mice

containing a human or altered form of mahogany gene, may be used to identify compounds capable of ameliorating symptoms of the disorder. Such animal models may be used as test substrates for the identification of drugs, pharmaceuticals, 5 therapies and interventions. For example, animal models may be exposed to a compound suspected of exhibiting an ability to ameliorate symptoms, at a sufficient concentration and for a sufficient time to elicit such an amelioration of body weight disorder symptoms. The response of the animals to the exposure may be monitored by assessing the reversal of the 10 symptoms of the disorder.

With regard to intervention, any treatments that reverse any aspect of body weight disorder-like symptoms should be considered as candidates for human therapeutic intervention in such a disorder. Dosages of test agents may be determined 15 by deriving dose-response curves, as discussed in Section 5.5.1, below.

5.4.3.COMPOUNDS AND METHODS FOR THE TREATMENT OF BODY WEIGHT DISORDERS

20 Described below are methods and compositions whereby body weight disorders, including obesity, cachexia, and anorexia, may be treated. Such methods can comprise, for example administering compounds which modulate the expression of a mammalian mahogany gene and/or the synthesis or activity of a mammalian mahogany gene product, so that symptoms of the 25 body weight disorder are ameliorated. Alternatively, in those instances whereby the mammalian body weight disorder results from mahogany gene mutations, such methods can comprise supplying the mammal with a nucleic acid molecule encoding an unimpaired mahogany gene product such that an 30 unimpaired mahogany gene product is expressed and symptoms of the disorder are ameliorated.

In another embodiment of methods for the treatment of mammalian body weight disorders resulting from mahogany gene mutations, such methods can comprise supplying the mammal with a cell comprising a nucleic acid molecule that encodes an unimpaired mahogany gene product such that the cell expresses the unimpaired mahogany gene product, and symptoms of the disorder are ameliorated.

Because a loss of normal mahogany gene function results in the restoration of a non-obese phenotype in individuals exhibiting an agouti mutation (e.g. individuals that ectopically express the agouti gene in all tissues) a decrease or elimination of normal mahogany gene product would facilitate progress towards a normal body weight state in such individuals. Methods for inhibiting or reducing the level of mahogany gene product synthesis or expression can include, for example, methods such as those described in Section 5.4.3.1.

Alternatively, symptoms of certain body weight disorders such as, for example, cachexia and anorexia, which involve a lower than normal body weight phenotype, may be ameliorated by increasing the level of mahogany gene expression and/or mahogany gene product activity. Methods for enhancing the expression or synthesis of mahogany can include, for example, methods such as those described below, in Section 5.4.3.2

25 5.4.3.1. INHIBITORY ANTISENSE, RIBOZYME AND TRIPLE HELIX APPROACHES

In another embodiment, symptoms of body weight disorders may be ameliorated by decreasing the level of mahogany gene expression and/or mahogany gene product activity by using mahogany gene sequences in conjunction with well-known antisense, gene "knock-out," ribozyme and/or triple helix methods to decrease the level of mahogany gene expression. Among the compounds that may exhibit the ability to modulate

the activity, expression or synthesis of the mahogany gene, including the ability to ameliorate the symptoms of a mammalian body weight disorder, are antisense, ribozyme, and triple helix molecules. Such molecules may be designed to
5 reduce or inhibit either unimpaired, or if appropriate, mutant target gene activity. Techniques for the production and use of such molecules are well known to those of skill in the art.

Antisense RNA and DNA molecules act to directly block the translation of mRNA by hybridizing to targeted mRNA and
10 preventing protein translation. Antisense approaches involve the design of oligonucleotides that are complementary to a target gene mRNA. The antisense oligonucleotides will bind to the complementary target gene mRNA transcripts and prevent translation. Absolute complementarity, although preferred,
15 is not required.

A sequence "complementary" to a portion of an RNA, as referred to herein, means a sequence having sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense
20 nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA it may contain and still form a stable duplex (or
25 triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

In one embodiment, oligonucleotides complementary to
30 non-coding regions of the mahogany gene could be used in an antisense approach to inhibit translation of endogenous mahogany mRNA. Antisense nucleic acids should be at least

six nucleotides in length, and are preferably oligonucleotides ranging from 6 to about 50 nucleotides in length. In specific aspects the oligonucleotide is at least 10 nucleotides, at least 17 nucleotides, at least 25 nucleotides or at least 50 nucleotides.

Regardless of the choice of target sequence, it is preferred that *in vitro* studies are first performed to quantitate the ability of the antisense oligonucleotide to inhibit gene expression. It is preferred that these studies utilize controls that distinguish between antisense gene inhibition and nonspecific biological effects of oligonucleotides. It is also preferred that these studies compare levels of the target RNA or protein with that of an internal control RNA or protein. Additionally, it is envisioned that results obtained using the antisense oligonucleotide are compared with those obtained using a control oligonucleotide. It is preferred that the control oligonucleotide is of approximately the same length as the test oligonucleotide and that the nucleotide sequence of the oligonucleotide differs from the antisense sequence no more than is necessary to prevent specific hybridization to the target sequence.

The oligonucleotides can be DNA or RNA or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, e.g., Letsinger, et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86, 6553-6556; Lemaitre, et al., 1987, Proc. Natl. Acad. Sci. U.S.A. 84, 648-652; PCT Publication No. WO88/09810, published December 15, 1988) or

the blood-brain barrier (see, e.g., PCT Publication No. WO89/10134, published April 25, 1988), hybridization-triggered cleavage agents (see, e.g., Krol et al., 1988, BioTechniques 6, 958-976) or intercalating agents (see, e.g.,
5 Zon, 1988, Pharm. Res. 5, 539-549). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

The antisense oligonucleotide may comprise at least one
10 modified base moiety which is selected from the group including but not limited to 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-
15 galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, 20 beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-
25 5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

The antisense oligonucleotide may also comprise at least one modified sugar moiety selected from the group including
30 but not limited to arabinose, 2-fluoroarabinose, xylulose, and hexose.

In yet another embodiment, the antisense oligonucleotide comprises at least one modified phosphate backbone selected

from the group consisting of a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, and a formacetal or analog thereof.

5 In yet another embodiment, the antisense oligonucleotide is an α -anomeric oligonucleotide. An α -anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gautier, et al., 1987, Nucl. Acids Res. 15, 6625-6641). The oligonucleotide
10 is a 2'-O-methylribonucleotide (Inoue, et al., 1987, Nucl. Acids Res. 15, 6131-6148), or a chimeric RNA-DNA analogue (Inoue, et al., 1987, FEBS Lett. 215, 327-330).

Oligonucleotides of the invention may be synthesized by standard methods known in the art, e.g., by use of an
15 automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein, et al. (1988, Nucl. Acids Res. 16, 3209), methylphosphonate oligonucleotides can be prepared by use of
20 controlled pore glass polymer supports (Sarin, et al., 1988, Proc. Natl. Acad. Sci. U.S.A. 85, 7448-7451), etc.

While antisense nucleotides complementary to the target gene coding region sequence could be used, those complementary to the transcribed, untranslated region are
25 most preferred.

Antisense molecules should be delivered to cells that express the target gene *in vivo*. A number of methods have been developed for delivering antisense DNA or RNA to cells; e.g., antisense molecules can be injected directly into the
30 tissue site, or modified antisense molecules, designed to target the desired cells (e.g., antisense linked to peptides or antibodies that specifically bind receptors or antigens

expressed on the target cell surface, can be administered systemically.

However, it is often difficult to achieve intracellular concentrations of the antisense sufficient to suppress translation of endogenous mRNAs. Therefore a preferred approach utilizes a recombinant DNA construct in which the antisense oligonucleotide is placed under the control of a strong pol III or pol II promoter. The use of such a construct to transfect target cells in the patient will result in the transcription of sufficient amounts of single stranded RNAs that will form complementary base pairs with the endogenous target gene transcripts and thereby prevent translation of the target gene mRNA. For example, a vector can be introduced e.g., such that it is taken up by a cell and directs the transcription of an antisense RNA. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art. Vectors can be plasmid, viral, or others known in the art, used for replication and expression in mammalian cells. Expression of the sequence encoding the antisense RNA can be by any promoter known in the art to act in mammalian, preferably human cells. Such promoters can be inducible or constitutive. Such promoters include but are not limited to: the SV40 early promoter region (Bernoist and Chambon, 1981, Nature 290, 304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto, et al., 1980, Cell 22, 787-797), the herpes thymidine kinase promoter (Wagner, et al., 1981, Proc. Natl. Acad. Sci. U.S.A. 78, 1441-1445), the regulatory sequences of the metallothionein gene (Brinster, et al., 1982, Nature 296, 39-42), etc. Any type of plasmid, cosmid, YAC or viral vector can be used to prepare the recombinant DNA construct which can be introduced

directly into the tissue site. Alternatively, viral vectors can be used that selectively infect the desired tissue, in which case administration may be accomplished by another route (e.g., systemically).

5 Ribozyme molecules designed to catalytically cleave target gene mRNA transcripts can also be used to prevent translation of target gene mRNA and, therefore, expression of target gene product. (See, e.g., PCT International Publication WO90/11364, published October 4, 1990; Sarver, et
10 al., 1990, Science 247, 1222-1225).

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. (For a review, see Rossi, 1994, Current Biology 4, 469-471). The mechanism of ribozyme action involves sequence specific hybridization of the ribozyme molecule to complementary target RNA, followed
15 by an endonucleolytic cleavage event. The composition of ribozyme molecules must include one or more sequences complementary to the target gene mRNA, and must include the well known catalytic sequence responsible for mRNA cleavage. For this sequence, see, e.g., U.S. Patent No. 5,093,246,
20 which is incorporated herein by reference in its entirety.

While ribozymes that cleave mRNA at site specific recognition sequences can be used to destroy target gene mRNAs, the use of hammerhead ribozymes is preferred. Hammerhead ribozymes cleave mRNAs at locations dictated by
25 flanking regions that form complementary base pairs with the target mRNA. The sole requirement is that the target mRNA have the following sequence of two bases: 5'-UG-3'. The construction and production of hammerhead ribozymes is well known in the art and is described more fully in Myers, 1995, *Molecular Biology and Biotechnology: A Comprehensive Desk*
30 *Reference*, VCH Publishers, New York, (see especially Figure 4, page 833) and in Haseloff and Gerlach, 1988, Nature, 334,

585-591, which is incorporated herein by reference in its entirety.

Preferably the ribozyme is engineered so that the cleavage recognition site is located near the 5' end of the target gene mRNA, i.e., to increase efficiency and minimize the intracellular accumulation of non-functional mRNA transcripts.

The ribozymes of the present invention also include RNA endoribonucleases (hereinafter "Cech-type ribozymes") such as the one that occurs naturally in *Tetrahymena thermophila* (known as the IVS, or L-19 IVS RNA) and that has been extensively described by Thomas Cech and collaborators (Zaug, et al., 1984, Science, 224, 574-578; Zaug and Cech, 1986, Science, 231, 470-475; Zaug, et al., 1986, Nature, 324, 429-433; published International patent application No. WO 88/04300 by University Patents Inc.; Been and Cech, 1986, Cell, 47, 207-216). The Cech-type ribozymes have an eight base pair active site which hybridizes to a target RNA sequence whereafter cleavage of the target RNA takes place. The invention encompasses those Cech-type ribozymes which target eight base-pair active site sequences that are present in the target gene.

As in the antisense approach, the ribozymes can be composed of modified oligonucleotides (e.g., for improved stability, targeting, etc.) and should be delivered to cells that express the target gene *in vivo*. A preferred method of delivery involves using a DNA construct "encoding" the ribozyme under the control of a strong constitutive pol III or pol II promoter, so that transfected cells will produce sufficient quantities of the ribozyme to destroy endogenous target gene messages and inhibit translation. Because ribozymes unlike antisense molecules, are catalytic, a lower intracellular concentration is required for efficiency.

Endogenous target gene expression can also be reduced by inactivating or "knocking out" the target gene or its promoter using targeted homologous recombination (e.g., see Smithies, et al., 1985, Nature 317, 230-234; Thomas and Capecchi, 1987, Cell 51, 503-512; Thompson, et al., 1989, Cell 5, 313-321; each of which is incorporated by reference herein in its entirety). For example, a mutant, non-functional target gene (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous target gene (either the coding regions or regulatory regions of the target gene) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express the target gene *in vivo*. Insertion of the DNA construct, via targeted homologous recombination, results in inactivation of the target gene. Such approaches are particularly suited in the agricultural field where modifications to ES (embryonic stem) cells can be used to generate animal offspring with an inactive target gene (e.g., see Thomas and Capecchi, 1987 and Thompson, 1989, *supra*). However this approach can be adapted for use in humans provided the recombinant DNA constructs are directly administered or targeted to the required site *in vivo* using appropriate viral vectors.

Alternatively, endogenous target gene expression can be reduced by targeting deoxyribonucleotide sequences complementary to the regulatory region of the target gene (i.e., the target gene promoter and/or enhancers) to form triple helical structures that prevent transcription of the target gene in target cells in the body. (See generally, Helene, 1991, Anticancer Drug Des., 6(6), 569-584; Helene, et al., 1992, Ann. N.Y. Acad. Sci., 660, 27-36; and Maher, 1992, Bioassays 14(12), 807-815).

Nucleic acid molecules to be used in triplex helix formation for the inhibition of transcription should be

single stranded and composed of deoxynucleotides. The base composition of these oligonucleotides must be designed to promote triple helix formation via Hoogsteen base pairing rules, which generally require sizeable stretches of either
5 purines or pyrimidines to be present on one strand of a duplex. Nucleotide sequences may be pyrimidine-based, which will result in TAT and CGC triplets across the three associated strands of the resulting triple helix. The pyrimidine-rich molecules provide base complementarity to a
10 purine-rich region of a single strand of the duplex in a parallel orientation to that strand. In addition, nucleic acid molecules may be chosen that are purine-rich, for example, contain a stretch of G residues. These molecules will form a triple helix with a DNA duplex that is rich in GC pairs, in which the majority of the purine residues are
15 located on a single strand of the targeted duplex, resulting in GGC triplets across the three strands in the triplex.

Alternatively, the potential sequences that can be targeted for triple helix formation may be increased by creating a so called "switchback" nucleic acid molecule.
20 Switchback molecules are synthesized in an alternating 5'-3', 3'-5' manner, such that they base pair with first one strand of a duplex and then the other, eliminating the necessity for a sizeable stretch of either purines or pyrimidines to be present on one strand of a duplex.

In instances wherein the antisense, ribozyme, and/or
25 triple helix molecules described herein are utilized to inhibit mutant gene expression, it is possible that the technique may so efficiently reduce or inhibit the transcription (triple helix) and/or translation (antisense, ribozyme) of mRNA produced by normal target gene alleles that
30 the possibility may arise wherein the concentration of normal target gene product present may be lower than is necessary for a normal phenotype. In such cases, to ensure that

substantially normal levels of target gene activity are maintained, therefore, nucleic acid molecules that encode and express target gene polypeptides exhibiting normal target gene activity may, be introduced into cells via gene therapy methods such as those described, below, in Section 5.9.2 that do not contain sequences susceptible to whatever antisense, ribozyme, or triple helix treatments are being utilized. Alternatively, in instances whereby the target gene encodes an extracellular protein, it may be preferable to co-administer normal target gene protein in order to maintain the requisite level of target gene activity.

Anti-sense RNA and DNA, ribozyme, and triple helix molecules of the invention may be prepared by any method known in the art for the synthesis of DNA and RNA molecules, as discussed above. These include techniques for chemically synthesizing oligodeoxyribonucleotides and oligoribonucleotides well known in the art such as for example solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by *in vitro* and *in vivo* transcription of DNA sequences encoding the antisense RNA molecule. Such DNA sequences may be incorporated into a wide variety of vectors that incorporate suitable RNA polymerase promoters such as the T7 or SP6 polymerase promoters. Alternatively, antisense cDNA constructs that synthesize antisense RNA constitutively or inducibly, depending on the promoter used, can be introduced stably into cell lines.

5.4.3.2. GENE REPLACEMENT THERAPY

Mahogany gene nucleic acid sequences, described above in Section 5.1, can be utilized for the treatment of a mammalian body weight disorders, including obesity, cachexia, and anorexia. Such treatment can be in the form of gene replacement therapy. Specifically, one or more copies of a

normal mahogany gene or a portion of the mahogany gene that directs the production of a mahogany gene product exhibiting normal mahogany gene function, may be inserted into the appropriate cells within a patient, using vectors that
5 include, but are not limited to adenovirus, adeno-associated virus, and retrovirus vectors, in addition to other particles that introduce DNA into cells, such as liposomes.

Because the mahogany gene is expressed in the brain, such gene replacement therapy techniques should be capable
10 delivering mahogany gene sequences to these cell types within patients. Thus, in one embodiment, techniques that are well known to those of skill in the art (see, e.g., PCT Publication No. WO89/10134, published April 25, 1988) can be used to enable mahogany gene sequences to cross the blood-brain barrier readily and to deliver the sequences to cells
15 in the brain. With respect to delivery that is capable of crossing the blood-brain barrier, viral vectors such as, for example, those described above, are preferable.

In another embodiment, techniques for delivery involve direct administration of such mahogany gene sequences to the
20 site of the cells in which the mahogany gene sequences are to be expressed.

Additional methods that may be utilized to increase the overall level of mahogany gene expression and/or mahogany gene product activity include using target homologous
25 recombination methods, discussed in Section 5.2, above, to modify the expression characteristic of an endogenous mahogany gene in a cell or microorganism by inserting a heterologous DNA regulatory element such that the inserted regulatory element is operatively linked with the endogenous mahogany gene in question. Targeted homologous recombination
30 can be thus used to activated transcription of an endogenous mahogany gene that is "transcriptionally silent", i.e., is

not normally expressed, or to enhance the expression of an endogenous mahogany gene that is normally expressed.

Further, the overall level of mahogany gene expression and/or mahogany gene product activity may be increased by the
5 introduction of appropriate mahogany-expressing cells, preferably autologous cells, into a patient at positions and in numbers that are sufficient to ameliorate body weight disorder symptoms. Such cells may be either recombinant or non-recombinant.

10 Among the cells that can be administered to increase the overall level of mahogany gene expression in a patient are normal cells, preferably brain cells, that express the mahogany gene. Alternatively, cells, preferably autologous
cells, can be engineered to express mahogany gene sequences, and may then be introduced into a patient in positions
15 appropriate for the amelioration of the body weight disorder symptoms. Alternately, cells that express an unimpaired mahogany gene and that are from a MHC matched individual can be utilized, and may include, for example, brain cells. The
expression of the mahogany gene sequences is controlled by
20 the appropriate gene regulatory sequences to allow such expression in the necessary cell types. Such gene regulatory sequences are well known to the skilled artisan. Such cell-based gene therapy techniques are well known to those skilled
in the art, see, e.g., Anderson, U.S. Patent No. 5,399,349.

25 When the cells to be administered are non-autologous cells, they can be administered using well known techniques that prevent a host immune response against the introduced cells from developing. For example, the cells may be introduced in an encapsulated form which, while allowing for an exchange of components with the immediate extracellular
30 environment, does not allow the introduced cells to be recognized by the host immune system.

Additionally, compounds, such as those identified via techniques such as those described, above, in Section 5.4.2, that are capable of modulating mahogany gene product activity can be administered using standard techniques that are well known to those of skill in the art. In instances in which the compounds to be administered are to involve an interaction with brain cells, the administration techniques should include well known ones that allow for a crossing of the blood-brain barrier.

10

5.5. PHARMACEUTICAL PREPARATIONS AND METHODS OF ADMINISTRATION

The compounds that are determined to affect mahogany gene expression or gene product activity can be administered to a patient at therapeutically effective doses to treat or
15 ameliorate body weight disorders, such as obesity, anorexia, or cachexia. A therapeutically effective dose refers to that amount of the compound sufficient to result in amelioration of symptoms of such a disorder.

20

5.5.1. EFFECTIVE DOSE

Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the
25 population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD_{50}/ED_{50} . Compounds that exhibit large therapeutic indices are preferred. While compounds that exhibit toxic side effects may be used, care should be taken to design a
30 delivery system that targets such compounds to the site of affected tissue in order to minimize potential damage to uninfected cells and, thereby, reduce side effects.

The data obtained from the cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the IC_{50} (i.e., the concentration of the test compound that achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography.

5.5.2. FORMULATIONS AND USE

Pharmaceutical compositions for use in accordance with the present invention may be formulated in conventional manner using one or more physiologically acceptable carriers or excipients.

Thus, the compounds and their physiologically acceptable salts and solvates may be formulated for administration by inhalation or insufflation (either through the mouth or the nose) or oral, buccal, parenteral or rectal administration.

For oral administration, the pharmaceutical compositions may take the form of, for example, tablets or capsules prepared by conventional means with pharmaceutically acceptable excipients such as binding agents (e.g., pregelatinised maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose); fillers (e.g., lactose, microcrystalline cellulose or calcium hydrogen phosphate);

lubricants (e.g., magnesium stearate, talc or silica);
disintegrants (e.g., potato starch or sodium starch
glycolate); or wetting agents (e.g., sodium lauryl sulphate).
The tablets may be coated by methods well known in the art.
5 Liquid preparations for oral administration may take the form
of, for example, solutions, syrups or suspensions, or they
may be presented as a dry product for constitution with water
or other suitable vehicle before use. Such liquid
preparations may be prepared by conventional means with
10 pharmaceutically acceptable additives such as suspending
agents (e.g., sorbitol syrup, cellulose derivatives or
hydrogenated edible fats); emulsifying agents (e.g., lecithin
or acacia); non-aqueous vehicles (e.g., almond oil, oily
esters, ethyl alcohol or fractionated vegetable oils); and
preservatives (e.g., methyl or propyl-p-hydroxybenzoates or
15 sorbic acid). The preparations may also contain buffer
salts, flavoring, coloring and sweetening agents as
appropriate.

Preparations for oral administration may be suitably
formulated to give controlled release of the active compound.

20 For buccal administration the compositions may take the
form of tablets or lozenges formulated in conventional
manner.

For administration by inhalation, the compounds for use
according to the present invention are conveniently delivered
25 in the form of an aerosol spray presentation from pressurized
packs or a nebulizer, with the use of a suitable propellant,
e.g., dichlorodifluoromethane, trichlorofluoromethane,
dichlorotetrafluoroethane, carbon dioxide or other suitable
gas. In the case of a pressurized aerosol the dosage unit
may be determined by providing a valve to deliver a metered
30 amount. Capsules and cartridges of e.g., gelatin for use in
an inhaler or insufflator may be formulated containing a

powder mix of the compound and a suitable powder base such as lactose or starch.

The compounds may be formulated for parenteral administration by injection, e.g., by bolus injection or continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampoules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing and/or dispersing agents. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, e.g., containing conventional suppository bases such as cocoa butter or other glycerides.

In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

The compositions may, if desired, be presented in a pack or dispenser device that may contain one or more unit dosage forms containing the active ingredient. The pack may for example comprise metal or plastic foil, such as a blister pack. The pack or dispenser device may be accompanied by instructions for administration.

6. **EXAMPLE: GENETIC AND PHYSICAL MAPPING
OF THE MAHOGANY LOCUS**

In the Example presented herein, studies are described which, first, define the genetic interval on mouse chromosome 2 within which the mahogany gene lies, and second,
5 successfully narrow the interval to approximately 0.29 cM. Further, the physical mapping of this interval is described.

Mouse crosses were performed to obtain homozygous mg/mg mice. First, LDJ-Le-mg mice were crossed with CAST/Ei mice. The F1s were back-crossed with LDJ-Le-mg mice and the
10 resulting litters scored for coat color. Mice showing coat color of mg/mg homozygotes were genotyped to using D2/NDS3 and D2/MIT19 markers to identify meiotic events. Mice showing recombinant events were fine structure mapped using various markers shown in FIG. 1. All genotyping was
15 performed using PCR-SSLP and then analyzed using PAGE.

After 2300 meioses, the mahogany gene was mapped to a 0.99 cM interval FIG. 1. This corresponded to an interval width of 700 kb.

20 Physical Mapping of the Genetic Interval: The 700 kb mahogany region on mouse chromosome 2 is shown in FIG. 1. Genetic markers, clones spanning the region and open reading frames in the interval are shown in the figure.

25 7. **EXAMPLE: IDENTIFICATION OF A CANDIDATE
MAHOGANY GENE**

In the Example presented herein, a gene is identified within the cloned DNA described in the Example in Section 6, above, which corresponds to a candidate mahogany gene.

Clones spanning the 700kb region were sequenced and open
30 reading frames were identified and analyzed through this interval. Nucleic acid sequencing was performed using ABI sequencers and the manufactures recommended procedures. Many

novel sequences encoding proteins are located in this integral, see the bottom of FIG. 1. With each open reading frame identified, mutational analysis, primarily via SSCP analysis, was used with the three alleles of the mahogany phenotype mice to identify which of the open reading frames within this interval contain a mutation in an mg mouse.

A mutation was found in one of the genomic/cDNA sequences found in the integral in mg33 mice. Figures 3 and 2 provide the genomic and cDNA sequences surrounding the mutation, FIG. 6 shows the mutation in mg33, and FIGS. 8 and 9 show splice variants in the 5' end of the murine mg gene. The mutation in mg33 mice is a deletion of a GCTGC sequence which results in the creation of a frameshift. Based on the chromosomal location and mutation identification, the cDNA provided in Figure 2 and the corresponding genomic DNA which contains the contigs provided in Figure 3 represent the mg gene/locus.

Further analysis of cDNA clones identified two distinct splice variants in the 5' end of the mg gene. Figure 7 provides an analysis of the structure of the two splice variants, denoted akml003 and akml004. Figures 8 and 9 provide the nucleic acid and amino acid sequence of the 5' ends of these splice variants and structural analysis of the protein encoded by the 5' regions.

Analysis of libraries of human cDNA sequences led to the identification of three forms of the human ortholog of the mg gene: a long form (FIG. 18) and two shorter splice forms, each of which is shown in FIGS. 19 and 20.

8. EXAMPLE: CHARACTERIZATION OF THE MAHOGANY GENE

In the example presented herein, the nucleic acid sequence of the mahogany gene transcript identified in the example presented in Section 7, above, is used to generate

Northern analysis data which characterize the expression of the mahogany transcript in a number of tissues both of wild type mice, and of mice exhibiting the mahogany phenotype. The results presented in this example are consistent with the 5 mg gene being the mahogany gene.

For Northern analysis, polyA RNA was isolated from wild-type and the original mg mutant, mg3J and mg-Lester mice and utilized from the Northern analysis following standard protocols. Northern blots prepared from this mRNA was hybridized with a probe obtained from sequences common to the 10 akml003 and akml004 sequences. Specifically PCR primers TTCCTCACTGG and GGACACACAG were used to amplify cDNA from the akml003 sequence which had been radiolabelled by random priming using a Gibco-BRL kit according to the manufacturer's recommended protocol.

15 An mg transcript was found in all mice examined in mRNA isolated from brain (minus the hypothalamus), kidney, heart, testes, liver, skin, and hypothalamus. No expression was seen in muscle.

In a Northern blot run on RNA samples from mahogany 20 mice, the mg transcript was found to be expressed at a reduced level in all tissues in mRNA isolated from mg3J mice, as a varied size fragment in mg-Lester derived mRNA, and at different levels and sizes in original mg mutant mice derived mRNA.

25 These results are consistent with the mg gene disclosed herein as being the mahogany gene.

9. EXAMPLE: EFFECTS OF THE MAHOGANY GENE ON GENETIC AND DIETARY OBESITY

This section describes experiments which examine whether 30 the mg gene acts specifically within the agouti pathway. Specifically, these experiments test whether mg can suppress the obesity of other monogenic obese mutants as well as

whether it can suppress diet-induced obesity. The results show that *mg* does not suppress obesity in any of the monogenic obese mutants. However, *mg* can suppress diet-induced obesity. Thus, the *mg* gene and its corresponding gene product and compounds that modulate *mg* expression and/or activity have implications in the treatment of diet-induced obesity disorders, as well as in the treatment of disorders related directly to the *mg* or *agouti* gene.

9.1.

MATERIALS AND METHODS

Genetic crosses: The crosses, and the number of animals for each (n) were (LDJ/Le-*mg*/*mg* X CAST/Ei) X LDJ/Le-*mg*/*mg* (n=1588), (C3HeB/FeJ-*mg*^{3J}/*mg*^{3J} X CAST/Ei) X C3HeB/FeJ-*mg*^{3J}/*mg*^{3J} (n=324), (C3HeB/FeJ-*mg*^{3J}/*mg*^{3J} X MOLF/Ei) X C3HeB/FeJ-*mg*^{3J}/*mg*^{3J} (n=216) and (C3HeB/FeJ-*mg*^{3J}/*mg*^{3J} X C57BL6/J) X C3HeB/FeJ-*mg*^{3J}/*mg*^{3J} (n=309). The 2437 N₂ mice were analysed by coat colour to determine their genotype at the *mg* locus. As mice change color slightly at each hair molt and because the phenotype of *mg*/*mg* vs. *mg*/+ can be subtle, all mice were phenotyped at the same age by a single person. Genomic DNA was made from a tail biopsy of each mouse and analysed for multiple simple sequence length repeat polymorphism (SSLP) markers. The first ~100 mice were typed for a series of polymorphic Mit genetic markers (Deitrich, W.F. et al., 1996, Nature 380:149-152) from distal mouse chromosome 2 in order to accurately delimit the position of *mg*. With the first ~100 mice it was determined that *mg* mapped approximately 15cM proximal of Agouti between markers D2Mit19 and D2Nds3 (FIG. 13). All remaining animals were genotyped for D2Mit19 and D2Nds3. Animals recombinant in that interval were typed with all available Mit markers between and for the ever growing number of markers developed during the project which, finally totaled 265 markers.

9.2.

RESULTS

The murine mahogany (*mg*) gene is known to act in a dosage dependent manner within the agouti pathway, to compensate for the agouti overexpression and for lack of signaling from the nul allele *McIr* (Miller, K.A. et al., 1997, *Genetics* 146:1407-1415; Dinulescu, D.M. et al., *Proc. Natl. Acad. Sci.*, in press; Robbins, L.S. et al., 1993, *Cell* 72:827-834). The phenotype of mice homozygous for both *mg* and a null allele of *McIr* (recessive yellow, *McIr^e*) is yellow, the same as the phenotype of *McIr^e/McIr^e* mice, indicating that *mg* is not acting downstream of *McIr*. A similar experiment was performed with obese *Mcr4* knock out mice (FIG. 11). For both sexes, all the animals homozygous for *Mc4r*^{-/-} were approximately equally obese and were heavier than the mice wild-type at *Mc4r* independent of the genotype for *mg*. This data strengthens and confirms the *McIr* data previously published, strongly suggesting that *mg* acts at or upstream of both melanocortin receptors.

To test whether *mg* acts specifically within the agouti pathway, experiments were performed to determine whether *mg* can suppress the obesity of other monogenic obese mutants of the mouse and whether it could suppress diet-induced obesity. Appropriate genetic crosses were set up to produce mice segregating *mg* and one of the mouse obesity mutations *Cpe^{fat}*, *tub*, or *Lepr^{db}* such that all combinations of homozygous and heterozygous animals were on the same mix of genetic background. No suppression of obesity was seen for any of the monogenic obese mutants (FIG. 12) lending credence to the assumed specificity of action within the agouti pathway. To ask whether *mg* can suppress diet induced obesity C3HeB/FeJ-*mg^{jj}* and C3H/HeJ mice were placed, at weaning, either on normal chow having a physiological fuel value (PFV) of 3.63 kcal/gm with 9% fat, or onto a high fat diet having a PFV of 4.53 kcal/gm with 42.2% fat. Food consumption and body

weight were measured weekly. Converting the grams of food consumed to calories indicated that C3H/HeJ mice on normal chow and high fat diet consumed -97 kCal/week and -96 kCal/week, respectively. C3HeB/FeJ-*mg*^{3J} mice on normal chow and high fat diet consumed -83 kCal/week and -81 kCal/week, respectively. Despite the equal calorie intake, the C3H/HeJ mice on the high fat diet readily gained more weight than the C3H/HeJ mice on normal chow ($p=0.0004$). In stark contrast, the C3HeB/FeJ-*mg*^{3J} mice on either diet showed no statistically significant difference in weight (FIG. 12D). Female data showed the same trends, although there was no statistical significance between any of the mice on either diet.

10. EXPERIMENT: MAPPING AND SEQUENCING OF THE MAHOGANY GENE

15 This section describes experiments wherein the murine mahogany gene was genetically and physically mapped to an approximately 0.6 cM interval, and then sequenced. The murine *mg* sequence obtained was then used to isolate and sequence the human *mg* gene. Northern and *in situ* analyses of *mg* expression in mouse tissue are also described, and sequence motifs of the predicted MG polypeptide are discussed.

10.1. MATERIALS AND METHODS

25 Physical Mapping: More than 36,000 individual sequences from the region were compared by BLAST (Altschul, S.F. et al., 1990, *J. Mol. Biol.* 215:403-410) to publicly available sequence databases and analyzed using GRAIL (Guan, X. et al., 1992, *Proc. Eighth IEEE Conference on AI Applications*:9-13) to identify potential coding sequence. In addition, sequences from overlapping BACs were assembled using phrap (Sing, C.F. et al., 1998, *Genome Res.* 8:175-185; Ewing B. and Green, P., 1998, *Genome Res.* 8:186-194; Gordon, D. et al.,

1998, *Genome Res.* 8:195-202), and the resulting contigs were also analyzed using BLAST and GRAIL to aid in gene prediction. This data was displayed in ACEDb (Durbin, Richard and Mieg, Jean Thierry, 1991, *A C. elegans Database*, Documentation, code, and data available from anonymous FTP servers at lirmm.lirmm.fr, cele, mrc-lmb.cam.ac.uk, and ncbi.nlm.nih.gov) to further visualize predicted exons and their relationships to each other.

10 Northern Blot Analysis: PolyA⁺ RNA was extracted from the tissues indicated from wild-type, C3H/HeJ and the three mutant alleles of *mg*, C3HeB/FeJ-*mg*^{3J}, LDJ/Le-*mg*, and C3H/HeJ-*mg*^L, according to the manufacturer's instructions. RNA STAT-60 (Tel-Test, Inc., 1511 Sounty Rd. 129, Friendswood, TX 77546) was used to isolate total RNA. PolyA⁺ was isolated
15 using Poly(A)Pure™ mRNA purification kit (Ambion, Inc., 2130 Woodward St. #200, Austin, TX 78744). 2 µg of each mRNA was separated on a 1% agarose-formaldehyde gel, transferred to nylon, and hybridized with a probe for *mg* corresponding to nt 990-1406 of the murine cDNA sequence with Rapid-hyb Buffer
20 (Amersham LIFE SCIENCE, Gaithersburg, MD). Filters were washed with 0.11x SSC, 0.1% SDS and exposed to KODAK X-omat film overnight.

10.2. RESULTS

25 A positional cloning strategy was undertaken to identify the *mg* gene. Multiple genetic crosses were set up to produce second generation mice (n=2437) segregating *mg* which were used to genetically localise the *mg* locus (FIG 13B). When the genetic map critical interval for *mg* was resolved to -0.6 cM physical mapping was initiated. Approximately 1 Mb
30 was contiged with 30 BACs (FIG. 13C), most of which were made into random sheared libraries for shot gun sequencing. At completion of the project it was estimated that 85% sequence

coverage across the interval had been achieved and that all genes within the region had been found. Twenty-nine genes were identified, 15 of which are novel genes. Within the final minimal interval for *mg*, indicated by the arrows in FIG. 13, there were eleven genes of which nine were unknown. All of these genes were tested as candidates for *mg* by examining the three mutant alleles of the mahogany locus, the original allele, *mg*, that arose in a stock of Swiss x C3H mice, and two alleles that have independently arisen on the C3H background, C3HeB/FeJ-*mg*^{3J}/*mg*^{3J} and C3H/He-*mg*^L/*mg*^L. Each gene was examined by Northern blot analysis and RT-PCR analysis of RNA from tissues from wild-type and *mg* mutant mice, by Southern blot analysis of DNA from wild-type and *mg* mutant mice, and by SSCP analysis of genomic PCR products designed to cover the intron-exon boundaries of much of each of the genes. In all, 20 genes were analyzed in this manner, one of which showed a northern blot difference between the wild type and mutant alleles (FIG. 14).

The wild type expression pattern of this gene gives three bands of size ~9 kb, 4.5 kb, and 3.8 kb, of which the largest message is the most prominent (FIG 14). The smaller two bands can be seen in all tissues but, depending upon tissue, may require extended exposure. Each of the different *mg* alleles gave a different expression pattern. C3HeB/FeJ-*mg*^{3J}/*mg*^{3J} has extremely low expression, the 9 kb message only being very faint in brain, hypothalamus, and fat on northern blots. C3H/He-*mg*^L/*mg*^L expresses a single aberrant band of approximately 9.5-10 kb in kidney, heart, muscle, fat, and, most prominently, brain and hypothalamus. The LDJ/Le-*mg*/*mg* shows an altered ratio of the three wild type messages: the 9 kb message is reduced, while the two smaller messages are more highly expressed, in particular being very abundant in fat and hypothalamus. *In situ* analysis was used to look more closely at *mg* expression in the brain and specifically the

hypothalamus. Overall hybridization in LDJ/Le-mg/mg looks equivalent to that of wild type, and the C3HeB/FeJ-mg^{3J}/mg^{3J} shows an overall reduction of expression. Close examination of the hypothalamic region in both wild type and mutant
 5 alleles revealed differences in the ventromedial hypothalamic nucleus (VMH). Both C3HeB/FeJ-mg^{3J}/mg^{3J} and the LDJ/Le-mg/mg have reduced VMH expression (FIG. 15) which is particularly interesting as many neuropeptides and receptors known to be involved in body weight regulation are expressed in the VMH,
 10 including Mc4r.

Initially, two overlapping mouse cDNAs of 1051 bps and 2419 bps were identified. Using these cDNAs as a starting point it was possible to build over 7990 bps of human sequences, using both the public EST database and an in house
 15 liver library. The 23 ESTs used in the contiging are listed in Table I below. Using the derived human sequence, it was then possible to estimate the intron-exon boundaries within the mouse genomic sequence. These were verified by PCR amplification and sequencing. In total, 4079 bps of mouse
 20 sequence was obtained, of which 4011 bp are coding sequence. The mouse genomic locus spans over 160 kb, and has 31 identified exons, at least one of which is differentially spliced.

TABLE I

25	<u>Gene Bank Accession #</u>	<u>Clone ID #</u>	<u>Clone Source</u>
	NA	NA	Human Endothelial Cell (MPI)
	AA062169	482948	Soares mouse P3NMF19.5
	NA	NA	Human Liver (MPI)
30	AA350292	151062	Infant Brain
	R87660	194640	Soares Fetal Liver Spleen 1 NFLS

	T69367	82898	Stratagene Liver
	T92696	118881	Stratagene Lung
	H11351	47626	Soares Infant Brain 1 NIB
5	AA350293	151062	Infant Brain
	AA297697	149184	Fetal Heart II
	AB011120	NA	Human Male Brain
	AA297214	129808	Embryo, 12 week I
	AA298732	184690	T-Lymphocyte
10	AI076479	1676623	Soares Total Fetus Nb2HF8 9W
	AA771958	1359202	Soares parathyroid tumor NbHPA
	R84298	194640	Soares Fetal Liver Spleen 1NFLS
	D81046	1178923	Human Fetal Brain (Tfujiwara)
15	AA378603	183010	Synovial Sarcoma
	D60710	962349	Clontech Human Fetal Brain (#6535)
	D20236	pm1235	Human Promyelocyte
	AA345684	147210	Gall Bladder I
20	H45413	182870	Soares Breast 3NbHBst
	AA044305	486349	Soares Pregnant Uterus NbHPu

The mutant mahogany alleles were also sequenced, checking all intron-exon boundaries. A 5 bp deletion at 2809 nt was found in the coding sequence of the *mg* gene from C3HeB/FeJ-*mg^{3J}*/*mg^{3J}* which introduces a stop codon a position 937, two codons 3' of the deletion. This mutation will result in a seriously truncated protein lacking many interesting domains, as discussed below. The *mg^{3J}* allele is the same allele that showed extremely low expression levels. The combined Northern blot analysis, *in situ* hybridization

analysis, and sequence analysis of the mutant *mg^{3J}* allele strongly suggest that this gene is the mouse mahogany gene.

The 4011 bp of open reading frame (ORF) of mouse MG predicts a 1336 amino acid polypeptide with molecular mass of 148,706 D (FIG. 17, top sequence). BLAST searches of the NCBI and SwissProt protein databases identified two human paralogues with a similar modular architecture (KIAA0534, Genbank accession no. 3043592; and MEGF8, Genbank accession no. AB011541), as well as a *C. elegans* homologue (YC81_CAEEL, Genbank accession no. Q19981).

Another human protein, Attractin or DPPT-L (Duke-Cohen, J.S. et al., 1998, *Proc. Natl. Acad. Sci. U.S.A.* 95:11336-11341), appears to be a 1198 amino acid residue, approximately 134,000 D, secreted splice variant of the MG polypeptide. An alignment of the predicted MG (top) and Attractin (bottom) amino acid sequences is shown in FIG. 17. Attractin has not identified as being involved in the regulation of body weight. Rather, the protein is reported to mediate an interaction between T lymphocytes and monocytes that leads to the adherence and spreading of monocytes that become foci for T lymphocyte clustering (see Duke-Cohen et al., *supra*).

Searching the MG polypeptide with the SMART domain tool (Schultz, J. et al., 1998, *Proc. Natl. Acad. Sci. U.S.A.* 95:5857-5864) revealed sequence motifs that may provide further clues to its biological function (FIG 16B, FIG. 17). The single transmembrane spanning MG protein has a large extracellular sequence of 1289 amino acids containing three EGF domains (Nakayama, M. et al., 1998, *Genomics* 51:27-34), two laminin-like EGF repeats, a CUB domain (Bork, P. and Beckmann, G., 1993, *Mol. Biol.* 231:539-545), a C-type lectin domain (Drickamer, K., 1995, *Nat. Struct. Biol.* 6:437-439; Weis W. I., and Drickamer, K., 1996, *Ann. Rev. Biochem.* 65:441-473), two plexin-like repeats (Maestrini, E. et al.,

1996, *Proc. Natl. Acad. Sci. U.S.A.* 93:674-678), and six consecutive kelch repeats (Bork, P. and Doolittle, R.F., 1994, *J. Mol. Biol.* 236:1277-1282). Multiple EGF domains are commonly found in Type-1 membrane proteins involved in cell
5 adhesion and receptor-ligand interactions (Schultz, J. et al, 1998, *Proc. Natl. Acad. Sci. USA* 95:5857-5864). Laminin-EGF-like modules are found in a variety of proteoglycans such as perlecan and heparin sulphate proteoglycan. As CUB domains also frequently occur in glycosylated proteins and c-type
10 lectins are known to be carbohydrate binders, it is likely that MG is heavily glycosylated and that carbohydrate interactions are essential for its function. Many kelch motif containing proteins have been found that, like MG, have multiple consecutive domains. Such consecutive four-stranded β -sheet Kelch motifs form a bladed beta "propeller fold" that
15 is common in many sialidases and other enzymes (Maestrini, E. et al., *supra*). Unlike the other well recognized domains, the "plexin" repeat is less well defined. It was first recognized as a triple repeat in the *Xenopus* gene plexin that has similarity to MET (Bork, P. and Beckmann, G., 1993, *Mol.*
20 *Biol.* 231:539-545). Since then, this cysteine rich repeat has been found in 6 MET gene family members, three of which signal via tyrosine kinase and three of which are hypothesized to have putative signaling function via a novel conserved cytoplasmic domain. However, it is fascinating
25 that there is an eight amino acid stretch that is 100% conserved in the four proteins shown in FIG 16A from human, mouse, and *C. elegans*. The conservation of sequence across such widely evolutionary divergent species strongly indicates a functional domain, possible a putative signaling motif.

30 The multi-domain structure of MG is complex, but draws many similarities from receptor and receptor-like proteins. The full-length MG polypeptide is predicted to be a large membrane-spanning protein with multiple extracellular domains

that may have a binding or gathering function as well as a highly conserved putative signaling motif in the cytoplasmic tail.

5

The present invention is not to be limited in scope by the specific embodiments described herein, which are intended as single illustrations of individual aspects of the invention. Functionally equivalent methods and components are within the scope of the present invention. Indeed,
10 various modifications of the invention, in addition to those shown and described herein, will become apparent to those skilled in the art from the foregoing description and accompanying drawings.

All publications and patent applications mentioned in
15 the specification are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

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WHAT IS CLAIMED IS:

1. An isolated nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1 (FIG. 2A), SEQ ID NO: 8 (FIG. 8A), SEQ ID NO: 10 (FIG. 9), SEQ ID NO: 12 (FIG. 10),
5 SEQ ID NO: 14 (FIG. 18A), SEQ ID NO: 16 (FIG. 19A), or SEQ ID NO: 18 (FIG. 20A).
2. The isolated nucleic acid molecule of Claim 1,
wherein the nucleic acid molecule comprises the nucleotide
10 sequence of SEQ ID NO: 1 (FIG. 2A).
3. The isolated nucleic acid molecule of Claim 1,
wherein the nucleic acid molecule comprises the nucleotide
sequence of SEQ ID NO: 8 (FIG. 8A).
- 15 4. The isolated nucleic acid molecule of Claim 1,
wherein the nucleic acid molecule comprises the nucleotide
sequence of SEQ ID NO: 10 (FIG. 9).
5. The isolated nucleic acid molecule of Claim 1,
20 wherein the nucleic acid molecule comprises the nucleotide
sequence of SEQ ID NO: 12 (FIG. 10).
6. The isolated nucleic acid molecule of Claim 1,
wherein the nucleic acid molecule comprises the nucleotide
25 sequence of SEQ ID NO: 14 (FIG. 18A).
7. The isolated nucleic acid molecule of Claim 1,
wherein the nucleic acid molecule comprises the nucleotide
sequence of SEQ ID NO: 16 (FIG. 19A).
- 30 8. The isolated nucleic acid molecule of Claim 1,
wherein the nucleic acid molecule comprises the nucleotide
sequence of SEQ ID NO: 18 (FIG. 20A).

9. A vector comprising the isolated nucleic acid molecule of any one of Claims 1-8.

10. An isolated host cell genetically engineered to
5 express the nucleic acid of any one of Claims 1-8.

11. An isolated nucleic acid molecule comprising a nucleotide sequence that hybridizes to the complement of SEQ ID NO: 1 (FIG. 2A), SEQ ID NO: 8 (FIG. 8A), SEQ ID NO: 10 (FIG. 9), SEQ ID NO: 12 (FIG. 10), SEQ ID NO: 14 (FIG. 18A),
10 SEQ ID NO: 16 (FIG. 19A), or SEQ ID NO: 18 (FIG. 20A) under stringent conditions comprising hybridization in 0.5 M NaHPO₄, 7% SDS, 1 mM EDTA at 68 °C.

12. A vector comprising the isolated nucleic acid
15 molecule Claim 11.

13. An isolated host cell genetically engineered to express the nucleic acid of Claim 11.

20 14. A method of producing a mg gene product comprising culturing the genetically engineered host cell of Claim 10 so that the mg gene product is expressed in cell culture, and recovering the mg gene product from the cell culture.

25 15. A method of producing a mg gene product comprising culturing the genetically engineered host cell of Claim 14 so that the mg gene product is expressed in cell culture, and recovering the mg gene product from the cell culture.

30 16. An isolated gene product encoded by the nucleic acid molecule of any one of Claims 1-8.

17. The isolated gene product of Claim 16, wherein the gene product comprises the amino acid sequence shown in Figure 2B (SEQ. ID NO. 2), Figure 8B (SEQ. ID NO. 9), Figure 9 (SEQ. ID NO. 11), Figure 10B (SEQ. ID NO. 13), Figure 18B (SEQ. ID NO. 15), Figure 19B (SEQ. ID NO. 17), or Figure 20B (SEQ. ID NO. 19).

18. An antibody that immunospecifically binds the gene product of Claim 16.

10

19. A method for diagnosing a body weight disorder in a mammal, comprising: measuring the level of *mg* gene expression in a patient sample and comparing the level to that of a control sample, so that if a difference between the levels is detected, a body weight disorder is diagnosed.

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20. A method for diagnosing a body weight disorder in a mammal, comprising detecting a *mg* gene mutation contained in the genome of the mammal that correlates with presence of the disorder.

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21. A method for diagnosing a body weight disorder in a mammal, comprising: measuring the level of *mg* activity in a patient sample and comparing the level to that of a control sample, so that if a difference between the levels is detected, a body weight disorder is diagnosed.

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22. A method for identifying a compound that modulates *mg* activity, comprising:

- a. contacting a compound to a cell that expresses a *mg* gene;
- b. measuring the level of *mg* gene expression in the cell; and

30

- c. comparing the level obtained in (b) to mg gene expression level obtained in the absence of the compound;

such that if the level obtained in (b) differs from that
5 obtained in the absence of the compound, a compound that
modulates a mg activity is identified.

23. A method for identifying a compound that modulates
a mg activity, comprising:

- 10 a. contacting a compound to a cell that contains a mg polypeptide;
- b. measuring the level of mg polypeptide or activity in the cell; and
- c. comparing the level obtained in (b) to the level of
15 mg polypeptide or activity obtained in the absence
of the compound;

such that if the level obtained in (b) differs from that
obtained in the absence of the compound, a compound that
modulates a mg activity is identified.

- 20 24. The method of Claim 22 or 23 wherein the compound
identified is capable of treating a body weight disorder.

25. A pharmaceutical composition comprising the
compound identified by the method of claim 24.

- 25 26. The use of the pharmaceutical composition of Claim
25 for treating a body weight disorder in a mammal.

27. The use of the antibody of claim 18 for treating a
body weight disorder in a mammal.

- 30 28. The use of a mg antisense, ribozyme or triple helix
molecule for treating a body weight disorder in a mammal.

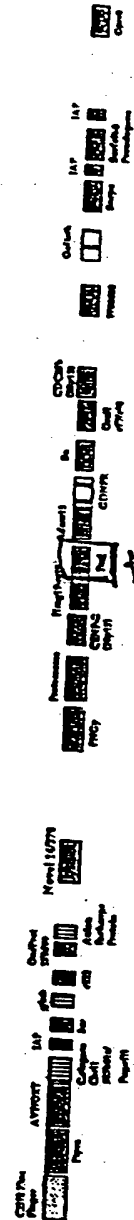


FIG. 1

GAATTCGGGGCGAAGGGGAGCCGGCGTGGGGGTGTGTATGTGTTGCTGGGGCGCCGGCTCAGCCCCAGGAAGATGGTG
CGGTGGCGGGCGGGCGGGCGGACTGAGGCGCGGCTGAGGGGGAGCACGAGGACGACAGCAGOGCTGGGGGAGGAAGG
GCAGGCAGCACCGACCCCTGCACCGCGACAGGGGCTGGAGGCGGGGACCGCGCGCCGGCTGTGTCTCCCGGGGTGCT
GTGCGGGGCGCTGCCCCCGCCGCGCTGTGCGCTGCTCTTTTGGCTGTGCTGCTGCGCGCTGCCCCGGAGGCGGAG
GCCGCTGCGGTGGCGGGCGGGCGGTGTCCGGCTGGGCCGAGCCGAGGCCAAGGAATGTGAACGGCGCGTGTGTCAACGGCG
GCCGCTGCAACCCCTGGCACCGGCCAGTGGCTGTGCCCCACGGGCTGGGTGGGCGAGCAATGCCAGCTGTGGGGGCGG
CTTCAGGACATCTGTCTCAGCCTATAATCAGAGCTGTTGGAAGGTGAGGCTGGAGGAACAGTTGAGGCAAGCTTCG
GCTACAGAATAAGTTCAAGAGTAACCTGGGGCAACTTGGGCTGTCTCCAAAACCAAAATGAGOGAAAAGGAGCAAGCT
AGAGTCTTTTGGGAAAATTTTAGCTGACTAATTTTTCACCGAGAACTAATCGCTCTTCTGGATTGTAAACAGATGGAC
CTGGGAATTATAAATATAAGACGAAGTGACATGGCTCATTTGAAGGACAGCCAAATAGAATAATGAGACTTGGCTTCAA
CCATTTTGCTACAGAATGTAGCTGGGACCATTTATATGTTTATGATGGGGACTCAATCTACGCACCTCTGATTGCTGCC
TTTAGTGGCCTCATTGTTCTGAAAGAGATGGCAATGAGAGGGCTGCTGAGGTCACTGTCACTTCAGGTTATGCACTGC
TGCAATTTTTCAGTGATGCTGCTTATAATCTGACTGGATTAAATATCACTTACAATTTTGACATGTGTCCGAATAATTG
CTCAGGCCGAGGAGAGTGTAAAGAGCAGTAACAGCAGCAGCGCTGTGAGTGTGAATGTTCTGAAAACGGAAGGGGAG
TGCTGTGACATTCTCACTGTACAGACAACCTGTGGCTTTCTCACCAGGCATCTGTAATGCAAGCGATAACCAGAGGGT
GCTCCTGCTTTCTCACTGGCAGGGTCTGGATGTTCAATCTCTGTGCCAGCTAACCAGTCTTTTGGACTCGAGAAGA
ATATTCTGATTTAAAGCTTCCCAGAGCTCTCATAAAGCTGTGGTCAATGGAAATATAATGTGGGTGTGTGGCGGATAT
ATGTTCAACCATTACAGATTACAGCATGGTTTTAGCGTATGACCTGACTTCTAGGGAATGGCTTCCACTAAACCAATCTG
TGAACAGTGTGGTTGTAAGATATGGTCATTCTTTGGCATTACATAAGGATAAAATCTACATGTATGGAGGAAAAATGA
TTCAACAGGGAACGTGACCAATGAGCTGAGAGTATTTCATATTCATAATGAATCATGGGTATTGTTAACTCCGAAAGCT
AAGGATCAGTATGCAGTGGTTGGACACTCAGCACACATTGTTACACTGGCATCTGGCCGTGTGGTCATGTTGGTCATCT
TGGTCAATTGCCACTCTATGGATATATAAGCGTTGTGCAGGAATATGACTTGGAAAAGAACATOGAGTATATTACA
TACTCAGGGTGCTCTTGTGCAAGGGGGTTATGGCCACAGTAGTGTTTATGATGACAGGAGCAAGGCTCTGTAGGTTTAT
GGTGGCTACAAGGCTTTTACGCGCAACAAATACCGGCTTGCCAGATGACCTCTACAGATACGATGTGGATACTCAGATGT
GGACCATTTCTTAAGGACAGCCGATTTTCCGTTACTTGCATACAGCTGTGATAGTGAGTGGAAOCATGCTGGTGTGTTGG
AGGGAACACACACAATGACACTTCCATGAGGCAAGGTGCCAAATGCTTCTCTCGGACTTCATGGCTTATGACTATTGCT
TGTGACCGATGGTCAGTGCTTCCCAGACCTGAGCTCCATCATGATGTCAACAGATTTGGCCATTCAGCAGTCTTGTACA
ACAGCACCATGTATGTGTTGGGGCGCTTCAACAGGCTCTCTCAGTGACGCTTGGTCTTTACCTGGAGCAGTGOGA
TGCACACCGCAGTGAAGCTGCTTGTGTGGCAGCAGGACCTGGTATCCGGTGTCTGTGGGACACACAGTGGTCTOGATGT
ACCTCTGGGAGTTGGCAACTGAAGAACAAGCAGAAAAGTTAAATCAGAGTGTTTTTCTAAAAGAACCTTGAGCATG
ACAGATGTGACCAGCACACAGATTGTTACAGCTGCACAGCCAAATAGCAATGACTGGCACTGGTGCATGATCACTGGGT
CCCTGTGAACCACAGCTGCACAGAAGGCCAGATCTCCATTGCCAAGTATGAGAGTTGCCCCAAGGATAAGGCGATGTAC
TACTGCAATAAGAAAACCAGCTGCAGGAGCTGTGCGCTAGACCAGAACTGOCAGTGGGAGCCCCGGAATCAAGAGTGCA
TGGCCCTGCCGGAAAATATCTGTGGCAATGGCTGGCATTTGGTTGGAAAACCTGTGTCTGAAAATCACTACTGCTAAGGA
GAATTATGACAAATGCTAAATGTCTGTAGGAACCACAATGCTTTTGGCTTCCCTCACATCCAGAAAGGAGTGGAG
TTTGTCTTAAGCAGCTTCGATTAAATGCAATCATCTCAAAGTATGTCCAAGCTCACTCTGACTCCATGGGTGGTCTTC
GGAAGATCAATGTGTCTTACTGGTGTGGGAGGATATGTCTCATTCACAAATAGTTTGTGTGAGTGGATGGCATCTGA

FIG. 2A(1)

[illegible]

FIG. 2A(2)

TTCCCCATTTATGGTGCTCTGTATTCTGGCATTATGCAGCAGCCTCCAGAAGCTCTCTTCTGCTTCAAAAACCTGGGAT
CTCTGGCATTACCCATTATGGGATGGACCGCTGGACAGCAATGCTCGAGTTTGTGAATTTGGAGAGATACTCAAAAGAGC
TAAAACTGCAGCATTTTACCTTTAAATGCAGTGCCTAGAGAGAGAGTATTGTCTCTTCCCCAACACTAAGCCCCACTCCC
ATGAAGAATTGCCTGGAAAGATGTTTTCAAGGAATTTGAACCATAAAACACTATCTGATGCACAGAACACCTCTACTTT
GAGACTCACCTCTCATAAAGCTCTTTTTTCACATTACTGTTAAAGACCAGACGTTCTAGAAAAGACCCCTCCTCTCATG
AGCTCCCCCATCCCTGCTACAGAACACAGCACCCATGGCGCCTGCAGTGGACTGGCCCCCTTAATTCCCACAGGCCCCCC
CAGCAAGGCCAAAGGGAGGCCCTGGGTATTGTCTCTCTACAAGGAAGATCCTCTTTGTTTGTTCAAAGGACCAGTTT
CCTAGGCCAAAGAAGTCTCTTCCCCATGTTAGTCTATGCCTTGAATATCATGCACCATGACCCACAGCCATCTGGTT
ATGTCTTATTTTTTTTCTAAAAGATAATGTTTATTTTTTAAAAAGGAAGGAAGAAGCAAGTGAAGTTTCAATCTGCTCCA
GCGGTGGGAAGCCGCTGAATCCACCTGCTTCTCCTTTGCAACCGACAGCAACAGCTTTCTCCGGCCTCAGGGCAGAA
AAAGGGAATGGCAGGGAGTAAGAGGCGCTGGGCTCGGAGCCTGTTTCCAAGAAGGAATTGGTTGTCTATCTGGCAGTGT
GCGCGTCACAAGAGAGCCTGTATATAAATTAAATAGTCAAGACAACACTGACCTTGCACCTGTACATAACTATACAGT
AGTGTCCAGAATGTTTCAGACATTGGAGTGTACATAAAACAGAAAAATCTTCATGTATTTTTTATTAAATATAACAATG
TCTGAGTTTACCTAAGATGTTTTTGTGCCATATGCTGGATATCCAGGTTCTCGCCAGGCCCGATACATGAATAACAA
ACCCAAGAAACGCATCCCCATTGTGTGATGTGTTTCAGATGCATCTGGCACCATTAGGTATTTCTTAAAAACAGGACTCA
TCTGTTCAGAGTGCACATGAAAAATCAGGCAGGGAATCGAAACGACAGCGCTGGAGGAGACTCAGGAAGCAGAGGCGTCC
CTGCCGCTGCCCTTGGCCCTGCAAGCACATCATGACCCCTTCTGGCAGCCTCTTGGTGCTCTGGGTAGTGAGGGATGAC
CAGTCTTGTCTGAGAAATGTTTCTCTTAGTCTTTAAGTTCAAAGACTAACCCTGTAGCAATCAGACTTTCCAAAAGGGG
GTTCTCCATTTTTTGTAGTTTTGTCTAAATTTTTAATGACCATTTCCTGGAATCAGTTTATTATACTGAAAACCTGGGGG
TGGGAGTAGGGAGCTAGTTTGTGATTAATAGTTCCCATTTCCCCGTGGAGAATTGACATACCCTGGACTCCTGTGTG
CCTCCTGCCATCCCTGCACACAGCCTGGGGAGAAGCCTGTGCCTCCCCGTGTGGAGAGAAGGCAACCCAGATCCCTG
AGCTAACCCGGAGGAAAGGCAGTCTGGACAGAAGACTGTTCAGCAGAAGGAAAGTACTGGACTACCCGTGGGTAAGTCC
TGCCATTCAAGACTGGAGACACCTGGGAAATAAAAAGAGCAGGGCAGTGTGGTGGGAAGAGGCATTTTACCTTCCAGT
GCAAATCCTGCTCCTTTGATTTAATGGGGTGTACTGGGGCCAGGGGCTGATTCACCTTCTTGGGAGATGGTGGTGT
CATGAACATCTTTGATCCTTCCATTTCAATTTATTCATCCATCCATTCAACAAGTATTTGCTAAACACTAACTTAAGCTA
ATGCTAGGGTAGTGACTGAGATGTAAAAATAGATTTTAGAATTAACAACAAATCCAAGTCTCACACCCCTGTCTATCCC
AGGAGATCTTTCTTGTGGTGGTTTCTGTGAGAATTGGCCATCTGAGGACACAGCCAGGACCGGCAGAGGCTCCTGGC
CTCAGGGCATGCCCTGCCTACCTTCTGAAATGTTTACCCCATTGACCAAACTTGGCTCCAGCCATTGOGGTGGTTTCTA
GATAGCCAGGCCCAACAGAGATATTGCCCTTGTATGAGAGTCAACAGCCTGCCTACAAGGAGATGTTTTGAAATGGA
GAGGAAATTTGGCACCTCATCTTTTAAAGGCAGTAATOGAATTTGATTTTCAGTAAGTGAATTTGTGCACAAAACATTCT
AAACACTAGTGAAGCCTGTTTCTGTTGAACATAATCTGGCTCTGGAATGTTTTTGTGTTTATAGTTATTTACGATTTGGT
TTGTTTGGATTCAAGCTTAGTTTGTAAATATGTATAATTTAGCATCTATTACACTCATGTAAATATGGAGTAAGTATTG
TAACTATTTCAATGCGGGGATTGTGGGTGTTATACATACATTTAGGACTGCAATTTTTTGGTATTTTTTGTATTGTAA
AATAACAGCTAATTTAAGCAGGAACAAGAGAACTAAGGGAGGTCTGTGCATTTTAAACACAAATGTGAAGAAGTGTAT
ATAAACAAAAGTAAATACTATAATACAACTTCTCTGAAATAAAAGTAGATCTGGT

FIG. 2A(3)

MRLRFNHFATECSWDHLYVYDGDSDIYAPLIAAFSGLIVPERDGNETAPEVTVTSGYALLHFFSDAAYNLTGFNITYNFD
MCPNCSGRGECKSSNSSSAVECECSENWKGESCDIPHCTDNCGFPHRGICNASDTRGCSCFPHWQGPCCSIPVPANQS
FWTREEYSOLKLPRAHKAVVNGNIMWVVGGMFNHSDYSMLAYDLTSREWLPNHSVNSVVVRYGHSALHKKDKTYM
YGGKIDSTGNVTNELRVFHIHNEVWLLTPKAKDQYAVVGHSAHIVTLASGRVVMLVIFGHCPLYGYISVVQEYDLEKN
TWSILHTQALVQGGYGHSSVYDDRTKALYVHGGYKAFSANKYRLADDLYRYDVTQMWTLKDSRFFRYLHTAVTVSG
TMLVFGGNTHTNDTSMHSHGAKCFSSDFMAYDLACDRWSVLPRPELHHDVNRFGHSAVLYNSTMYVFGGFNSLLSDVLVF
TSEQDAHRSEAACVAAGPGIRCLWDTQSSRCTSWELATEEQAEKLEKSECFSKRTLHDHRCDOHTDCYSCCTANTNDCHW
CNDHCVFVNHSCTEGQISIAKYESCCKDNPMYYCNKRTSCRSCALDQNCQWEPRNQECIALPENICGNGWHLVGNCSCLK
ITTAKENYDNAKLSRNHNAFLASLTSQKKVEFVLKQLRLMQSSQMSKLTLPWVGLRKINVSYWCWEDMSFFTNSLL
QWMPSEPSDAGFCGILSEPSTRGLKAATCINPLNGSVCPANHSKQCRTPCALRTACGECTSSSSECMWCSNMKQCV
DSNAYVASFPFGQCHEWYTMSSCPPENCSSGYCTCSHCLEQPGCGWCTDPSNTGKGCIEGSKGPVKMPQASAGNVYP
QPLLNSSMCLEDSRYNWSFIHCPACQCNGHSCINQSIKCECEDLTGKHCECTCISGFYGDPTNGGKQPCCKNGHASL
CNINTGKCFCTTKGVKGDECQLCEVENRYQGNPLKGTCTYTLIDYQFTFSLSQEDDRYYTAINFVATPDEQNRDLMF
INASKNFNLNITWATSFPAQTGTGEEVPVVSNTNKEYKDSFSNEKDFRNHPNITFFVYVSNFTWPIKIQIAFSQHSN
FMDLVQFFVTFFSCFLSLLLVAVVWKIKQSCWASRRREQLLREMOMASRPFASVNVVALETDEEPPDLIGGSIKTVPK
PIALEPCFGNKAAVLSVFVRLPRGLGGIPPPGQSGLAVASALVDISQMPIVYKEKSGAVRNRRKQPPAQPGTCI

FIG. 2B

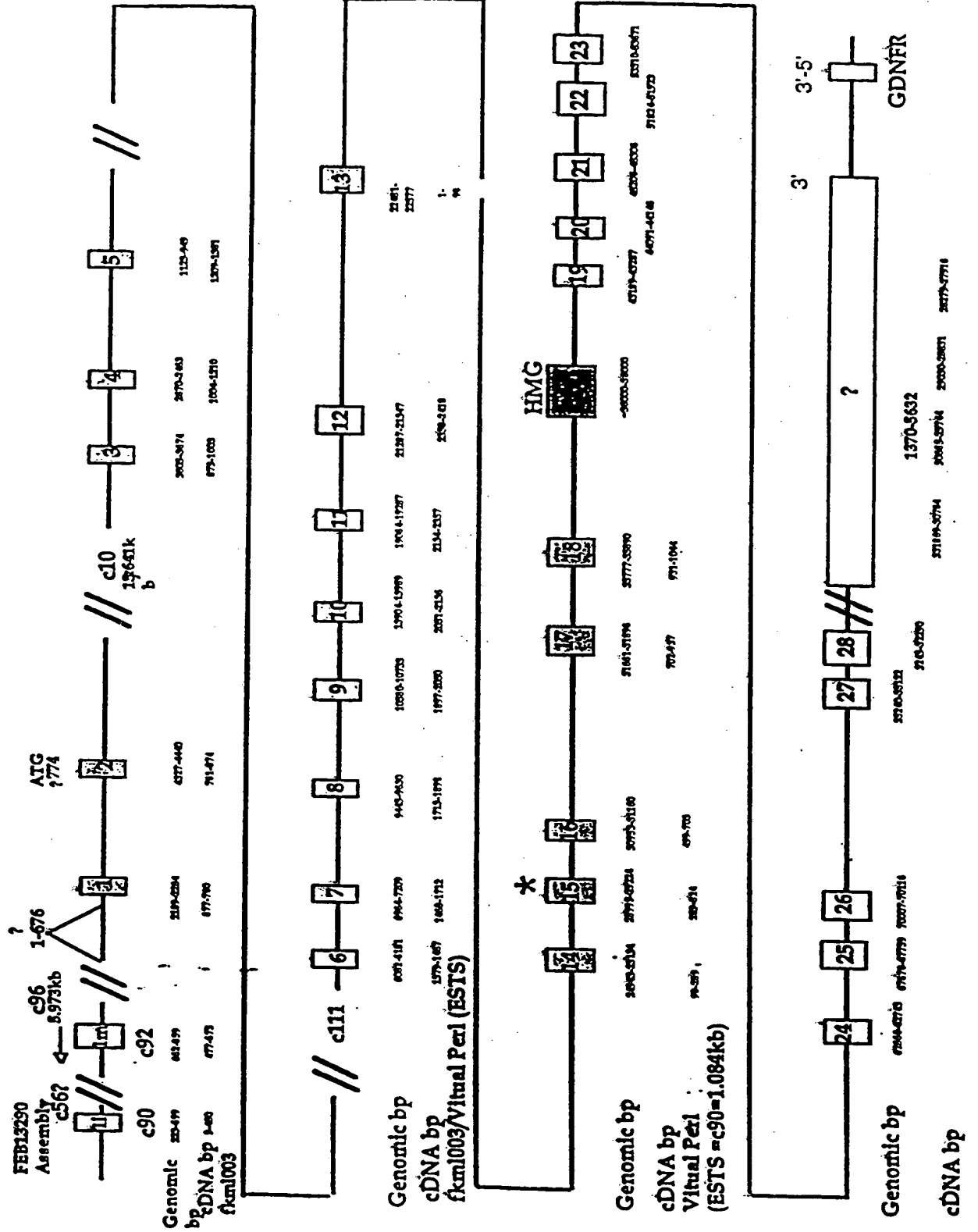


FIG. 3B(1)

AAACCCCTGGGAATTGTTAGACAAAGGCCATTTAATACTAATAAGCTATAA
ACTGAAACCATCTGATATATGAAAACTATTAATAAAATCAAGATAAAATA
ACCCCTATTTATATACTTACTATATACCTAAAGCAAAATATCAAAGAAA
GTACCTTAAAAAGATAAATTATTCTTATTTTGACAATGAATTCTTTGGGG
CGTTAAATTGTAGAATATCAACACATATCAAGAAAGTTTAGAAGAAAAC
ACCAAAGTTTAAACAGACTTTCCTCGGTAATTACTGGTGATTTCTTGGCT
TTTTTTTTTTTACACTGCAGTTTTTCAGGGTGGAACTTAAGCTTTGTACA
GAAGCACTTACCACCCTCTCAGAGCTGGAAATGGCTCAAAGGGCAAAGC
ATTACAAGCCTGGCAACCTGAACCAAATACCCAAAACACTTGCAAAGGTG
AAAGGAGAAAACTAACTCCAGGAAGTTGTCTTCGAGCTCCTCTTGCACA
CCACTGTATACACCCCTTATATACACTCAGTTACCATAAAATAAAATGTT
TCATTATAAAGACACTTACGCTAAAACCATGCTGTAATCTGAATGGTTGA
ACATATATCCGCCAACCAACCCACATTATATTTCCATTGACCACAGCTTTA
TGAGAGGCTCTGGGAAGCTTTAAATCAGAATATTCTTCTCGAGTCCAAAA
AGACTGGTTAGCTGGCACAGGAATTGAGCATCCAGGACCTAATAAAAAAA
AAAAAAACAACAACAACAACAATAGCTTCACAAAATGCAGCCTGAAAGT
TTATAGTATTCCAAGTTCCAATCTAAGTGCAAAGAATATTTAAAGACTTG
TGGGGCTAGAGAGATGGCTCAGTGGTTAAGAAAACGACTGCTCTTCTTG
GAGGTCTGAGTTCAAATCCCAGCAACTACATGGTGGCTCACAACCATAT
GTAATGGGGATCTGATGCCCTCTTCTGGTGTGTCTGAAGACAGCAACAAT
GTACTCACATGAAATAAATAAATTAATTTTTTAAAAAACAGACCAGAAAA
AAAAAAAAAAAAAGACTTGTGTTTCCTTTAGCACTTAAGCGCAAACATC
TTTAACCTGTGGGGTTTTTAAAGGTTTTTACATGTACAGGTATTTTGTTTA
CATGTATGCCTATATACCACTTGCTTGCTTGGTACCCAATGATGTCAGGA
AAAGGCATTGAATCCCTGGAACTAGAGTTACAGATCTTATGAGCTACTT
TGTGGATGCTAGGATCAAACCTGAGTCTCTGGAAGAGCAACCAGTACTC
TTAACCAAGAAGCCATCTGCTTAGCACCTAACATGAGTTTTTTAACTTACT
CAAGATACAGACCAAAACCAATCACTCCCTTATAAAATTTAATACTACAC
ACTTTCTGATAATTTGGCAATTTCTGATAATCAGGTAAACTTTTTTAGA
GGTAAAAATCTTGCTGAAGCAACATTTAGTAGAAAGGGTAGACCAAGGGG
TTATTATATTAATCATGTGGAAAAGGCATTAGGGTTGAAATATAATGAC
AGATCAAAATCGATCTTCTGGCAAGTCCAGGCGCTGAATAGATGAAAGAG
ACAAAGGGAGAATTGGACAACTAAAAACATTTACATGAACACTTACTTT
CTGAGGACCTAAGCATAGAAGGAAAATCACTAAACCAACGATGACTGCTT
CCTCAATACCCCAGGGAATTGCCTACAGTACCTTAGTAGCCGGTTGTGTT
GGGTAATGGCACTAGATGACAGCACTGAGACTCTAAGGAACGCTTGTCTT
CCTCTCAGCTTGAGTCTCTGCTTCTCTATCACCAGACCATGTTCCCTAAT
TCCCACGAATGAGTTGCAAAGGATTTGTCAAACCTTTCCACAATTCTAAG
CACATAGATAACAACCATATATGTAAATTCAAAGAATCTGAATAAATG
GAGATGAATGCTTAAATGCCACCTGATACATGATTAACATAAGGCGTATG

FIG. 3B(2)

GCTGCTAAAATAAACTCCCTACAGTTCACCTAACTCAGAACTTTCTGTGAG
GGAAAGGACTTTGAAGGGCAGCTCCTACCCTGCCAGTGAGGAAAGCAGGA
GCACCCTCTGGTATCGCTTGCATTACAGATGCCTCGGTGAGGAAAGCCAC
AGTTGTCTGTACAGTGAGGAATGTCACACGACTCCCTTTCCAGTTTTC
GAACATTACACTCAACAGCGCTGCTGCTGTTACTGCTCTTACACTCTCC
TCGGCCTGAGCAATTATTGGACACATGTCAAACTACAAAGACAGGAGA
AAACGAAGTCAACAATTTCAACTAAGCAACATTGCAACTAATGCAGACCT
TCCTCCTCAGTTTAAAGTTCAGTTCATTGCAAGTGTGACTGCAGGACTT
ACCAGTTAGCCCAAGTGTGCTCACAGAGCTCTGTGTAGCTAGAGCCCCAG
GCTCAAGTAATGAAATCAAATCAACCTTGCTGCATTACATATGAAGAAG
GAAGAATAAATAACTCACAAAGTTAGAGAAATTACAAAACAATAGACATT
TGTGCAAAATCACTTAGACTTAGCTCAAGACTGGCAACCAGGATCCTACT
CTTCTGGTAGCTCATTAGTAAAGAGTTCTACAAAAGCAGCAAGGTCATG
CTAGGAAGTGGAGGAAGGAGAGGAAGCCAATGAGCTGCCAACATTACCGG
TATACATTTCTCTGTAAAGATTCTGAGAATTAACAGAAATTAAGATTATT
TTCCAGTGATGTAGTTAAAGGTCTTTAGTAACTTTTATCAGCTTAGAAGG
AGAAGAGCAGTTAACTTCATGTATGAGTTTAAAGTGTCTCATGACTTAAGA
TAACAGTTTTGCTACAATTTGAAATGCCATCTCAGACTTTTTAAAGGG
GTGCATTAGTGGACTATTACAATAGCTTAAAAATATAGATTTCTCCTACT
GATGATTATTACTGAGACACTACTAGTCTTTATTAAATTCAGTTAGCAAA
ACTCCTGACATTTTCTTCCAGCAGCGGAAGAAATGTCTCTCTCTCTAGGA
GATCCTCAGTGACAAGATCTAGAAAGACCAAGAACTGTGGTCCCAACCAG
TGGGGCTGATATTTGTTTTAACCTTTTAGCTCCTGTTTCTTCAATTATGAA
AAAAAAAAAAAAAGAAGAAGAAATCCATGTTAAATTTAGCAAGGAG
CCTGACTAGCTAGAAGCCTCCCTCCAATATATTAGTGTTATTAAGTCATT
TGAGTAGTATCACAAATATTAAATCTAAATATCTTACTGTAAAGTGATAT
TAAATCCAGTCAGATTATAAGCAGCATCACTGAAAAATGCAGCAGTGCA
TAACCTGAAGTGACAGTGACCTCAGGAGCCGTCTCATTGCCATCTCTTTC
AGGAACAATGAGGCCACTGAAATGTAAACACAGACCAGATTACAGCAACT
TCAACAGAACTGTCTATATGTTACTATTTGATCCTGCTGCTCCTGTTCC
AACACACACTGTAAATGTGACTCTAGCTGGCCTCAAATTCACAGACCCAC
CTGCTTCCACCTCCTGGGTTATAGGCATGCGCTACTATGCCCAACATCTA
AAAGGATTTGAAATCTATGACTTTGATTGAATTTTGGGTTTTTGTTTTT
GCTATAAACTTTTTATTATAATACTCTCAAGTCTCTACAATAACATTATT
AACAACTTTATGAATTGACAACTGTCAAATATATACTGTTGAAGAAAA
TACTTTACATATTTTTGTAAATATGTATCATATAATCTTTTTAATGTATTT
TATAGATGTCTTATATAAGTAAAAATAGAAAAGTTTACTGATTTATAATC
CTTATACTATTAGCTTTCAGACGTATTTTGTGTTGTTAAACTGGTAACACA
TTTTATGTTTATAATTCACAATAAGCACTGCCACTGAAGGTGCCAAAGGC
TCCTTAGAATCTCAGTAAGAACCTAGTGGGTAATATTTGAAGTTTGGAT

Fig. 3B(3)

GCCAGTAAATTCATGTGTAAAGATTTATTGAGTAAGTGACTIONACCAGCGGG
ACAGTGGTGGTGCACGCCTTTAGTCCCAGCACTTGGGAGGCAGAGGCAGG
CGAATTTCTGAGTTCGAGGCCAGCCTGGTCTACAGAGTGAGTTCCCAGGA
TAACCAGGGCTACACAGAGAAAACCTGTCAACCTGTCTCAAAAAAAAAA
AAAAAAAAAAAAAGAATATACCATTTTTTAAGGCATTTGATCCACAAAAATCA
TACCACCTTGTTTTACAAAAGATATATATTAACCTGAAGGCTGGAAATGG
TGGCACATGTC'TTAGTCCCAGTATTGGGAAGACAGACCCAGATGGATCT
CTGAGTTCAAGACCAGCATGGTCTACATAGTGAATTCATGTAAAGTTTGT
CCGTGTGTGTAACCTTGAAACCTCATTATAGAATGGAAGTGTCTACCCAC
CCCCTTACCAACAGTAAGGAATATTATGTTGGTCCCGCTCATTTAATAC
ATGGTGTACTCCCAAGGTAATCATTTTTCATGTTTAGTCCCTCCTATTAT
TTTTTCCATTATCAATTCACTACAACACTACTACCACCAATCACATTTAGCC
ACTAGAAAAGCCATGTGATTTGCTCCACACATACAACCTCACTCAATAAA
TAAACATCTTATCAGTACTACTCTCTCTTTCACTCACTCAATCCCTAGTC
CCCTAAGTTTTTGGACGATTACACCAGGTAATTCCTACTTCAGGGTAT
GACCATCTTAAAACTAGGACCTAGCAATTCTCTTTGTATAAGAAATACT
TCCCGGTATATACACAGAAAAACAAAGAACACTACTACAGCACTATTAG
ATGACAACTGACTAAAAGTCACCTAATTGCTTATTTATGGGAGTGTATTA
AATTAGTCATTACAAATCTGTAGGTCTGCAAGACTAACCAAGAGCTTCGT
GAGGACAATAGGTAGGGCTACCCAGAGAAAACCTGTCAACCTGTCTCGAA
AAAAAAAAAAAAAAAAAGGGAGGCACAGAGAAAAACAACAGGCCCGGGTA
CCTGTACATCTATGTAAGCGTAGGTACATGCACATAAAAGTGACTACAAG
AGAACATAAACAGAGAGCGCGATGAGAAGAGGATGGGATTTTTTCATTTA
ATTTGCGTGTATGAGAGCACCTATATGTGCATGTTATCCGCACCAAAGTG
TGTAGGGTACATTATGTGAGTGTGCTGCAGAGGTCACTGTCAAGTGTCT
TCAATCACTCCGCTCCTTTTTCTCTCGGAGATAAGAGTTTCATGAAGTAG
TACTGGCTGGACTAGAACTCACTATGCAAAGCAGGCTGGCCTTGAATCT
CAGAGAGCCTCTTGAGTGTGGAATTTATATGCATGTGCGGCAACACAGCC
CACCTCATTTTGGGGGGTAGGATCTTTCAGTGAAGCTGAGCTCACTGATT
GGTTAGACCGGACTGGCCAGTAAGTTCCAGGACCTCTCTTGTCTCCGCT
CTTCAGCACTGTGATCACAGGCTCACAACCAACACTGGACTTTTACTTGA
GTCTGGAGATCTAAACTCAGCTCTCATGCTGTGCAGAAAGGAATTA
CTGAGCCAGCTGTCTCAGTATCAAGAGAGAACATAGGAACGTGAAGATTC
TGACAGTACTCTAGGGCTTACAGAACCCGACACATTTTCTACTATGTAT
TCAGTTAATAAAAGAATAAATACAAACAAAAAACATGAGAAACATATAG
AGGCAGAGACAGACAGACACACACACACACACACACACACACACACAC
ACACACACACACACACGCACTTAGACGGGTGTGGGGGAAGAAAGAGCAAG
GCCACCTAGAAACAGGTACGTTCCATGCAAAATGATCACAGGAAAGGATTG
GGGATTTTAAACACTTGTGGGAAATGCTGTACTCTCCTATTCTAGCACA
GATTTGAGGAAAAAGTAGAGCAGAGAGTCTGTCTTCCACATATCCTGGA

Fig 3B (4)

AAGTCACTGACATGTCCAAGTTTGGATTTCCTTCATAGGGACAATGAGAGA
AACCAGACTATCTCACAGCAGCACAGCAAGGACCAACCAGCAGAGCAGG
AGAAGTGCTTACAGCAGTGTGCTGCTAGAAAGGTGCAACAGTCTTCTTACA
GAGGGCATTAAATATGCAGGATGGATAAGTTTGCCAACTACAACCTACAG
AGGCTGGACAAGGTAGGACAGCTTCTTCACTGTCAAAGACGTTTGGGCAG
TTGCTTCTATTTACCTTAAATCAAACCTGTGACAGCTGTGGCATATATAG
ATTTCTCCCAGAATGAAAACACATTAACTCACTTATGTCAATAATATGGA
GTAAACACAAACATAGTCTATCTAGCTCAGCATGCAAGACATGTGAGGAA
GAGGAGCTACTGTGAGTCCCTATCCCTGTCCCTAAGGAAAACCAATATATG
TAAATGTAGTCTAAGCTGCAGGCAGTTCTTCAACTGCCTACCCAGGCTG
CTCACCACTTCACATTCTAAGCACAGACTAGAAAGTATGATCAACCTCTG
AACACTGTGCTATAATGTTACCATCAATCTCACACACAAATTTTATAACA
TTTTAAGTAAGTCTATGATGATTCTATGTTGTGTCCAGTTATATAAGAT
CCATAGGTACACAGGCTAGACATTCAAGGACACCAACATTTGGAATTTTGG
GTTTTTTTGGTGTACTGTATATACTTGCTAGTGACAGGTACCCATGCTCAT
GTGTGTAGAAGTTGGGCGTCTTCTTCTATCACTGTCTACTTTATATTTT
CTTTATTGTTTCATTTGATATGTATAGGTGTTTGCCTGCATATATGTGT
ATGTTTGTGTCAGAGAGGGTATTGAATTCCCTGGGACTAGAGTTACAG
GTGGTTGTGAGGCACCATTTATGGGTACTGGGACTCAATCCTGGGTTCTCT
GGAAGGGCAGCCAGTACTTTTAATCACTGAGCCATCTCTTTAGCTTCCTT
CGTTCATTGTTGTTTCATTTCCTTCATTTCCTTCATTTCCTTCAGAGG
ATTGAGATACCTTCCTCAGTTAGGCTGGCTAGCCAATGGACTCTGGGAAT
CTATCTGTTTCAGCTATTCTCTCCTTCCCATCCAAGTGCTGGGGATACAG
GCAGGTCTACTGGGTTTCATTTTGAAAAATTACAGAACTATGTATTTTCT
TCATAAATCTGAACTCAGCATAACTGTCTCAGGCTAACATGGAATCCCT
AAATATATATGAGGCACAACCTGACTTTACCAACTGTACTATGTAAATTT
GCTAGTATATTAGTCAACACTTAATGGAAAAACATCTGATAAAAACAACT
TACAGGCCAATAGGCAAGGAGACACTTGGGGAGGTGGATTCAAGGCAGTC
ACTGGATTCTTGAATTTAAGTCCAGCCTAGGCTACATGAGATTCTGCTTC
AAAAATAAACAAATTAAATTTATGGGGGAAAGAATGATGATTTTGGTTT
CAGAAATTCATCCTATCATCCAAGGGAGATATTGTATAACAGCGAAGTT
CCTCAGCTCACAGCAGTCAGTAGCATATAGACAATCCTGGCTCCAAGCCT
ATGAAAACACAGCCTGTACTAAAGGTGTGTTCCCTGTGTTTTGAGTGAGAT
GTGCCCCCTAAGTCTTGTGTATTTGAATACTTGGCACTCACTTGGTGGCG
ATTTGGGAGGAATTAGGAGGTGTGGCCTTGGTGAAAAAGGAGCATCACTA
GGGTCAAGGTTTCAAAATCCTCCTGCCATCATCCCCAATATGTCTCTCT
GCCTCCTGCTTGCAGTTCAAGCTATGAGCTCTTAGTTACTACTTCCACCA
CCTACCCCTGCTATCTCTGCTCCATCATCATGGACTCCTATTCTGGTGGA
ACTGTTAGTCCAAAAAGTCCCTTCTTCTACAACCTTGATTGATGCCAGA
TCTAGCCCCCAGCCTAGCTAGCAATATACCAAGGTATACCATCTTGAAC

Fig. 3 B (5)

TCTAGGTGTCTCTCAATCCAATCAAGCTACATAAGATTAAACCATCATACC
TAGTCATCCCCAAATCAGTGTATCTCTCTCCTCCCAAGACTATAAGCTCC
TCAAGGGTCAAAATATGTAGAAAGGAAGAAAGATTCTCAAAGGTCAAGGA
TCAGACCTTGGTGAGGATTGAGCACTGTCTACACTTTGCCTGGTAAAGAA
GGGTCCACAATGTAAAAGAGAACTGACCTGAACAGTTTTCAATTAGGTGC
TAACAAATGTCTCATACGTATTGAGTTTCTTATAAAATAAATAAATAAATA
AATAAATAAATAAGCAAGCAAGCAAGCAAGCAAGCACTTAAGAGCACTAGCTGC
TTTCTTCTGAAGACCTGGTTTCAATTACCCAGCACTTATACAGAGGCTC
ATACCAATTGTAACTCCAGTTTGATGATATCCAACATCTTCTTCTAGCCT
TCAGACACCAAGCACCAAGCATGTAATGGTATAACACATGTATACCAAAC
ACCCATACAAACCAATTTTTTAAAAAATATTGAGCCGGCGTGGTGGCGC
ACGCCTTTAATCCCAGCACTCGGGAGACAGAGGCAGGTGGATTTCAGAGT
TCGAGGCCAGCGTGGTCTACAGAGTGAGTTCCAGGACAGCCAGGGCTGCA
CAGAGAAACCTGTCTCGAAAAACCAAAAAAAAAAAAAAAAAAAAAAAT
AGTCATTTTAGGGCTGGAGAGATGGCTCAGGGGTTAAGAGCACTGACTGT
TCTTCCAGAGGTCTTAGTTCAATATCCAGCAAGCACATGGTGGCTCACA
GCCATTTGTAAATGGGGATCCAATATCCCATTTCTGGTGTGTCTGAAGACAG
CTATAGTGTAATAAATAAAGAAATCATATAAATAAATAAATAAATCT
TTTTAAAAATATTAAATTAACCCAGGCTGAACCTAAACTTACAACTTCCC
ACATTAGGCTCTTTAATGCGGGTGTATAGGTCTGAATACCAGCTTAAGA
ATAATATTCTTCTGAAGAATGTGCCCTGGTCAATCACCATGACCACACCT
GCCAACAGGTCCCTCATAAAAATACTTGGTATATGTTGAATGTTCCATAAA
ATTATGGAGCTAGAAAAGGTAGTGAGCTAGAAGGATATTAAAGATATAAA
CCATTGCCCCAGTGGTCCCTCACATTTGTCTAGTAATAGAAGCTTGTAA
CTGTTTTTATTTAGAAATTTCAATATATAAAAGACAAATATGAAATAGTCC
GGAAGCAAATTAAGCTACAGCTTGCAGCAAAGCCAGATAGAATGCAGATT
AAACTAACACAGTACCTTTGTCTTATGTTTTAGATGCTAAAGTCTAGTCT
ACAACCCCAGCTGCCCTTGAACCTTTAGCAGTCTCTTGCCTTCAGGCTCT
CATGCTGCTAGGGTTAAAAGTATGTGCGACCACACACAGTTTTGAAGTTT
AGAGCACTTAAATGATCTATTTCAGCAACTCAGGCAGGATTTACACTGAAA
GTAAATTATCTTATGAATCCTTTTTGGTTTTCTTTTTATTCATTPCATTC
ATGCACCTTACATGAACTATCTATTGCTAGGCTGTCTCTATACTGGATGC
TCAGCACATCACCACATGCCGATTCTTCTACTGGTACAAATGGCAATGCT
GAGAAAACCAACAACTAAGACAGTAGGGAGGTGGTGTCTGATTGTTG
GTGTTGTTGTTGTTGTTGTTTTGGTTTTTCGAGACAGGGTTCTCTGTGT
AGCCCTGGCTGTCTAGAACTCACTCTGTAGACGGGCTGGCTCAAACCT
CAGAAATCCGCCTGCCTCTGCCTGCCAAGTGCTGGGATTAAAGGCGTGTG
CCACCACGCCGGGCTCTGGTGTCTGATTTTTTAAATACAACAATTTTCAG
CTAGCAATGTAACTCAGTAGTAAATGCCTGECACAGCATGCACAAGGCTC
CAGACTGGACCTGAGCACCAACACTTTTTTAAAAGATGTGTTTTTTTT

FIG. 3B(6)

ATTTTATGTGCATGAGTGTGCTTACATGAATGCTGCACTGTGTTTA
CCTGGTGCCTGTGAAGGTTAGAAGGCAATGGAGCTATGGAGAGTTGTAAA
CTACCATGTGGAAATGGAGCTATGGAGAGTTGTAACTACCATGTGGGTA
CTAGGAATTGAATCAGGGCACTCCTCTGCAAGAACAACAAAGGCTCTTAA
CAGCTAAAATATTACTACAAACCCACACCACAAAATTTTAAATTGATAGA
CATTATCACCTTAGTTCTAGATAGAGAATGTGCTTGGCATTGTAAGTACT
AAAAAGGTTTTGGGGTGGATCTTTTATATTATCTCACTATAATTTTATAA
AATTAATACTCAAATATGTTATAAGTTAAGGTTTTTATTTTGTGTTTTCA
TTTCTGTATTTTGTCTATGTAGCTCTGCCTGGCCTGAAACTCATGGGAAC
TTGACTGGCCTCAAACCTCAGAGAGACCTGAACGGCCCTGCCTCCAAAGAG
CTGGGACTAACCATGCCCAACAGTAGGTAGCTTTAATACCTAACCAGTGT
ATTAGTTTATGCTCTCAATTAACCAACATTCTCTACATACAGAAATTTTT
ATGCCTATTTAATCAAATACACAGTCTAAGTAACTCTAAGTACAACCTGC
TTGGCTCATATTTTACAATGGCTATGGCTAGCTAATTCAAAGGCCAGTC
ACATAAAAGGGTCTCTATGAATTCTGATTAAACAAATGCAGTTAAATAGAT
GAATTCCTAAAAGTAGTATCATAATAATATCATATTTAGTTTTTGTGCT
TCCATTATAGTTTGAGGTGCCTCCTCCATAATGCAAGGTATATTTCAA
TAATAGATATATACATGGTTAACACATGGCAAATGCCATTTTAAATGCTT
AGCACAGCCTGCTCTTTGGCTCCATTAAGTGAAACTCTTAAGTTCTCAGT
TAAAATAATTGTTGGAGAGCTATAGGAGCAATGGGTGGAGAACTAGTCTT
CTAATTTGTCTTTGCCTCCTTGCGTACTAAGTAGTCCCTCCCTCACTAT
GTGGCATTCCAGCAGACTACCACCAAGAGAAGAACAGAAAAGTGTGATT
TCTTTCTAAAGTAAAGAAATAAGGGGCCAGTGAGATACCTCAGCAGGTCA
AAGCCATTTGCCTAGAAACCAAAGTTCAATCCTTGGAAGCCCTGTAAAGG
TGGAATTAGAAAACAGACTCCACAAAACCTGTCTCTAACCTCCACTCGGG
CACACATGTGCCAACCCCTCCATTCTCCCTCCCCCACATACAAAGTAACA
ATAAACTTTTCAAAAAATTTAAGTTGCTACGCATGGTGATTGATGAATGTC
TTTAATTCTAGCTCTTGGAAGCAGAAGTGGGTGGATCTCTGTCTAGTTCA
AGACCAACCTGGTCTATATAGTGTGTTCCAGGCATCCAGGACTACACACA
CACACACAAAATTACGTGAAGGAAGTAGAATGTTTGAAGGAAAGAAGTCT
GGAAATGGGGATGGAGAGAGACCTCAGCAATTAAGAAAAGGTCTTGCACC
GGACGTGGTGGTGATGCCTTTAATCCCAGCACTCGGGAGGCAGAGGCAG
GCGGATTTCTGAGTTGAGGCCAGCCTGGTCTACAAAGTGAGTTCCAGGA
CAGCCAGGGCTACACAGAGAAAACCCAGTCTCGAAAAAACCAAAACCAAA
ACAGAAAACCAAGTATGATAGGTCAGGCAATTGGATCGAGACAGGACACTC
AAGATAGCTAGCCTGTGCAATATAGAAAGAAGTCTCATGGAAGAGAGAGG
GAAGGGAAGGAGGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA
GAGAGAGAGAGAGAATGAGAGCGAGAGAGCGAGCGCACCTCAGTTGATAC
AAGATTGGGGCCCTGAGTTCCATCCCCAGCATCCCATAAATTGGGTGTAG
CAGCACACACCTGTATCCCAGCAGAGAGGCAAAAGACAAGTTCAAAGTCC

FIG. 38 (7)

TATATGGAAAAAGTGTGAGATCAGCCTGGAGACCTGGTGTGTGGCAGTGG
GGTGAGGGGTGTCATCAAGGAGAAGGCTTAGTAAGTAAAGGACCTGCGTT
GGTTCTTGAGTTCAAGTCTCCAGCAATCAGAGAAAGCCAGAACCATTGCA
CAAACCTGTAAAGCCAAGTGTGGACTGGACAGAGACAGGCCAAATGTTTGA
GGTCCAGGTTTCAGTAAGAGACCCTATCTCAAAAAATCTGATGGAGAGTAA
CACTGGAAGAACTCAGAGTGAGTCACACATGCACACACAGGTGAATGTGT
ATACAAAGGGGGCAGGGAGGGAGAATGAGAGGAGACTGGGAGATATCTGT
AGTTCATGTCTGTAATTCTAGCACTTCAGAGGCAGCTGGAGCTACACAGC
AAGACCCCGTCTCAAAAACAAACCCAAAGCCTGACAGTGGTGAGGTACACC
TTTAAGCCCAGAGGCAGGAGAATCTCTGAGTTCAAGGGCAGCCTGAGTGA
GTTCCAGGACAACCAGGGCTCCACAAAGAAACACTGTCTTGAAAAAACC
AAAACCAACCAACAAAAAGAATCAAAAACAACCACCACCCTACAACA
AAGCAAACAAGGGAGAAGGTATAAAATGCTTAGGAGAGTCTTCCTTTAGT
CTCCATCCTTTGGGTACTCCTTCCCCACAGAAAGCCACTACTACCAATTT
CTTACATAAGCTGCTGTTTGTAGACACAGGTTTTTTTTTTTTTAAATATA
GTAACATATTTCATGTGTAGCTCATTTTCTAGTGAGTGGTTGGTCCTTCT
TTTAACAGTTTAAAGGACCTCTATGTTTAAAGGCGATTGGGCGCTGTCTG
GAGTATGGGTGTATTTTCCCAATTTGTGAGTTTACCCAACCTATTGCC
TATTACCTATGGCCATTTATTCTTGTGATAAGTAGTTTCCAATTGTATG
ACTATGGTCACAGTGTTCATGGACTCTCTGCGCTAGACAGCGCGTGG
GTCTGAATTTGAGATGGTTACAAGGGTGATTGGCTCTGCTCCCTGGGTGC
TGGGATTAAAGGCGTGACCTCCACACCCAATTTGTCTGTTTTGTAAAGA
AATGAGGTTTATTGTGTGTGCTCAGGCTGATCTCAGTCTCCTGGCCTCAA
GGTATCCTCCCATGTGATACACAGCACAAGGCGTAGGAAAAGTGGCAGA
TTTTTTTAAATTAAGTTTCTTTCCAAAATATAGATTTCAGAAATGTGAGA
TTTTTCACAAAGTGAACCTGCTCACTTCCCTGGCTCTMGAATCTCCATTGT
GGCTCCCGCCCATCCCTTTTGCCCAACAGTGGCTGTGTATTGACTTCTA
TCCCATTCCCTTAACATATACCTGTCTTGGTCTTGGCTGTGAACCTGCTTG
GGCTGAGAATCACCTGTTCGGGCACATCAGGTCACTGAGGGTGTTCCT
AGAGAGTTTTTAACAGAGACCAGAAGACCCACTCCAAATGTGGGPGGCAAT
ACCTGATGTCTGTCTATCCTGGACTGGGTAGGAAGAGGAAAGTAAGAAGC
AAACGGCACCCCACTCTCTGTCTGCTTCTCTGCGGACACAAAGTGACC
AGGGCCTCCCACTCCTGCCCCCTCAGCTAGAGACACTTGCTGCCATCTTT
CCAACCACTCTGAGACTGTGCTACTAACCCTGACCCAAAAATAAATGTTT
CCTTCTTAAGGTTGCGCTTTGTTAGCTCCTTTAATAGAGCGGTAGGACAT
GTAACGCCACAGGCAGGCATCGCTGCCAGCCCTCCCACTGACCGTCTG
AGAACCACACTCAGCTGTAGGCACAGCTCTCATAGCTGTGTGGCGGTAGC
TCTGTCTACTCGGTCAATCCCCCTGCTGCCGAGCATTTATTGTTTTCAGTT
CCTGGCTGATGGGTAGCACTGTATGAACATCCTAGTACAAATCTCAGGG
TGACACGGCGCTTCATTTTCTCTGAGAAAATGGCCAAGGATAAAATGCTA

FIG. 3B (8)

GGGCCAAGGGAAGAATATTTACCATTAAGAGACACTGGTCAGGACTGGA
AAGATGGCCCAGTGGTTAAGAGCACTGACTACTCTTCCAGAGGTCCTGAG
TTCAATTCTCAGCAACCACATGGTGGCTCACAACCATCTGTAATGGGATC
CAATGTCCTCTTCTGGTGTGTCTGAAGACAGTGACAGTGTAACCTACATAC
ATGAAATAAATAAAATAAATATCTGAGAGAGACAGACAGACAGACTGGC
TAGTCATCTCACAATGTTCTCATGTTTAAATATGATACCATTGTATATA
AGCAGAAACACAGGAAAAATAAAATCTGTGGTATTATATTTGATTTTAA
ATTAACCTGATTAGTGAAGTTAGCAGCTACACTGGGCAGGGGTGGGAGT
GGGGTACTCTGAAGTGCTGGTATTTCTGGTTTTGTMTTGTGTTGTTGT
TTTTTTATCTTATTTATATTACATAGAAAGCCATTTTGCTAATACACTTA
CCATGTGTATATATTGTGCTTGAATTACAGCTAAGTAATTATTTCTGAGG
GGCTTTAGACTACTGAAGATTGGGCCCCAATGAGCCCCACCCCAAGTAGTC
TCCAACATCCCTCTTGGAAGTACTTGAGAGCAAAGATTCAAGTCACATGT
CCCCAAACCCCTCAGCAGCCACCACCCTTTAGGTGTGGCTTTTGCTCTCGG
TCATCCTGGAACATCTTGCCATCTTTGGTTTGTCTCTCCCTGTCTTGCC
TCTGGTAGAGCTGGGTTCTGTGCTTCTATTCAACCATGTACAAGAACCA
TGTGCCACCTGCCATGTGCCAAGCCTGTGCCAGTCCCTGTGAGCGAGCAG
CCCACCCCGTGAGTTATCATGTGAGGAGCTATGAGGAGCAGGAAGGGGCC
CGGATGACTTCAGCAGACAGTATGAAGCAAGCACTGTGCGATTTATGCTC
CCTGGCCACATGCCACAGATGGTGTCTGAGACACTAGCGTTTAATATTT
GAATTCTCCACATTCTAGCCTAGACATTTTGGTTGCAAGAAGAAAATTGA
CTCCAGTTGTATCCTGGAATGAAATTTATTGGAGGAAAATACTGGACAGG
CTCCAGAGAAAATACGATATTTCAGGCACAAAAAGAAATGGGGACTGAGG
ATCTGAAGTTCAAGGTCATCTGTAATGAGATTGAAGTCAGTTTGGGCTAC
ATGGGACCTGGTCTAGGGGGAATGGGGAAGAGAAGGGAAGGGATCGAGAT
AGGGAT

FIG. 3B(9)

CAATGTGCTCTGACGATTAATGGGCTAGAAATGTGTGGCTGTTGATTAGT
GAAAAGATGTCATGGTTCAGGAGATTGGTAGTCTCTGTGGGAAGACAAC
CACTGAAAGGGAGGAAATAGCCTGGAAGAGATAAAGAGACAGTGATCAGC
TAGGAAGCTTAAAATTTAAATTTTGTGGAAAGTACTGTTAGGAATACTAG
CAGAGGCCAGATGAATGTATGGTTAAGTTATAGCAAAGGAAAAGATTGTT
AATGGTGAGGTTAGGAATGCAGGGTGACACCAAGCTGTAATGTCAGCATT
AGCGAGATAGAAGCAGGTGTTTAAGGCCATTCTCTGCTACTTAGCAAGTT
GAGGCCAATCTGGACCACATGAGACCTTTTTTCAAAAATAAATCTCCTTA
AACAAAAGAGGCTGGGTTTTTTTGATAGATTCTTCAAGATGTTAATGTAAA
TAAATGGAAGACCAAGGATGGCATGCTAATATCCTCAGTGTCTGAAGAAG
GACTATGTAGTGTGGCTGCTGACTCTGAAGTAAGTGCTCATTACTGACA
GATAGTGTATCTTAGAGCCTGGCAGATGGGATGGAAGTGAGGAAGCAAGT
AGCACCTTTGTATATTATGTTCTAAGTAGCCAGAGATACTTGACACAAA
CAAAGTTGAGAAAATGTATCTTCTAGAAAATACAGACATGGAAGGTGTC
CTTCTATATAAAGAGGTATTAAACATTAACTGAAAAAAAAGTTAGCAA
TTGGGCTTTGGCAAATGAATATAGTCAAGTTTCATTTTTATTTTGTTTTT
TGTATATGACTGTTTGGCTTGTGTACCATGTGTGTTCCTGGTGCCTAGG
AAGTCAGCTGGAGTTACAGATGGTGTGAGTTGCCATGTGGGTGCTGAGAG
ATGAACCTAGGTCCTCTGGAAGAGCAGTTAGTGCTCTTAACCACTGAGCC
ATCTCTCTAGTTCTCTGTAGAATTTTCATTAATTTACAAAGGAGAAAAG
TATAAATGATAAAACCATGAGAAGATAGACCGGCACTAGAATTAGTGGAG
TCAAAATGTTAATGATATGTCAGATACGCCTTATATGAGGAAGTTGCAA
ATTATGAAAATCCAGGCACTCCACTGAGTTAGAAATCTAGGCTCTGATGC
ATACTGCTATGGTAAGGTAGCAAGTGGCCATTGAGTGCAGAAGTGAGTCT
GGATGGGTCTTCTGGTGTGTGGAGCACACAGACTGCTGTCTTCTGCATT
GCAGTTTCACCTGTATTTCCCTTGGAACTACTTAGCTTTGCAACTAGGCGT
TAAAAAAAACCTTTATATTTATGGTTTTAAGTTATTTATTTGTTTTATTTT
ATTTTATGAGACATAGTCTCACTCTCTAACCTAGGCTGGCCTGGAACGTC
CTAGGTAACCTGAGCTGGTGATTCTCTTGCCATAGCCTTCTAAAATTTTA
GATTGCAGGCATAAGCCAGACCACTCCTGACTTTTGTAGCCATTTTTCTG
ACATGAAGTGTAACCTTTGCTTTTCATAACTAAAATGATTTAGTTGTTTTGT
TATTGTTTAATCCCTTTTGCTTTGAATGTATCTTTTGTGTGGGTGGCAG
ATATATAACCACAGACTTTTCCACAGGCATCCTACCTAGGTCCAGAAAT
GACTCTGAGACGTCCTATATATGAATGAATGCTAGGCCAATAGCTTTGG
CTGATTTCCACGGGTCATAGCTCAGTTATCCATTATAAAGTAGTCTAAG
TCATGCCATGAGGCTACATAOCCCTCCTTCAGTTTCAGGCGACTGTCTTC
TCAGTTGTGTAATGTCTATCCTCTGTTGCTGCTGCCCCAAGCGGCATGCT

FIG. 3C (1)

TGCGTCATAGTCCGTCGTCTCGTCTCCCCCATTTACTTGCACAACGG
ACTCTACTCTAGAAGTCCTCTCTGTGCTGGAGCTTGCACCTCCGCTCTCC
CCGTCTAAGCTAATAGGCAACAGCATTGTACAGACAGGTGATGCTTCCAT
ACATCGCACAGGAGATTCTCCCTACACAGATACTTATTTCATCCAGCGTGA
ATGCAACCGTCCAGGCGTGTCTCTCTAGTTGTAGTACATGCTGTTGTATC
AGTCTGATGAATTTCTTTGTCTTTACAACCAAGAAAGATAATACTGTAAG
AAATTTTGACTAACATTTTCTTTTATTATAAATTACAGACTAACTGGCTC
TTCTGGATTTGTAAAGATGGACCTGGGAATTATAAATATAAGACGAAGT
GCACATGGCTCATTGAAGGACAGTAAGTTATAATGGCTGACTTTATTTTA
ATTTATTATAAGAGCACAGTATAGCACAAAATACTTCCATGTGTGTTATT
GCTATTTCTTGAGACAGGACCTTTCTGACTGAGTAACTCAGGCTGACCTT
GAATTTTGCTATGCTACCTCTGCTTCCCAAGTGCTAGGGTGGTAGGTGTG
GACCACCATGCCCTGCTGCTAAAATACCGTTCATTGATGCTTTTCATTTG
GATAGTGTCTTGCTTTTTTAAAATTTACTTTTTGGGGGACAGAGAGATG
GCTCAGTGGGTAAAGTGCTTGCTGAACAAGTCTGGTTATGTGAGTTAATC
CCTGGCTCCACAGTGGAGAGTGACTCCTGAAAGTTGTCTTCTGACTCC
CACGCTTGTCATGCACGCACACACACAAAATAATAAAATAAAAAATTAAA
AGGAAATTTCTTTTTTGGGTGATAGGGATTGAACCTATGACTTCACTAA
GCAAGTGCTCTATTGTTAAATAATTCCTTTAATTGTGGGTTTTTTTTTT
TTAGGTTCCAAGTTGACTTAATGTTATAAATGAAAGATACATACCAGAAA
TTTGCAATTTCTAATAGTTTAAAAAACTTAGTTAAATCTTTTAAATAG
TTTGCTTAAATCTTTATATAATAATGCTATTATATCATTTTTCTAAATAT
TGATTTTATTATCAGCAAAACAGTAAATGAGCCATCAGAATAACCACTGT
AGCCTGTTTCCCTGGCCCTCTGTCTTCCATCTGTCTATCTCTCTTTTT
TTTCTTTTTTGTGCCCTGTCATTTAGGGCAAAGCATTTTAGTCTCTGAAC
AAAATTTGAAATTTCCAAGTAACTCTTGTTTATTGTTGTGCTCATAT
TCAACCCAAGAAATATTATTTACTAACTCATTTAAAAGCAACAATTATAA
CCCCTACATGTTAGCAGAAAAACCTATTGTTTTTATTGAGACGGGATC
ACACTAGTAAGCACTACATGGCATGGCGTTCACTGTGTAGATCAGGCAGG
CTGGCTTCGTGCTCTTGACAGTCCCTCTGTGTTTGTCTCTCACTTCTGAG
TGCTGGGATTATAGACATTACCAACACACCGATTGTTTTGGGGGGTTGGGTAC
TGGGATCAGTCCAGAGTTGCATGGATGCTAGGCAAGCACTCCACCAACTT
AGCTATATCCCTGGTCATAAATGTCATAAGGAAAAAAATTCCTTATATTT
AAAGAAATTTAAGAATTGCATTGTTTAAAGATTTCACAGATCTCTTTGCT
ATCTGGCAATCTTTTTGATATTTTGTGTTTTTAAAAATATGTGGTA
TGTAACAACCTTAAATATGAATGGGACAGTTCCAGATGAGAGTGAAAAG
TTAAATATTTGGGAGAAAAATTGATAGGTTTATCTATTATGGAAAAATTC
AGAGATTTTAGTAAAAATTTGAAAAATGGAGCTGGGAGGTCTGAGGTAGTCA
TCTAAAGCTGCCAGTTGTAGAGCGTGTGGAGTGTGGAGTCAGAGGGAGT
TACTGATACACTTGTTGAAATTGCCAGGCTTCATGGGAAGTGATGAGGG

FIG. 3C(2)

GCTGTTACTGTGACTCTGGGCAGGGCTTGTTAGTTTCCTTTGGATTAGT
CTCAGTCAGAGTTGATACATAGTTTCTGAGGACGTGGCTTTTGGTACA
GTGCTGTGAAAAGGCAGAGAAGCAGGTAACTTAGAAAAATGTGTGTTTT
AAAGTGATGTGTTATGAAATCTTACGTAAGATGAATAAAGAAAGAAGTGG
GGACACTGAGGGCTCCTGTTTCTAAATGTTAAAAGCAAGGCTGGAAACAT
TCTTTGAAGGCCCCCTGAAGTCAGAGCCCGTGTCTCTTTTGGTTCCCAGGA
CATTTTTGATATTCCCTTACACATAGCAAATACTAAGTAGATCTCTGACA
AATGCAGGAAAGCTGTTTATATTTATATATATTTATATTGTATATTTTC
TCCTTATAAATCTTTAAAAGTCTGTTTATAGTAGTTAATGTTATGATTAT
TATAAATTACTTAATTATTTTTCTAGGCCAAATAGAATAATGAGACTTCG
CTTCAACCATTTTGCTACAGAATGTAGCTGGGACCATTATATGTTTATG
ATGGGGACTCAATCTACGCACCTCTGATTGCTGCCTTTAGGTAAGCCCTG
CTGCATTTTCATCTCAGGAAGTAAGTGTGTCTCCAGGATGGAGTCCGTGCT
GCATTTACTTTATCTGCAGTCACACTCATCTCATGGAATTAGTTCTGTT
CTGGTGAGCTACAGTTCACTTGGTTTTTATGTACTGGGTGCTTTTCCATB
TATACTAGTATGTAGCCACGGTTAGTCTTGAACCTCTGGTTCCTGCCT
CCACCTTCCAAGTGCTAGGAGTATAGGCTTGTGCCACTGTGCCTGACTCA
TTTCACATTCTTGAACGTGGAAGTTTGTAAACACTATTAAATTTAAGCTG
CTATTTGTGATTTTGTAAAGTTTGCATTAAAAAGTTTTTGACTATATTG
ATAATATTTTTGTGACAAATTTAAATCAGAAAGCATACCTTTCTGTCT
TGTATGTATTTCAATCCATAGGCCCTTAGGAATAACTTTTTTCAATAGTA
TATAGTTCTCTCAGTTTGTATATATGTATTATTAGGGATAGGAGGAGCTT
TCTGGAAGACTATTTATAAATTGGACAATGGCTAGCTGTTGAGAGTGAGG
AATTTGCTAGTTTGTTTTTGTAAATCCCTCCCCAATGCATCTGTATTAGT
GATTTAATAAAATAATGCAATTTTGTCTAGTTATATGGGTTGCACGAAAT
TTTGCTATTTTATTTTAAAGAAAGATTTTGTGTGTCTACAGTGTATATGA
GTGTATGATATGTGTGCGTGTGCATGTGTGTGTACTTCTATGCAGGTA
CTCACATGCTATGGTGTGCACGTAAGGTTGGAGTGCAGCCTCACATGTTG
ATCATTATATTCACCTTGTTAGAGATAGGTTGTCTTTGTGTGTTTGTCTG
GGCCTGGAGCTGGAGCTGGAGCTAACGAGTCTCAGCCACCTGACATGGGT
ACTGGGAACCAAGAGCAGCAAGACCTCTTCTTCTTCTTCTTTTTTCA
TTTTCGGTTTTTTCAAGACAGGGTTTTCTCTGTATAGCCCTGGCTGTCTGG
AACTCACTCTGTAGACCAGGCTGGCCTCGAACTCAGAAATCTGCCTGCCT
CTGCCTCCCAAATGCTGGGATTAAAGGTGTGTGTCACCACCAGCCAGCCT
AAAAGATTTTCTTACTAAAATATATTTCTAAATTAATTAGTTGGAATCTG
GTTTCATACTTCTTTTTGAAACAAAACAGCATTTTTTTTTCACTCTACATA
CAGAGACATTGACACTAGACACTGGTTATGAGTAGTTACTATAAGAATGG
GAAATTATCCACCCCTGTAAACCTTAATACAACCTTATCAGGCTCTG
AAGACTTTTTAAAAGCAAGAATTGTATATAACACACAGAAATGATTTAGA
CTATTTAGATCTTTATGTCATGGGATTTTAAAATTAATTATTGTATTTCTG

FIG. 3C(3)

GGGCATGTTTGTCTATGTAGCATATGTGCCTGTAGAGGCAACCACCAAG
TAGGTCCTGGGAATCAAACCTGGTACCCCTGCTCTTAGGTGTTCTTAACT
GCTGAGCCATCTCTCCAGTCCTC

FIG. 3C(4)

AGGCAAGAAAGAGCCAGCGAGCCTCCAGACAGACCATTAGAAATTCCACA
GTCAGCACAAATAGGGAGAACAGTAAATCTTACATTAAAAGAAGGCCAGGG
CCTGGTAGCAAAAGGTTTTAATTTAAGCACTTGAGAGGGAGAGGAGGCAA
ATCTCTCTGATTGGGGGTTGGGGTTAATGGTGAATGCCATGACACCCCTGC
TCAGAGTTAGCCTTCTCCCCCTAAAAAATTTTAAATTCATTTTCAATGCT
GACACAGTTAATCATAGACATTGTATCTCAGACACCTCAACATACTCCAG
ACTGCAGCACCAGCCCACTGCTGAGGCTGTCGTTTCAGTTGGTAGAAGGCA
TGCTCAGCATTCGCGAAGCACCAGACTTCATCCTTAGCACTACATAAAAC
TGGGTGTGGTCATGCACACTTATAACTTCAGCACCATGGAGGCAGAGGCA
GGATGATGAGAACTTGAGGATCATTCTCAGTTACATAGGGAGTTTGAGGT
TAAGCAGGGGTACAGGAGGCCTGTCTCAAACAAACAGACAAACAGACAAA
CAAACAACTTCAAAAACTCTTGAAGTACTAGGCCTAGTACGTGCTGAG
ATTGTAGGTATATGTCATCATGCCCTGTTGTAGAAATGAGTGAGAGCGGACT
CCATAGGCTTATAGATTGGAATCTTGGTGTCTGTCTATGTCATGTCATCC
CTGCACAAAAGCCACACTAGGCCACACATTCCTCTCTGTCTGCTGCATG
TGGGTAGATGTGAGCTCTCAGCTGCTGCTCCAGTGCCATGCCCTGCCCTGC
TGCCAGGCTCCAGCCATGACGGTCAGGGACTAACTCTCTGAAACTGTAAAC
CAAGTTCCTCAATGAAATGCTTTCTTTTATAAGTTGCCTTGGTCATGGTGT
CTGCTTCACAGCAATAACACGGTGACTAAGATACCTGGCTCCTCCCTCC
CCACCCACCATTATTTACCATAAAGTAAACAATACACAGTTGGATAACA
TGATACTGAAGTTATTTTCTGTCTTCTCTGATGTAACCCAATTTTGGACAA
GATTAAGCCTTAAATAGCAAGCTGTGAGGCAGGATAAAGAAAAAGCTGGC
AGGCCAATGTCTGCTTTACCAAATTCGTTCAGCAGTCTAAAGCTGCCGT
CACCTCGACTCCTGTGATGGCATTTCATCACTATCTTAGATATTCCCTG
GGTCACAACCTTTTAGTACACAGATTGCAACTCTGATGGAATGGCTGACT
GCTTGGCTAATTAAAGCAAGCTAGAGTTTGTCTGGCTTCCTTGTCTGAAT
GGGGAGGTGGTATTTACAAAATTTTGTAATAAACTACTATATTTGCATG
ATGTATATAAATTTGATGTGGCTGCTTTTAAATCATTTAACCTAAACTGT
CCCACAGAAATCATCTGTTTGATTGGAAAGATTGTAGCTTCAAGAGAATTT
CTGCTGAACCTGAAATGATTATAATGATGTGTCTGAAGAATGTGTGCTA
TCACCTACGGTTTTTGTTTTTAGTTGATATTTGTACTTTAAGATTTCTTT
ATGTATGTGTGTGTGTGTGTATTTATGTGAATGTATACCTCATGTATGTG
GTGCTCAAGGACACCTGAAGAAGGGCTCTGGAGCTGGAGTTACAGGGAGT
TGTGAGTGCTAGGAAAGAAAGCTGGGTACACTGGGAAATCAAAAGGTGCT
TCTAACCCTGAGAAATCCTGCCAGCCCCCTGGTTTATTAAAAATATCAA
ACAAAACCAACACTAGTTACATAAGTATCTCTCTCTCTCTCTCTCTCTCT
TTCTTTCTCTCTCTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
CACACACACACACACACACACACAAAGGATCCATAATAGTTCTTCTGT
ATCCCGGTAAATATAAGTTCTTAGGGGCTAGAGAGATGGCTCAGCAGTT
AAGAGTGCTTGTGTCTTCCAGAGGACCCAAGTTCAGATCCTAGTACAC
ACATCAGGCAGCTCACAGCTACCCATATCTCCAGCTCCAGGAAGAACCAA
TCAATGCCTATGGCCCATGCAAGCACCAGCACATATGCTCCACAAACA
TCCATATATATAGCTAAAAGTAATAAAATAAATCTTCAAAAAATTAATT
CTGGTTGAACTGAAAAAGATCACCTAACATTTAGAAAAAGCAGTTTACTA
GTGAATAGGACATAAATCATGGTATCAAATATTCTGTTGTTAAAGGAAGC
AACTAGAAAAAGCATGTGTTTGAAATAACCAATGGATACAAAACAAATGA

FIG. 3D(1)

GGCAACCCCAACATCTGTCAGTACCTTGCAAACCAACACAATAAATTTGA
TTTTATTTTAAATCGTAGTTATTTTCATGCTAGTAGTTTGAACACAAT
AAATTTGATTTTATTAAATCGTAGTTATTTTCATGCTAGTAGTTTGA
AACCAAGATCTAGATTTTGTATAGCCACATAAATACACATTAGAATTGCA
AACTGATACGAGCTTCATCTTCATCAGTCTCTCTTCATGAAAAGCAGTTA
CAGGGACTGAGACATGACTCAGCAGTTACGGCATGGGCTGTTCTTCCATA
CGACATGGATTCAATTCCTCAGTGCCCAAATGTTGGCTCACAACCATTGT
AACTCTGGTCCCAGGGGATCTGACACTCTTCTTGGCTTCTATGGCCACTG
TATTCATACGGTACACAGACACATATGCAGGCCAAACTCAACAAAAAAA
TAAGGTTTAAAAAAAAGAATTAGAACTTAAAGGCACTTCATTCCGTCAGC
ACTAAATCAGCCTCTCTGGAGTCTTCCCACCTTCATGAGAAAATCGTCAGC
TCTCCACTGCTGTCTGTGGCTGAGGAGCAGGACCTGGACAACGTTTCAGAG
ATTGTCAGTGCATCTCTTTTCTTCTTTGGTTTGTCTGTCATCAGGTTCACT
GTCACATTCCTTTTGTACCATCCTTCCTTTAACAGCCTTTTGAAAATGCA
GAAATGTTGGATGCTGCCTTCAGTTCACACAGGCTGTCTTTTAGCTCCT
CATCTATCTATGCTTAATTTGTTAGTGGTGCTCACCATGTATGTGTTA
TGTCATGAAGCCACAAGATGAGCCTTGATTGAGTCTTGCTGTCAGTGTGG
ATCACAGAAATGACACCCTATCATCTTTGCTTCCTGCTTGTAGAAAGTCA
TTGATTCTGCTTATACTCAAGGCCACAGTATTATACCTGGGTGTGAACC
CCAGGAAGCAGGGAGGTGGGGGGTGTCTATGGATACTACTCAGATATCTGA
CTGTTGTGATATTTTCATCAGTCTTCATTGGTCTCTATCTTTAAATCTGCC
CTACATCTAGAGCTGGCTGTGGTGGTGTGTGGTGGCATCAGTATCAGT
ACTTGGATTACAGAGGCAGGAAGATTGTGATTTTGGAGGCCAGAATAGGT
GCATACAAAGATCCTGTCTGCAAAAGAAACAAATGTGCAATAATTATAA
CTACTTTACTAATAGCCTAACTAATAACCACTGCTAGTGCTGTGTCCACG
AAAAGGTGAAGTAACTGTGAAAATGACTTCCCCTTCTGTGTGACACACG
CCGTCATGTGATTTTACTTGTGTCTCATCATTTGTTTCTCTTCTGTTTGC
ATGTGTGAATGTTTACATGTGGAAGCCAGAAGTCAGTGTGAGTGTCTTC
ATAATTGATCTCTATTCTCTTTGTTTGTGAGACAGGGTTTGTGAGACTAAGC
CCAGTGCTCAGTGATTTCATCCAGTAACTGTAGGGAGCTTCCTGTCTCTG
CCTCCACAGTGTGGGATTACAAGCATGATCCAAATTATGTGACAAGCGC
TTTACTAACTTAGCCATGTCTCAGCTCCCCACTCCCCTTTTCTTTCTT
CTTCTTTTCTTAGACTTACTTGTATTATTTTATGAATGTCTTGCCGTGCA
TGCATACATGC
AAGCAATTCCAGAAGAGGGCATTGAATCCCTGAAACTGGAGTTCCAGTTA
ACTGTGAGCCTGTCTATGTGCGTACTGGGAGCTAAATCCGGGTCTCTGGA
AGGTCAGCAAGGTCTTACCTGGGAGCCGTCTCTTAGCTCATGTGTTTCT
CTCTTGAAGCAAGAACTTAGGAATCATTTTGAAACTTCTTCACAGCCT
TTATCATAACTTCACGTCAATTTTACCTACTCTTCAACAAATACATGT
TATATTTACTTATTTTATGTTTAGCCTGCTATTGGTTTCTACTTAGCCT
CTTGCAGTAGAGTTCTGTGAGATTTATGTTTCTATTGCTTTTAAATTTATT
TGTAAGGTGAATGGGAAAATATTTAAAAATTACAGATCCCATCATTTAC
TATATTCTTAAAGCCATGGCTAGCCAGGCTTGGTTGTGATGCTTGTAC
TCCCAGGACTCTGACAACTCAGTAAGGAGGAGAGTGAATCAGAAAATAGC
GCCAGCCTGTGCTGCTTAGCAAGAAACAGAAACAAGTACAATCACACACA
TAGAAAATCCCCCATTAATACCATCCCATTAGATATAATGGTCTGTATG
ACCATTCACCACTGTTTGTCTCTGTACTGCAGTAACAGTCTTCTGCCC
TTGCCCCGTGAAGCACGTGCGCACCCCGCCTCCAAGTGCTTTTGCAGTGGT
GTCTTCCGTCTAGATGTCTGTACTATATGTAAGGACTGGTTTCTCCTC
CTCTTTACAGTTCAATCTAATTGTCTCATGAAAAGATCTTTCCTGACCAT

FIG. 3D(2)

CTGGTTCAGACAGGTTCTCCCTGTTGTTGTTTGTGTTTTTGTGTTTTATAGT
TCTAAATTCCTTTCAGGAACCTTTTGCTTATTTTAAATTCCTTGAGTGCAT
ACGTGTGCTTGTGTTGCTCATGCTCGTTGTTTGGGCTTACTTTACTATC
AGCTCTGGATGTGGTTCACAGAAGGTGCTCAGGGGAGCACTCTCAGCCAC
TCATCTCACACGGGTTATAGATATATGTATTGATGCTACGTTTGCTTGTC
AGCCATGTTTTAAAGATTAGAATATCTTTTCTATGTGTACTCTATCAAAA
CACATGTTAGGGCTTTATCTATTTTATACAGATATTGGTGTCTTGCTTT
ACTAATTTTCATGGAATTTTCGGTGAATATTAGTATTTTAGATAGGAAGAC
TTGTCTCAAAATGTAGCTCAGCTGGTTGAGTGCCTGCCTGCATGTAGAAA
GCCCTGTATTCACTCTCCAGCACCTCAGAAGTGGGCCATGGTGCATATGC
TGTCATCTCAGCACTCCGGAGGGAGAGAAAAGAGAATCTGGAGTTCAAGG
TTATCCTTGGCTATATAACAAGTCCAAGATCAGCCTGGGCTACATGGCAT
CCTGCCTCAAAATCAAACACCAAATCAAAAAGCTCACATCTTGATCCAAA
AGAAGGTAGAGAGAATACACTGGGAAAGTCTTTGAAACCTCAAAGCTAAC
TCCAAGTGACAGTGACACCTCCTTAGCAGGGCCATAAATTCATCCTTC
CCCAAAGCCCACCAACTGGAGACCAAGTATTCAAAGATAAGAATCTATGC
AGTCCATTCTCCTTCAAACCTACCACAGTAGGTTTTCTTAAAAAAGAAAA
AAGAATATTTAATTGATTGTGATTATTCAGTATTATTATGAATAATCA
TGAACCTACATGGCAGGACTATAAACTATTATTTTAAAGATTTATTT
ATTTATTTTATGTATGTGAGTACACTGTAGCTGTCTTCAGACACACCAGA
AGAGAGCATCAAATCCCATTACAGATGGTTGTGAGCCACCAAGTGGTTC
TGGGAATTGAACTCAGGACCTCTGGAAGAACAGTCAGTTCTCTTAACCAC
TAAGCCATCTCTCCAGCCCCCTATAAACTATTATTATTTATAAAATATA
AATCCGTGAGTCTGTGCACCCCTGTGTGCACATGGATGGGACATCTTTGA
ACTGGATTATATCATACTTAGAAGAATACAAGATACTCTGTTTTGTCAAT
TGGGTGAAAATATGGTCTGTTTTATTTTGCAGGTATGACCTGACTTCTAGG
GAATGGCTTCCACTAAACCATTCTGTGAACAGTGTGGTTGTAAGATATGG
TCATTCTTTGGCATTACATAAGGTAAACTATCTCAACTCTTCACCAAGCA
AGAAGTTCAACTCTTCCTGTTGCTTTATGTCAATTGAATACTATCGAGCTT
TGGTTTTAGTTGGTATAAGCTTTGTTTTGATGTCAATGAGGTATATAATT
CACCAAGTTGTCACCAAGTTGTAATTGGAAATTGAAGTTAGAACGATTTT
AATCCATGGTGTCTTGCATTTGGATACTCTGATCACAGTTAACAATGAAG
ATTAAATAGTGTGAGCAAGCCTATGCCATTATCAAGTCTAGCATACTGC
ATGCGTGTGACTGAGTAGCCATTGTTATCTCCTTGTTTTGAGCGTATATT
GTAGAATGAGGCAACTGTATTTTCCACACCATTTTTCGTTCTGTAACACGT
TTCATGTAGAGAAGGTGATTTAGAGAGGGGAAGAATGTGATTGTATTGGT
TGGTTCTTTCTCTATGCTATTTCTAGCAAGTCACCGAAGAGCTCATGTTA
CTCACACTTCTTAAGCTGGGATCACAATGAGATTGTGAACCACTCATTGT
TGTTTTCCAATATAAATTTTAAAAAGATGTATTTATTTTATTTTATGTG
TGTGGGTGTTTTGCCTGCATGTATGCCTGTGTATACTGTTCCCTECAGAGG
TCAGAAGAGGATGGCATCAGAACTGGTGGCTGTTAGCTGCCATGTGGGTA
CTAGGAACATAAACC CGGGTCTCTGCAAGAGCAGCAAGTGTTCATAAACT
CTCTCTCCAGCCCTAGAGTTGATTTCTTAATGGTTTTAAAAATCCTGTTT
ACATCTTTCTTATAGGATAAAATCTACATGTATGGAGGAAAAATTGATTC
AACAGGGAACGTGACCAATGAGCTGAGAGTATTTTCATATTCATAATGAAT
CATGGGTATTGTAACTCCGAAAGCTAAGGATCAGTATGCAGTGGTTGGA
CACTCAGCACACATTTGTACACTGGCATCTGGCGGTGTGGTCATGTTGGT
CATCTTCGGTCATTGCCCACTCTATGGATATATAAGCGTTGTGCAGGAAT
ATGACTTGGGTATGTATTTTTCAGTGGAGGCATCTTGAATATCATACT
GAGAACCCTGCCCTTATTATTAGGACACCGTAACAAAATTCAGCATGAT

FIG. 3D(3)

CTTGATCCAGTACCTTGTCTTGAAATAGTATCAGTAGATAACTGGTGAGA
TTGAGGTTGTTGAAGTCCCTGTGCAACAGCTGTTTCTTACTTGTCAAGGT
CTAGTCTTGGCTTGGGAGGGGTCTGAGGAAAGGGGTGTCAAAAAACCCA
AAAAGTCCAATTGTAGGTCCAAGCTGGCAGCTGTATATTGCATTAAGGAA
AGCTGAGGGAAATTTGGGATATTTATTTTCATCTATTAGTCTACATCAAGC
AAGTCAAGCGCTCACAGTCAACGTTTGCACCCTCAAATTAGTAACAAAAG
AGGGGGAAGTGAAGAGTCCAGCATGGTCTTGGTGGGACAGAATGACATG
GTTCCAGCCCTGAGACAGGGGCAGCAGGTCCGGGCCTCCATGGATGTCAC
ACTATGGACATAAACCTGTTTGTATAATAATGTACATATTTTCATGCTCCT
CTTCTGAGTAATGTCTTCTGTTAATGTGAATGACTTCATGATAATCAGA
GCCAGTGTGAGTCTGGGAAGTAAATGGTGGGACCTTCAGGACAGCTCTTA
AGGCTGTGGAAGAAGACATGAGTTCAAAACCATATACTTCCTCAACTATA
CAAAAATAGAAGGATGCAATATGAATTGTATGAGGGGCTTCACAGATCTA
AAGGAACAAAAGCAGCTTCGCTGTGAGCCAACTTGTGAGAAAGATATTGA
GTAAGCAGTTAAAGAGATTTAGGGAGTGCTGATTGCTAGAGGAGGCCACC
CAGCTAAGTTTGTGCTTACAAAGGCAGACAAAGTCTGAGTTCAGGGTGG
GCCTGGAACAGAGCAAGGTTAGTTAGACCTTGGTGTGGTAGAAATGGTAA
TTTCCAGACAGGATACCCAACTAGTTTGTGCTTAAACAGAGGCAGGTAG
ATCTCTGAATCTTTTGTAAATGTTAAAGGAAATGTGTGCTTGTGTCTC
CCAAGGGGCCTGAGTCCCAGGATGCTGATTTATAGGAAACCTGGAGTAAC
TGGGTTTATGACCTGCAGGAGACGAGCTATCCAGAATGTTTTTTGCAATA
GCAAGAGAGAACTGCCTGGAGAACTGCCTTCAGCAAAGAATAGCAAGAGA
AAGCTGTCTAGAGAGAGAGCTGTCTGTAGAGAAAGCCGGTCAGAGAGAAA
GTAGACTGGAAAACCTGTCTCCAGCTTGGACCCACAATTTGACTTTTTGTT
TTTGTGACAAGTTGCCCTCCCCCAGAAACACCTTCCTCAGGACCCCTCC
CAAGCCAAGGCAGGGCCTTGGCCCTTCTTGTGACCTTGCAAGGAGCCAAA
GATAGCATTAAATGCTTTGGATATCAAAATAAGCAAAATGCAAAACAGTA
AACACTCTAAATAAATCTGGCTAGTCCCTTAAATATTAGGCCAGTGCAC
TGTTATTTTACCTTAATGTATAATCTTGTGTTACATTTTATTGTTTTAT
TGTATAATAGGAATGTCAGAATTATAATTTGTAAACATTTGTTTGACATT
CCTGTGAAAATGCATCTAAAGATCATTAAAGTGCATCTGAAGATCATAAG
GACTCACTGAGGAGCACAGGGAATTAAGTGTCTGCTTAAGAGAACTTGA
ATCTTTAATCTTTAGAATTTGTTTAAATAATTTGAATCTTGCCAGTGTGG
TGGCGCATCCCTTTGGTCCCAGCACTCAAGGGGCAGAGGCAGGTGTATCT
CCATTAGTGTGAGGCCAGCCTGGTCTACAGAGCAAGTTCAGGCCAGGCA
GGGTACACAGAGAAACCTAGCTTAACAAAACAAAACAAATATGAATCT
TTAAAACTTGTCTGTGAAAATTTTCATACATGTATACAATATAGCTTGT
TCATATCCACCGCCATTCCCTCCAGCTCCTCTAGGCTTTCCAGTGCATC
TCCTTCCTAGCCTTATGGCCTCCCTTTTCAGGGTGAAGGTTAGCACACTGA
GTCCAGTTAGTGTGATCCGATGCAGTCTTGTCTAGATGGTCTTCTTTAT
AATAAGGTGAAAGTATATCCTAAACTTCCGTCTTTTGTCTAAGGTGTTT
AGACTTTAAACTAATGTTTAAATCGTTTAAATAATTTATTATTTTATAAG
AAGAGGAGCCTGCAACATTGACTTTAACTATTGTCTCTTATCCAGAAAAG
AACACATGGAGTATATTACATACTCAGGGTGTCTTGTGCAAGGGGGTTA
TGGCCACAGTAGTGTATTATGATGACAGGACCAAGGCTCTGTACGTTTCATG
GTGGCTACAAGGCTTTCAGCGCCAACAAATACCGGCTTGCAGATGACCTC
TACAGATACGATGTGGATACTCAGATGTGGTGGGTGTTTTCTAGAGCTT
TCCCTTGGTAGTCTAGAATCTGCAGAGGCAATTGATTAAAAATACTGTGC
TATGGTTTGACTTTTGTTCAGCATTGTATGTAACAAAGTTAGGAGATCAA
TACAGTAATAGAGTTAAGGTACTAATGGTGTCTGTGCTGTCTGTAGTGC

Fig. 3D(4)

TTAGTGCTTTAGACCTGATTCACCTGAACCTCTAGCAAGGTTTGCTCTCTTC
AGAATTCTCAGCAATAAAAAGCTGTGCTGATTTTATCCATACTTAAAAAGC
ATATCCTTCCTTTTCTCTTTTGGGTGTTGGGGATCAAACCTTGTTACATGA
ATAGGCTATACCATCTTTATCCATTTACATCACCAAACAGGATGCTCTCG
TGCCTATTTGATAGGGTTTTCACCTCACTTCGAACTGAAACTTGGGTGTA
AGAGTATGGTACTTTTAGCAAATGGAATAAATTTGAGTTATGATGCAAT
TATAAAGCACTGGTCTCTCTGTATTTCCCTCCTCCTTCTACTCCCTCCCT
CTTCCTTTCTGACCCCCCTCTCTCAACATACATTAGAGACCATGCTTTGAC
TGTCAATTTATGCTGTGCTGAAGATCAGGTCTTTAGTGGCTGTGAACCAC
GGAGCCTATGCAGTGGAAGTCTGTGCTCTGGCTTTTGCCTTACTAATAA
AACACTGAGCATAAATTTTGATTTGTATTTTACAATTCTTACCTGGAATT
CTTAAGTGGAATTATGGAGCCATAGAGAATGAACATTTTAGGGCTTTTAA
TATAGTTTCCCGAAATTTTAAACAGATTTTTCATGATTGTTAAAGGAAGTGG
CTTACGTATAGGGGGAAATCAAGTATTTGCACATTTGAATCTAAAGTTATA
AAGTAATTACATTTAAATTTGGCAAATAAGTATTCTTTTAAAACTAACCTT
ATATTTATTATTTCTAAATAAACTCAAAAGGACCATTCCTTAAGGACAGCC
GATTTTTCGGTTACTTGCATACAGCTGTGATAGTGAGTGGAACCATGCTG
GTGTTTGGAGGGAAACACACACAATGACACTTCCATGAGCCACGGTGCCAA
ATGCTTCTCCTCAGACTTCATGGCTTATGACATTGGTAAAGCTTTCCAAAG
ATGTTTGTAGCTTCAGGAATATTTTCTTTGCTGATGGAAAGATCACTATGT
TAAAATAATTGCACCATTTAAAAGAAGTCCAGGTGGTAGAATTTGCATTT
AATTTGAGTAGGGTTACACATCTATTGAAAAGCATTATTTTGGATTAAAC
TACATTAATTTCTTTGTGAAATCACTCTTCTTAATTTGCTTTAATTTCTTTT
TTTAGGTTGAGTTAATTGGTATCTTCTTTCTTATAAGTGCCTTACATAGT
AGTGGTGGTAGTTGTAACCACCAGTGTATGTTAAGTTTGATGGGATATG
CTGTTTCTTAGAAACCTGGTTTACACATGCTGTTGATGTCAATATACAT
GTGGCCAGAAGAGGGCAGTGTCTGTTTATTCTTGGAAAATAAACATCAGC
TGCTCTGTTGTGTAAATATCACCCATGTGATGTTCTTTCTGTTTATTGT
CTTTGCATTTTGAGACAGCCCTCACTATGTAGTCTAATTGGCTGAAGCTCA
GTATATAGATCAAGGTGACCTTGAACCTTAGAGAAATCCTCCTGCCTCTTC
TGAGTGCTAAGATTAAAGATGTGTACTACGAATGAAAAAAAAAATGTGT
ACTACCACACCTGACTAGAGATTCAATTTAAAAATTATTCTTATTGTGAT
AAAATGCTCAGAATAACACTCACCATCTTAATGTTTTAAGTAGTTTAGAT
TTAAATATATTCTTAGTGTATTTCATGTTATAATACCATCTGCTTGCCGA
CTTCTTGTA AAAACTGAAACTCTGCCCTTAAACAATAGTTCTCTCTTCAT
CCCTCACTCCAGCCTCTTGAAATCATTTTCTATATCTCTATGATTTTGAC
TAGTCTAAATTAGGCATTTTAAAAAATAATTTTGTTTACTTGTATGT
GTATGAGTGTTTTGCATGCATGTATGTTAAGCACACCATGTATATTCACT
GCCCATAGAAGCCAAAAGTAGGCATAGATTCCCCAGAGCTGGAATTACAG
ACTTTTGTGAGCCACCATGTGGGTGCTGGATACTGTGCCCAAATCCTTTG
GAGGAATAGTGAGTCTTCTTAGCTGTTGAGCCATCTTGTGAGCCCTAGAT
GTTTGTTTTAAACAAACGTGTTTTTGGCCAGCCATTGAGTTTTTAAATTGA
GAAATGGGGGTACACTATAGTTAGTCTTCTAGCTTCAAGCTTGTGGAAGCA
GAAATGAGAAGACAATATAATCTTAACTCAGGAGGATTCTTGCTGGCTGA
AACAAAGATGTGAAATTACCTCCGAGCACTCCTAAGCCACTGGGGTGAGC
AGGGTGGTCTGGAGAGGCCTTGAAGAGAAGCTGTCTGAGCTTGTTCCTGG
GGACACTGGGAGTCAAATAGACCTCCTGGGCAGGGGGATTAGTGCAGAC
AAGAGGCAGGAAAGTACATGTCAAATATTTAGGACTTTTGAACGGCTACC
TTTCTTTTGTGATGGTAACACAGAAGGTAGCAGGTGACTGTTAGACTAGA
ATGTTCAAGATCTGATTCAGAGTGCCAGGGATCGTTGGTTGGTCTTGTGTA

FIG. 3D(5)

AAGTCTCACAAGTGATAGAATCATATGTGTGTCTTAGACTTTTTTTGTTG
TAGGTATTTTAGATTTTTCTTGTTTTTCTTTTGTAAAGTCTGGCCCTCA
CACTATGGTCCAGGCAGGCTTAAGACTTATGGTAACCATCCTACTCTGCC
TTTATGGGCCACCATGACCAATTTAAGAAGCTCTCTTGGGTGGCATTGTG
ATAAGTGATCTGGAAGGGGCATATTGACAGTTAGCAGGCTGCTACTGCAG
AAGTCCTAATTAGGTTTGTATCAAGGCCATGGAAGGAGCAGTGACTTCTA
GTACCTGGCTGTTGTGTGTCTTGACAAAAATATAACTGCCCTTTCTTCCC
AAGTGTCTACTATGGACCACCTTTGCCAAAATAAAGCAGATTTCAGAGA
AAAACATATCATGATTGCACATGGCTATAATCCCTGAACCTTAGGAGGATG
AGAAATATGGCAAGATTGAGACCAGTCTGAACTATCTAGTAAGACCGTGT
CTTTAATAAAAAATAGTAAAAATTATAAAATCAGGGAGTAGGATCTGGGAA
GAAGAGAATGAAGTAAGTGTGGGGCATATCCAATTGGAGATGTCTTTAGG
ACAGAGCTGATTGCTGAGAGGTGGTTGTAGGAGAGGTGAGTTATTGTGGG
GCATAAAAGATGAGCAAGAGTCAGAGACAGTTGGAGAACAGAGTCTGAAC
AAGAGTAGAGACTAAAGAGAGTGTGAGAGAAGCAGGGAGAAAAATAGGTGA
GATTGATGACCTGTGAGATATGTTAATGGCCAGAAGAGTGGCTAAAAATG
ACTGGAGAATCCTTCAGACTTGTCAACAAAGAAATCCTTTAGCCTAATTT
AGGGTGCAGGCGGCTGAGGAAGGACATAGGTGAAATATGTGCTCTGTGTG
TTCATTTTTTATTAAAGCTTATCTGCAAAGGCCCTCAGATTGTGCTGTGACT
TGTAAGCTGAGGCTCTTTTGAACCTCTGGTTCTCCTGGCTCCACCTTCCCA
AGTGCTAGGATTACAGATGTGTGCCCTAGTTAAAATAGCTGTATACCTAG
CATTAAAAATTTTAAGTTAGAAAATACTGTGGTGCTCCGGGATGCATCT
CAGCAGTAGAGTGCTTGCCTGCTATACACAAGGCCCTGGGACTGATCCCT
AGCACCACAAATACTAAAGCAGACATTTCTGGTAGGGAAAACCTGGTAGACA
GCAGAGTGGTGACCATCAGGAGGGGGTGTGGGTGATGAATGACTAGAC
TAATTAGAAGTTCTGTGCAGTATATTTATTTTCATGCCCTGAAACATTGCT
GCTGCTGTTGCTGCTTTTCTTTTACACATAATAACATAACTAAAAGACAGA
CAAGCATGTGGTATGAGGCTGTGGATGAGGCATTCTTTGTTTTCTTTT
TTTTTTTTTTTTGAGACAGGGTTTCTCTGACCTGGCTGTCTGAAACTCAGT
AGGTAGAACAGGCTGGCCTTGAATGCACAGAGACCCTCCTGCTTCTGCCT
TCTGAGTGCTGGGTTCAAATTTATGTTTTTTTTCTATAAAGACTGAGAGT
TCACATGGACTATATATGACAACCTACTCTGAAATGTGTTTTTCTCCCC
TTAGCTTGTGACCGATGGTCAGTGCTTCCCAGACCTGAGCTCCATCATGA
TGTC AACAGATTTGGCCATTCAGCAGTCTTGTACAACAGGTAATTGGA
GCAAAGGCTCTATTACTGTCTTACATCTTATATTCATTTTTTAAATATCAAC
TTCCTAACAGTTGTATCTGAATGGTAAGAGGTTTGGGGAGAAAAAAGGAG
AGAAGGCAGTTCTAAGTGCACGATAAGGTAAGGGGAATAGGACTGGGAGG
TTATGGGGTCAAAGAGCAAGTCTGAAGTCTGCACTATATCCAGGTGTGTG
CTCAGGAATACTTTTCTGACCAGCAGAGCTCTTTTCCATTTGCTCCAGG
AACCTTAGTCCCTGTAAAGGACATGCAAAGGACTAGGGTTGTGGGCCAGCA
ATAGAGTGTTTATCTAGCTTGCACAAGATCCTGAGTTCTGACCTCAGCAT
TTTGCCCTTCTGCAAACACAGCATTTGCCATAAGGGACATGCAGAATGGCC
ATTTTACCTAGTCACTTGAAAGTGTGCTTTAAGATTGAGAACTTAACAG
CCTGCTGATGCTGACTTTTCTTATTTTGCTTCTGTTACTGCTTTCTGCTT
CTTTCTTTAATACTCTAATGCTTACATTATATAGTCCTACAGGTATTCAA
ATTTTCTGTTGGAGTTTCTTAATACAAGTAATTTAACTTGCAATTAGGAAA
AGGATAAAAGTGCCATTCTGGAGTTGTGAAGAATGACCGTTTAGAAGCTA
GATAGTGGGGAAAGATGATATCTTTAATCATGTGATTATTTAGTGTTTTA
CAAGTATATAGGGGATTGTGGCAAGACCATTGTATGATTAGAGACTAAAG
TGGAAAGATTTTTTAAATATCTTGTTAACTTGAGTGTTATCTTAAATTAC

FIG. 3D (6)

AATCTGATGCTTTTCCTTCAGAAAAAGCCCTAAATGCCTCTTGAGGTTTTTC
ATCTGGCAAGTATCATGTACCTGGCCTTGCTGGTGGAAATCTGCCCCAGC
TCATGTGTGTTCTTAGTGTTCTCCTAGCACAGAGTTAGGCACGTGTGGGC
ATTTGCATACTAATGTATAGTAATAGTAACAATTGAATGAATTGTCTATT
AAAACATTCTTAAGTTTTACCCAAACACAGAGAGGTGACAATTGTGTCAT
AAAATGTAGTTTTATCCATGAATCAAAATCAGGAATGACTGTCTGAACAGT
GTTTTTATTTTTTATTTTTATTTTTATTTTTGTGTAATTTCTGTGATGTGTTT
GAATATCTCAGTTTTAGGCAGGATTGGAAATGTTAGAGGTTGGTAAGAGG
TCATGGTTGCAGTTTGATCATGAGAGAAATCGATGGCTCTCCCTTCATTG
CAGTGTGTGTCAGTCAGCAGTGTGGGATCACCTATGTCTAACAGTTGTCT
AATTGAGAGAGGATTACAGGAGGGAAAGCAGTGAGATTGTGAGGTGCTAG
ATGAGGAGATGGCATTTACCTAGCAGCCTTCTCTCCCGCCCTCCCATCAT
GTGACCTGAGAGATTACAAATTTCTGAAGATATCAGCTGTGCTTAGTTTA
AGCAATAGTTTTATTAACATAAATCCAACTTGATTCATGTTATTCCCAGGG
AACCAGTGGTAGGATTAAAAATGAATCCTAGTGTTCTTTTTGGTTATTGG
AATGTCAAGTTTTTCAGACACTGTAACGAATACAGAGCCATACAATCACTA
TATTTATTTGGTCCCTTTGTTGACTTAGAAAAATTGAAGCCCAGTTTAGGT
GAGCTACCAAATTTCTCATTTGTGGATTAGTATTAAACTTGCGTGGAGTTG
TGGGATCTTGGAAGTGGGGGCTAAGCATCCGTGTTTGTACAGCCCAGAA
GGAACAGATGAGGTTCCCTTTGAGGAGTCTTATGTCTTTATGAACTTGGA
CTTAGAAATATTTGATGTGTTTAATTTCTGCTGTAGTTTTTTAAACTCTAG
CTAGTGAGCATCTTTTCACAGGAGCGCTTGAGTCTGACCTACAGCCATTG
TCTGTCTCTGGTGTGTCATATTACAAATGCACTGGGAGCGTTTCTTGACCC
AAACATATAATTAGATTTTTCTTCTAAAAAGGTCTAGTTTGGGAAGGAAT
GAAAGGGATTAGAGAAATGTTGTGGGTTTGGTATTTATTTATTTATTTAT
TTATTTATTTAATGTATATGAATGATCTATCTTCATGTATACCTGCATGC
CAAAAGAGGACATCAGACTCATGATGGTGATGAACCATCATGTGGTTGCT
GGGAATTGAACCTCAAGACCTCTGGAAAAACAGCTGGTGATCTTAAGTGT
GAGGCATCTCTCCAGCCCAATTGTTCTGTTTTAGTTTGAGGATGAACATC
TAATTTAGAGATGCCCTGCTTTTCCAAAAGTGAGTTTTAAACACTAATTT
CCATTGTCAGTGGATTGGTCTTTTAAGAATATAGGTAGTGGTGGCACACG
CCTTTAATCCCAGCACTTGGGAGGCAGAGGCAGGTGGATTTCTGAGTTGG
AGACCAGCCTGGTTTACAGAGTGAGTTCCAGGACAGCCAGGGATACACAG
AGAAACCCTGTCTCGAAAAGCAAACAAACAAAAACAAACAAACAAACAA
AAACAAACAAAAAGAATATAGGTTGGAATAGGTTGGAAGCAGCCAATGAT
AGTGCATACCTTTAATCCCAGCACTTGAGAAGCAGAGGCAGGTGGAACCTC
TGAGTTTGAGGCCAGCCTAGTTAGTCTACAGAGTATTTTCTGGAGAGCC
AAGGCTATATATAGAAACCCTATCTTGAAAGGCCAAAAAAGGAGGAAAAA
AAAAAAAAGAAAAGAAAAAAGAAAAAAGAAATGCAGGTTGGGCAGTCAG
GGTAAGTGTCTAAGGTAAGAGGAATTTCTTCAAGGTGGAAGTCATGAGTT
CTGCGCCAGCCTAGGCTACAGAGTACTGAAAGGGGAAGAGACTGTCCATG
TGTCAGACCCTCATTTCTCCAAAAGTCACATGACTATATTTTTTCTGTAT
TGCCCACTCTTCCATACATGCACCTAACAAATAAATATTGAAGTTCACTCT
GTGGCACTATATCTATGTGATAGACTTCTAGAAAAGTGATTTAAAGTTCA
AAAGGTAAATACGTAGTTTTGTTTTCAAGTTGCCAAAATCCCTTTAGTAGA
CTCCTACAATCTTACATGCCAGTAGCAGTATAGAAGCTTGCTTGTGGCC
TTGAAGCCTCACCAATTCAAATATTAGGTAACATTTGTTACATTTTTCTT
TGTCAGCTGGATAGGTAATGAATGACACAACAATGTGTTCCCATTTTCTC
TGCATTACTAATTGAAGTCTTATCACCCACAGCAGACTGAAGAGTTCTT
TAATATTTTATGGACTTTGACAAAGCTAGGATTCATAGCTTCCATACAGA

Fig. 3D (7)

GAGGAATTTACAAATAGCAAAGTTGGGCTGTTAGAAGAATAAAAAGAGA
ATTCTGAGTACAGCTTCTCAAAGAAGAGTCCCACGTAGGTGTCCTCTGGG
ATGTGCCTAGATGCAGGGTTATTGTACAGGAGCTCTTCTGTCTGCTCTCT
GATACTTGAGATTATAGGGTTGCAGGGAAATGCATTAGATGGCATTACAA
ACTGATAAGATAAAGTTAGGAGCTATCAGAGATTTAGGACATGGTTTTTC
TCTGTAAATGGGGCTTCTGGTGAGATTCCTAGAAAATGCTGTTTATAGCT
AGGAATGGGGTTATAGCTAGGAATGGGGAAAGACCTTAAGCAGTTGTGAG
CTGTGGTGGAATGCATGTGTTTTTCAGTTTGCTAAGGCTTCCGGGAATACT
TTTCCTGTGCGATAATTTTCTTTCCTCTCTTTGTAGCCTTCTTTGTATTA
AAATCCTCTCTGCTTGTGTTTTGTGTGTGAATGTGTGTATGTGTGTGTTG
TGTATGTGTGTGTATGCATGTGCATGTAGGTCCCTACATAGGACAGAACA
TATTTCTGAGTTATAGGTGCTTGTGAGCAGCCTTTTAGGGAACCAAC
TCTGTCTCTGGAAGAGTAGCCCCCTTAACTGCTGAGTCATTTAGCCTC
AAGAATCTTCTCTTTTCCCTATTAGTAGAAGATGTCATCTTAGCTCTAGG
AACTACACCACCTCTGGCCTCAGTGGACACCCATTTACATATGCACATAC
AGCAGACAGACATATAACTAAAGATAAAATAAATCTTTTTTAAATGTCTAT
TTCCCTGTGTACTAATTTTCCATGTACACACTCACAGGTAGATTTTTTAA
CTATTCTGAGTGATCACAAGCAGAGCAGAAGGTGAAATTTGAGAGAATA
GATGATATTAGTGGATTTTGAGACCTTGAAAATAATGTCTCAGAGCATTA
AATTAATCACTCATGTATGTATGTATGTATATAAGTATGTATGCATGTAT
TATGTGGATGGGGGTGCTGTAGCACATGTGTGGAAGTCAGAGGACAACCTT
TGTGAAGTCATGTTTCTCCTTCCATCTTTATATGGTTCCAGTGATTGAGC
TCAGATTGTCTACCTGTGTAGCAAGTGCCTTACCTGCTGACCTGTGCGAC
TAGCCCTCTCAGAGGACTTTTAATATTTGGAATATTTCTAACGATTGACA
GTCAAAAGTTTATTGTGAGCCAGGCACTTAAATCCTAGCACTTGTGAGA
CACAAGATGGAGGTCAGTCCAGTCTACTGAGTTCTAGACCAGCAAGGGCT
ACACAGTGAAACCTGTCTCAAAAATTTCAAAAGCGGAGCTAGAGAAATTA
CCCAAGGAGCTAAAGGGAACTGCAACCTATAGGTGGAACAACAATATGA
ACTAACAGTACCTGGGAGCTCTTGTCTTTAGCTGCATATGTATCAAAAG
ATGGCCTAGTCGGCCATCACTGCAAAGAGAGGCCCATTTGGACTTGCAAAC
TTTATATGCCCCAGTACAGGGGAACGCCAGGGGCCAAAAGGGGGAGTGGG
TGGGTAGGGGATTGGGGGGGTGGGTATGGGGAACCTTTGGGATAGCATTG
AAAATGTAAACGAGGAAAATACCTAATAATAAAAAAAGAAATGATATCA
GAAAAAATAAAAAAATAAAAAATAAAATAAAATTTCAAAAGCAA
CAACTCAAACCAGCCCTACGTGCTGCCTCTGAGTTCTCAGTAAATTCCTT
CTCTCTCTCCTCTCAGCACCATGTATGTGTTTCGGCGGCTTCAACAGCCTC
CTCCTCAGTGACGTCTTGGTCTTTACCTCGGAGCAGTGCGATGCACACCG
CAGTGAAGCTGCTTGTGTGGCAGCAGGACCTGGTATCCGGTGTCTGTGGG
ACACACAGTCGTCTCGATGTACCTCCTGGGAGTTGGCAACTGAAGAACAA
GCAGAAAAGTTAAATCAGAGTGTTTTTCTAAAAGAAGTATGTTTTTCT
CTACTTAGAATTTAAATCTAATTTTATCTGAATTGTGAAGGAACCTAG
TCTCTGTACTTTCTGTTCACCTTACTCTCTAGTTATTTCTTAATAAAAA
AATACACAAGATCTTTGGATGGGAGGAAGCATGTGGCTCCTGGAAGCTGT
TAGCAGGTAATAAGTTGTCTTTGAATTACACAGGCTTTGTGTACCAACTC
CTGGTCTGGCTGCAGGTGATCTGAAGCCATAGCACAATGAAATTTGTTTT
CATTTTGGTTTTATGAGACAGGGTCTTGTCTATAGCTCATACTGGTCAA
GCTCCTTGTGACGCTCCTCCTTCAGCCTCTTGAATGCTGGGGTTATAGGC
ATGCATCACTGGCCCTACTTGGGAAATATTTTGATGACAGACATGCTATA
TATTTCTTTGTTTCAGTTTAGTAGCCACTAGCAATCTGTTATTATTAGATA
TTTGAATGTGGCTATGTAACCTAAGGGGCTAACTGTTTTCTTTCTTTAG

FIG. 3D (8)

TGTATGTAGTGAGGCAGATGTAGTAGCACACGCCTGCAATCCAGACACTC
ACGAGGCTGAGGCAAGAGGCAGTTCTAGGCCAGCCTGGGCTGTGTAATGA
GACCTTGTCTCAAGAGCCAAAACATCAACAATAAAAGAACAGTATGTGGC
TATTGGCTGTTATGTTGATGATGAAGGTCTAGTGTTAAGGATAAGAGCCT
CTAATGGTATGATCACATATAGCAAATTTGCTCTGGTAGACAGCAGAGAGC
TGCTGTTCTTGAAAAGTATTTCCAGCCCCCTTTAGCTGTATATAGCAAGC
AGTACAGCATAACAGACAAACTATGGTCCCTTCTTCTAGAGCCCCCTGGCG
TGCTCTTGTTATTTTTCTCTCCTTTGCTACTTGCTTAGTGGTTGCTCTGA
GCACCACTTCACCAACTCAGCGAAGTAACGTGCAAAAATGTTTGAAAAAT
AAGAATGCCTCCAAGATATTTGTCCATATCAATCTTTAAAGTATGAACT
ACTTCCTTATCTAGTTGTTGCAGTTACATGAGAGTTATATTAGGCAGAGA
CTACTTCTGTTTTCTGGTATGTGTTAAATAAAGTTGTGCAGGGACATAA
AGCTCCTGAGGCTGTGCTGTTGATTAGAATTTGGTTTCAATTTATGGAAAA
CAGCTTACCAGAACCTGGTAGGATTACATAATTCTCCCGAAACAGTTAGAA
TTGGTAGAATAACCAAAATTTAAAGTTAAGCTTAAATATACAGTGCATTG
GAAATAATATTATCTTCTGAGGTTTCAAGTATGAGCCCATTAGTTTACCTCA
CTTCTGAGGTAGACCTAATCCTGTGAGAGTAAACTTGGCAAGAAAAAGCAG
CCTACATGAAAACTGATCAGGCAGGGAAGTTTCTGTGGCCTCTCTTCCTG
CTTGTTGATGTCATATTCATGAAATGATTTATAGATGGCAACATGGCTTT
TAGCTTCTTGTTTGAGGATTTAATGAGAATTATGTTAGGTCTACAAAGAG
TGGAAGTTGTGAAATCCACAGGTTTGGAGTCACATGAGTATATAGAGTTC
GAGTTAGCAAGTGCCCTCCTGTGGGGTTGTGGGTCACCTGGGTATACCTGCA
CCCAGGTAGGCCTTGCATTTGTAAACAGGACAAATGTATTGGTCTCTCAT
ATTGCTTTCTTAGGCTTCTGCACAGCTTCTGGTGTAAATTCTGTGCTAG
TTGATGTTTGTGCTGGGAAGAAAAGCATCCATTACTTCTTAGAAGCTATA
AAATTAACAGACCTTTGCTTTTCACTTTCTGGACACTATGGGAGGACAGT
TATAAACAGTGTCTTCTCGGATTGTCTGCTTATATCTGTTTTATTTAAC
CTAACATGGCACTGCTTTTTTCTCCTTTTCACTTTGACTATACACTTTGCTT
CCTGACTATTGTTAGGAGCTTTCTTACCTCAGATTATACATAAGAGAGGC
TGCCGCATAGTTGATGGGTTTGTCTTCTCTCTGTAGCCCTTGACCATGAC
AGATGTGACCAGCACACAGATTGTTACAGCTGCACAGCCAATACCAATGA
CTGCCACTGGTGCAATGATCACTGTGTCCCTGTGAACCACAGCTGCACAG
AAGGCCAGGTGAGATGCTGTTTTTACCGGATTTTAGGGAATAGAAAAATG
CTAGATGAGTGTGAGTGTAGGGCAAATAATGAGTAGAGTTCTTTTTTAA
TGCGATATCGATTGGAATTCTACTGTTGCTCAGGTTTTCTCTTAGGAAGG
GATGCTATATACATCCTGATTCCAAGGATCGCTCCTGCTGCTGAGGTCTT
TGTGCACTGTTTTCCGAAAGCATGTTTTTACAGAATGCCCTTGGCCCATATC
TGACTCAGCATGACATCTGGGCTAATCATGTATGATTGTTATAGGTGAT
AATAGGCTATGAGTAAGGTGATCCAGCTTTTGCTGTCTTTGATGGCTTAT
GACATTTTTTTCTCAAAGTTTAAATGCATTTTATAAGAAATAAGACTTGAG
ATTGCTATGGTGGGCACGGGCTGGGAGGAGCTCTGGAAAAGCAGCAGGTT
CAGCTTTTACGTTTTTACAGATAAGCATTTGGCTGAGGCTTGGTGGTGCCAG
TGGTTCCGTTGGGCTGCTAGCTTGCCAGCTAAAAGCATGTTAGTGAGAAT
ACACACTGTGGTATTCACATTGCAGTGCTGCTTCTGTTTCAATTTCTAATTC
TATCATTCATCCATCTACCTATCTCTATCTATCTATCTATCTATCTATCT
ATCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCT
TATCTAATTTCTATCTGTCTGTCTGTCTGTCTTTCTGTCTATCTATCTCTC
ATCTAATTTCTATCTATCTGTCCACCTATCTATCATCTAATTTTATACATC
CATCCATCTATCCATCTATCTGTCTGTCTATCATATATGTAATTTCTAACC
ATTCATCTATCTATCCACTTATCTGTCTGTCTATCTAATTTCCATCCATTTA

FIG. 3D(9)

TGTATCTATCTATATATCTAATTCTATCTATTCAATTCTTTTCTTTTTT
CTATCTTTCTTTCTGTCAGTTACCATTTCTCAGTTAATTCTCACTGAGTTAT
TTGTGTGAATAACAAAACACTTCTCCCCGTGTGTTCCAGATCTCCATTGCC
AAGTATGAGAGTTGCCCAAGGATAACCCCATGTACTACTGCAATAAGAA
AACCAGCTGCAGGAGCTGTGCCCTAGACCAGAACTGCCAGTGGGAGCCCC
GGAATCAAGAGTGCATCGCCCTGCCGGGTAGGCCTTGACACAGGGATGTCC
TCTATAAGGTCCAAGCTTGGTCCTCCCTCCTCAGATCAAGGTGGACCTAG
GAACAAGATTGCTTATTCTGTCTATTTAGCCCTCTCACTATTGGGGGGGG
GGGGGGGCGATATTTTGTATGTTTTTAACCTTAAATGTGGTTTTTATGTAT
GTATTTACTAGCCTTTGAAAGAAAGTGAAGTGTGAGCTCATGTTCTGGAG
AATTGGGGGGTAGCTTAGATCCATGTTACAACTGTGTCCCACTGTCCCTT
CCTTCTGCTGTGAAGGAGAACCTGGCACTAGAGCTCTGTGGTCTCAGCAG
CAGTCAGGAACCTGCAGGAAGCACTTACTGACAGTTGTGTGAGAAGAGAT
TTCTGTACCAGCATCATCTCCCATGTGACCTTCCTTCCCGACTATTTTCAG
CAGAGGTGTTTCAGGGTATTAACCTTAGGTCCTGAGGCCAGCTAGCCCTGA
CTAAATCTCTATGATGTATTTGCTTGATCAGGATATCCAGGAAGGGGAGC
TTCTGTGCTCTCCAACATCGAGGTTTGAGGGGAAGTTGGTCTGACTCTTT
TGAAAGCATTTTATTTAGTTTGTGCTGAATGGGCTTTAGTTTAGCCAGTGTT
CTATTGCTGTGAAGAGATAACCATTTCCAACGTGTAACFTTTATGAAAGGA
AACATTTAAGTGGGGGCTTGCAGTCTCAGAAGCTATTATCATCATGACAG
GGAGCATAGAGGCACAAAGGCAGGCATTAGAGTGGTAGCTGAGAGCTACA
TCCTCATCTGTGAGCAGAGGCAGACAAGGTGTGAAAAAGACAGAACCTGG
CCTGGGCTTTTGAGACCTCAAAGTCTACCACCCCAAGTGAGACACTTCCT
CCAACAGCTCCTGCAACAAAGCTCCATCCCCCGATCCTTCTCCAGTCCTG
CCTCCTGCTGAATGAGCACTCACATATATGAGCCTATGGGGGTCAAT
CTTACTCAAGCCACTACAGGCTTTGTTTTGTGTCTCAGACTTTATGTCAA
TAGAATACCTAGACACCTTGTTACAAGACAGGCCTGGAAAGCCTGCAGTG
CTGACTCCCTGCCAGTAGCACATTCTGAGGAGCAAGTCCCTTAAGTCGCT
TACCTGCTCTTACATTACGCCTTTCCCTGACCATTTAGTGAGCACTGTTG
GTGTCCCCAACCTGAACCTGGTTCTGGGGAAACACTTGCTTATTCACCTC
CGTGCTAATGGCCAGGGAGCAAGCATGCTTTCATGCAACACTGTGAGTTC
AGTACAACCACAGGAGGAGATTGCAGACTTCCTTCGTGTACTGTATCACT
ATGAGGTTTTCCAAACCAGTCTCCCTTTACCTCATTTTTTGGCATGCCT
TATGTACTTGCTTATACTTTCTATCTTATGACATGAAAACAGAGTGGCAT
TTGGAGGCTTAAATTTATCACATTCCCAATTCAATTCCATTTTCAGTTTA
CTCTTTCTGTATATACATCAGTGTGCAGATAAATATCTCTTTGTGTGAGC
ATTGGAGGCCAGAGGTTAACCTCTGGTATATTCTTCTCTATCACTCTTC
ACAGGGTCCTTTGATGAATGTGGAGCTCACTGATTACATAGACTAGCTGA
CTCAACCCTCAGGCCTCATAACCCTGCCTCTAGCCCTCAGATGAGATTAC
AAGCAAGCAAACTACGCCTGGCCTTTTATGTGGGTGCTTGGAATTTGAA
CTGGGTACTTATGCTTGACACAAGTATTTTATCCACTGAACCATCTCCCA
AGCCTCCATTTGCAGTTTTTTACCTCACCTTCCAATATATATATTTATT
TGTATGCCCTTTGTTCAAGATTTTAGTCACCTTTTACATTTTTCTTCAAA
AATAATTGCACCAATTTCTTAATAATGGCACCCAAAAGTAGGAACATTAG
CCTAGAGTATAACCCTGTGAGCCAGGAAATGTGACTGGTGAGACTTGTA
AGGGTCTTTTTATTCTGGCCCTCAGCGGAGGCTCAGCAGTGGAGCATGCA
TGCTGTTCCCTCTGGAGGACCCGAGGTCCCCAGGGGCCAGGTCACAACCAC
TTGTAACCTTAACTCTGATCTAATGCCCTCTATGGCTTTTGTGCTATAGT
CTCTTGCACTAACCCACACTCAAGGCACACATACACACATTCTTTAAAG
ATAAATTATTTTATTTTCAAAGGTTTTTTTCTGCATATAGAAGTTAATAA

FIG. 3D (10)

TTTGTCTGTTATGCTCACCAGATCCTAACAAAGCACCTGAAATTCAAATC
AGGATGAGTTCAGATGTTTCAGTATTTTGAAGTAGTAAACCGAACTGCATA
ATTCCTAAAACTTTGTTTTCTTTCCCTCTTCCCTTTAAAAAGAAAATAT
CTGTGGCAATGGCTGGCATTTGGTTGGAAACTCGTGTCTGAAAATCACTA
CTGCTAAGGAGAATTATGACAATGCTAAATTGTCCCTGTAGGAACCACAAT
GCCTTTTTGGCTTCCCTCACATCCCAGAAGAAGGTGGAGTTTGTCCTTAA
GCAGCTTCGATTAATGCAATCATCTCAAAGTATGGTGAGTTAATGTGTTT
AGAACTTTGGTTTCTAGGGCACACAGCAGCTCTTATGTAGAAGGCCACA
GTTGTATGTTATTTGCCTGGTAAGAGAAAGAATTACAATAAATGATTAAT
AATATACTGTGGGCCTCTATTTTCAGAGGCTCTTCTTTTGATACCTTTCTT
CTTGTCTTAAAAAGTTCAGTACTTTGCATATTTTATTAGTTGTTATTATT
AAGTAAATTATAAGGTATGAACATATGGAATGAATGGTAATATGTGTACA
TATTCTGGTGACATCAGATTATTTTGTACTTGATTTATATCTAGATTCTG
CTTGGGAAAAGGGAGAGTAAAATGTTAGTTACCTAGGTGTCATTAAAGCC
ATCTACAGCCCCCTGGAGGTATTATTATAGCACATAGTGTAATCGTCAGTA
AGAAATGTAAATCTGCCCAGGTTTTATAGCCTTCTTCCTAAGGCTTCTG
AACTCAGAAAGTTCTCTTACTCTAGAGCCAACTCTCAAATGGCTTGTAG
TTACTATATAGTCTCATTTTGGTATTTTCTTGGTAAGTCTAATTTCTAAGA
CTTGTGATTTGACTGTGATGCTTCAGTCAATTAGATATTCACAGAGCAGC
TTTTCTGTCTATGCTGGCTGTGGTACAGAGAGATGTGAGGGACATGTTTT
TGTCTAGCCAGGAGAAGACAGAATGCAGCTCAGCATCTCTCATTTGGCAC
CACCTTCATGTGATGGGATGCCGGTATGGTGTGGGTCTCTGGTTGTTAAAT
CTCAGGAAGTCCATATATCCAGAAATGACCTCAACTATAGGTGGATTCT
GGCAATTAGGTAAAAGTCAGCATTCCTTGGGCACTTGGGAACTGGTTAC
CATCTGCATAAAGGAGTCATTTCCCTTCTATCTGGCAGAAGGGACATATG
GCTATCTATTGTGCCTGTGTCAGCATGGAAGCACATGCTAGTCTCCAGGTCC
CCCCAATATCACAAGTACCTATAGCAGTGAATTAGTTAAACTGATTTGGC
TCCCAATGGGTCAAGTACAGCTGCACCTGCCCAAGAGCTCTTTGGGTGTTG
CAAATGAGAGACACATAGTTAATTTTATATGCTTTGACTAGTTTCAGTTG
CTGGACATTTCTAATCCTCCCTGCAGTAGCATACATTAACCCCTCCAAC
TTCTTGAGTCAACTTACTAACTCAACATTTTCATCTCTGACACCCACAGAC
TAATGGCAGAGTGGCCCTTAGAGCCACTTTCCCAATTTTTTTTTTATCAG
ATATTTTCTTTATTTTCATTTCCAATGTCCCTTTCCCTAGTTTCCCTGTC
CTCTCCCCCTGCTCCCCAACCCACCCACTCCCTCTTCCCTGGCCTTGGCAT
TCCCTTATACTGGGGCATAGAGCCTTTCACAGGACCAAGGAGCTCTCCTCC
CATTGATGACCGACTAGGCCATCCTCTGCTGAATATACAGCTAGCACCAC
GAGTCCCACCATGTGTTTTCTTTGATTTGGTGGTTTAGTCTCAGGGAGCTC
TGGGGTACTGGTTAGTTTCATATTGGTGTTCACTTTCCCAAATTCCTTACAT
GGCTGGTTTAGTTCTTTCCCTGCAGCTCTTAGGTCTAATCCCTTTCCCTTCC
TCTGTCTATGGTGATTGCCTTCCCTCTCCTATCTCAGTTCCCTGGCTGTCTCA
ATCTAAAAGTCCCACCTCCATCTTTCTGCCCAGCCACTGGCTGTATGCAG
TTCTTTTATTATCAGTTGAAGCCAGCTAGGGGCAGAGACCTTCAGGTCTGT
AAGTGCTTTGGGGAGCAGAATTAAGACAAAGCATTAGAACCAATTCCCAA
CAAGTACCTGCTATACATTTCAAAGTCCATATTAGTCTCCTGGGTCTTCC
CTTCCCCAGCTACTTGTCTCTCTTGTAAATCCAAATGACAAGCTTTTTCAC
ACATCTCTTTATCTCACATTTCCCTAGCCCTGGCCATGTCCACTTGTCTCT
TTTACTCTCTGCTCTGCTCTCTTTCCAAATGCCTCTGGATATTTTCTCTCT
CTTATTACAAATAAAAACCAAAACCAAAACCAAAACCAAAAGCTTACCCTAA
TAATGGAGTGGTCACGCCTGAGGTTTCCCTTACTGCTCCCCCTTGCACACG
TCTTGTGTCTGACACACTGGCAGGCTTTTATTAGCAGCAGGCTCTAGGAG

FIG. 3D(11)

CTGAGAGAAGCAGCAGGCACCTCTGAGGTGGTAGTTACTAGAGTGATTAG
AACAGACAGTGGAGACGTGGCTGGAAATATGGACTCTGGTGTGTTGGAGCC
AAGTATGGTAGGCGGCAGAAGCCAGCAGAAGCATGATCCACACCTTCACC
AGGTGCTTCCATTGGGAAAGGCTGGACCCCTTGGGAAGGGGTCCCTTTG
TGCTTCCTAGGTGTTTCGGAGCCAGGTGTGTGAGGGATACAGTAAAGGGA
CTGACTGCATGACTGCTCCATTAGGGTGAAGGGTTTTGTGTGTAATAGGA
GAAACAAAATGTGCAGAGGCATCTGGGAGAGAGCAGAGCAGAGTGAAAAG
GAAGCAGTGTAGGCATGGTCAGGGCTAGGGACAGCGGAGACAGCAAGATA
GCGAGTGGGTGATAAGGTGAGAGAGAGTGTGTGTGTGCGGTGCACACATC
ACGTGCATTATAAGGAGGCTGAGTAGCTAGCTGGGGGGAGGGAAGGGCCA
GAAAAC TAGCATGCACTCTGAAACGGGTACTTGTGATGCTGAGGGAGCTT
GGGGGAGAAGGGCATGCCCTCAAGACCAGAAGAGGGAGTTGGAGTTACAGT
TTGTAAGATGCCTAATTTGAATGCTGAGATCCAAACTCTGATCCTTTGGC
TGAACATCATATCTGCTGAGCCATCTCTCCAGCCCCCTAGAAAGGTGGTGA
TGGTGGTTGTTCTTGTGTTTGTGTTTATTTGTTTAAATGGGGAGCCAGGTA
CAGTACATCATGCCCTTTAATCCCAGCAGGAGATTCAGGAGATAGAGACAG
GTAGATCTCTTTGAGTTCAAGGGCACCTTGGTGTGTATAGGAAATTCAT
CCACCCAGGGCTACAGAAGGGTACCTTGTCTTTAAAAAAGAAATTCAT
AGAAAGAAAGAAAAAGAAAAAAGAAATGAAATTTTCAGAGTTATGC
AAGATAGGAGCTCAGTGGTAGAGTGTGTGCCCAGGAAGTGCTGGGTTTGA
CTCCTCAGAACAACAGCAGGGGCAGAAACTAGTCTACAGGTTTCATGAGTG
GTGTTTGTGTTTGTGTTTACATAAAATGTGTTGAATTAGATAAGTAGATAA
AATGTGACTCATACACAGATAAAATAGATAAAATGTGATACATGTACCTGT
ACATAGAAGATTATGATCTCACCTTTAAAAAGGAGGAAATAGAGAGTTTT
GGTAGTTACACCACAGGAAAACCTGGAAGAAAGAAATGTATATATGAGGCTG
TGCCCCATGGCTAAAGGAACATGTTTTTAAGTCATTTGAATTCACCAAAC
AGTTTTAGGTAATGATATATGGTTTTGCATACAACCAGTATTTTATAAAT
ATTAGCAAGGTCACATCATTTATGAACCAACATTTAAACTAAATTTGTAA
ATCATCATTTCTTTATAGCACTTGTCATAGAACATAAGTAGTTTAAATG
TGATTATTGCTTTGCTCTTGATGTCTGAAATCTTCATGTATTCTCTCT
TTATTTAATCTACCTTGCCTGAGTTTGGGGAATAGATGGTTTCCACATG
TCTGTGGGTTATGCCTAAGCTAGTGGTTTTTATGTTAGAGCTTGTGTTGG
GGAAGGCACTGGTTGCATTCATAGCTGTGTTTCTTTTGCTGTAGTCCAA
GCTCACTCTGACTCCATGGGTTGGTCTTCGGAAGATCAATGTGTCTTACT
GGTGCTGGGAGGATATGTCTCCATTCACAAATAGTTTGCTGCAGTGGATG
CCATCTGAGCCCCAGTGATGCTGGCTTCTGTGGGATCTTGTGAGGCCTAG
TACTCGGGGATTAAAGGCTGCAACCTGCATCAACCCTCTCAATG**GCAGCG**
TCTGTGAAAGGCCTGGTAAGGACATGGGTGCATATAGTGCTCCAGGAGGA
GCCAAGACAGCAAAGGAGGCACAGCTGAATGAGCGCTGAGGTGATGAAGT
ACTTATGGCAGCAGGGAGAGGAGCACCATTAGGCATATGTATTTCAA
CAGAACCCGATTCCAGATAGTCTTTCTTGGCCTCTGACTGCTTTAAGCCA
TACTGAAAACCAAAAATAAAATTGCTGAAAGAACCCAGTTTATATTGAGC
TGCACTGTTTCGTTGGTCTCAAAGTGTGAGAATTGTTCTAGAAGATTAT
TTCCTTGGTGTGTTGGCAGAGAAGTGCTATGGAGGAAACAACAACCTGAAAC
CAAAGAAACATTTAGAAAAGCAGCAAGTCAGGACACTATTTCAGACACTGC
TGGGGTGGGGGAGAGGGGCATGGCCAAAGAAGCCGACAGAGCCAACACC
AGGCTGTGGCAATGTCCTGCGCTGAGGTTAAGGTTAGACTCCATGAGGCC
AGGCCCAGAACAGCCATACACAAATGAGGACTCCAAAACAAGAGGTGCAA
GTGTAGTGGAGACTCCATCCCTGCAGGTCTGTTTCAGGAAATGATTGTA

Fig. 3D(12)

CTTTGCCTGAGTAATACAGCCTAGGAGCTACTTTCTGATAGGGTTTTTTTA
AATACTTACAAAGAATTATTTATCTTTAATCATGTGGTTTTGTATGTGTG
TGCTTGCACATGCAGTGCTTGTGAGAGAGAGTATGTGTGAGAGCATGCAT
GTATGAGAGTGTGAGAATATATGTGAGAGAGTGTGAGTGCATGTGTGCGT
GTGTGCATCTGTGTGTACAGGTGTGTGTACATGCATGTGTGTATAAGAGT
ATGTGAGAGTGTGGGTGTGTGTGTGAGAGTATGTGAGAATATATGTATGA
GTGTGTGTGAGTATGAGTGTATGTGCGTGCCTGCATGTGTGTGTGTGTGT
GT
GAGTTGTCAGATCTCTTAGAGATATAGTTGCAGTTGGTTGTGAGCCATCT
CATATGAGCGCTGGAAGTTGAAATTGGGTTCTCTGGAATCCTCTGGGTTCT
CTTGTGTAAGCCTGAATATTTTGATAAATATTTATGTCATTATCCCTCAA
AATTGTAAATGTAGAATTTAACAACTCAGGTCTTGAGTCATCTTTGTCC
CAAGGTTTGTGTTTGGTTTTTTTGTTCCTCCACCTTTTCTTCAGTGCTT
TTAAAAAAGAGAGTCCATTTTTTCTTAAATGTTTAAATACAGTTGAGGAA
TAGAACATCTGACTCCAATTTCTTGGGTTTCTCTCCATGTAGTGTAGTGC
TGACCTGATTTTCAGTGTGCATTGAAAACCTTGATCACTTGGAAGGCAGCT
ATGCTCACCCTATACTACCAATGTCTGCAATCCTATAGGAGAAACAACA
ATATGAACTAACTAGTACCCCCCAGAGCTGTGTCTCTAGTTGCATATGTA
GCAGAGGATGGCCTAGTCAGCCATCATTTGGGAGGAGAGGCCCTTGGTATT
GCGAAGATCATATGCCCCAGTACAGGGGAATGCCAGGACCAGGAAGCAAG
AGTGGGTGGGTGGGGGAGCAGTGCAGGGGGGGGGGGGTATAGGGGGTTTTG
GGGATAGCATTGAAATGTAAATGAAGAAAATAACTAATAAAAAATTGCCT
TAAAAAAAACAAAAAAGAAAAGTTTTTGATCTTAGCTGACCAGTGTCTC
TTTGGGTCTTAATTTCCAGCAAACACAGTGCCAAGCAGTGCCGGACACC
ATGTGCCCTGCGGACAGCGTGTGGCGAGTGCCTAGCAGCAGCTCGGAGT
GCATGTGGTGCAGTAACATGAAGCAGTGTGTGGACTCCAATGCCTACGTG
GCCTCCTTCCCTTTTGGCCAGTGTATGGAATGGTATACGATGAGCAGCTG
CCCACGTAAGTGGAAGGAGCTTTTGAACATTTGCAGGCAAGTTGGGCTTG
ACTTCTGCTCAAGTCCATGCAGAAGCTGGTTCGGGCCGGCCCTTCCAGAT
TAACATGTATGTATAGAATGCAGCACAGTGTTCATGCAGTAAATCAGTT
ACATCAAGGAGAAGGCACAGGGTACAGAAATACCTTTTTCTTCTCAGGGT
AATATTATAATTCAATCTGTATAATGTTTCTACATCTTAATCTACCAGTA
TGTAAGTGCTTTCTAGTAGAGGCCCTCCCCAGCTCCCTTTTTTCATCCAAC
ATCCTGATATTAAAAGGTTGGAAGAGTCCCTGTTATATATTATGTAAAT
GTGGGGCCCTTTAAATTATTTTCAGTTCAATAATCACTATAGGGTACTATT
TTTAATTCATGGAAGTTAAATCATCTGTTAAAAGAAAAGGTAATAACAGT
AAATTCAAATCTTGTGATAGTGAATTACAAGTTGGATTGTTTTGCCTTGT
TTTTTAATAGCTGAAAATTGCTCTGGCTACTGTACCTGCAGCCATTGCTT
GGAGCAGCCAGGCTGTGGTTGGTGTACTGATCCTAGCAATACTGGGAAAG
GAAAATGTATTGAGGGCAGCTATAAAGGACCTGTGAAGATGCCGTCACAG
GCCTCTGCAGGAAATGTGTATCCACAGCCCTTCTGAACTCCAGCATGTG
TCTAGAGGACAGCAGATACAACTGGTCTTTTCATTCAGTGTCCAGGTAAGA
TGCCTGTGTATCCTAGTTCAAATCTCGTACATAAACTAGACGCCCAGATC
CCTTGGCTCACTTGTTTTCTTGACTGTGTTTGAGTTCTTTCTGTGTTCTG
CATCACCTTGTGGATCATAGCTGGCAAAGGTGCTCTCCTTTCTGTGGGC
TTTTTCTTTACTTGATTGATTGTTTTCTTTGGTTGCACAGAAGCTTTTTAG
CTTCTGAAGTCCCATTTGCCAGTTGTCTTAAATTCCTGGGCGAGTAGAA
GCCTCATAAAAAAAGTTCTTCTACACATGTATCATGTAGGGCACTGC
CTATGTTTTATTCCAGAAGTTTCAGAGGTTCGGGTTATGTCTTTGATGCA
TTTAGGGTTACTTTTTGTGAAAGGTAATGGACACAGTTCTGTTTCATFCA

FIG. 3D(13)

TTATTCTACATGTGGACATCTACTTTTCCCAGCACCAGTTTTGAAGATGT
TATCTTTTCTGCAGGTTGTTTGTGCTTGTTTTGTCTCTTCAGAAAATC
CCAGATGGCGGTAGCTGTGAGTGCTTAGGCTTGGCCTACCTGTTTCATTA
TGTGCGCTTGCATGTCTGTTTGTGTCAGTGCCACCATATTGTCTTAATTG
CTATAGCTCTGCAATCTATCTTGACATCTGTGTTGGCAATCCTGCAGTTT
CGACCCTTCTGCTCAGCAGTGCTTTGGCCATCTGGGGTCTTTTCTGGGTT
CATAATGAATTTTAGGATTTTTTTTTTCTATTTCTGAGAAAGTATTGTTGA
TATTTTGATTGCGATTGAATTGAATCTGTAAATTGCTTTTGGTAGAATGG
TCATTTTCACAATATTAATTTTACTGATCCATGAACATAGGATGACTCCA
GTCTCTCATGTCTCCCTATAGCCCTGTCTTAAGAGATTGAGTCTTCAT
TGTAAGAGTCCCTCACCTCCTTGGTTAAGTTTATTTCTAGATATTGTATT
GTCTTTGGTATTATAAATGGTAGTATGTCCATGATCTTGTCTCAGTGTT
TTTTTAGTTTAGTTTTTTTTTAATTTATGTGTATGAGTGTGTTTTATAT
ATGTGTATATGTGCATTCATGTCTCTGGGCATCAGATCCCCTGGGACTG
GATTTACAGACAGCTTTGAGCTGCCTGTAGGTGCTGAGAATTGAACCCAG
GTCTCTGCAAGAACAGCCAGTGCTCCTACTCCCCAGCCCCAGAAGTACT
AATTTTTAAGAGCTGATTTTCTACCTTTGCTGACATTGTTGATTGTTTCT
AGAAGTTTAGTGATAGAGTTTTTGAGATTTCTTATATATCTTATGTTATC
TGTA AAAAGGGATAATTTGACTCCTTTTCTTATTTATATCCTTTATTTCT
TTTCATTTGCCATATTGTTCTAGCTAGTGCTTCCCGCTCAGTATTGAAAA
GAGTGGTGATTGTGAACAGCTTTTCTTATTTCTTATTTTAATGGGATTAT
TCACCCATTTAAGATAATGTTGGTTATGGGTTTGTGCATACACAGCCCTTC
TTATATTGAGGTATGTTCCCTTCCAGTCTGTCTCTCTAGGACTTTTTTTT
TTTTTAATCAAGAAAGCATATTGGGTTTTTTTGTGTTGTTATTTTTGTTTT
GTTTTCTAGACAAGGTTTCTCTGTGCAGCCCTGGCTGTCTGGAATTCA
CTCTGTAGACCAGGCTGGCCTTGAAGTCAAGAAATCCACCTGCCTCTGCCT
CCCGAGTGCTGGGATTAAAGGCGTGCAACCACTGCCTGGCACATGTTG
GTTATTTTGCAAGCCCTTTCTACATCTACTAAGATGAGCATGTGGTTTCA
TCTTTGTCTGTTTATATTGTCTGTTGTATTTATTGACTTATGTGTGTTGA
GCCAACCCTGAAGTCTGGGATAAAACCCACATGCTTTGGATGATTTTTGT
GCTATGTGCTTATATTGTGTTTGTGTTAGTGCTTTATTGAGGACGTCTGCAT
CCGTGTTTCTGCTGGGGTACTGTCTGTAGTTTGCTTATTTTGTGTTCTTTA
CCTGCTCTGCATTTTAGAGTAATCCTGGATTATAGAAAGCATTGGGGAG
TAGTCCTTCTGTTTATTAAAAAATAAAGAAATGATTGGTTGTTGTG
TGGTGGAAATCTGCTGTGAACCCATCTGGTTCTGGACTCTATTCCGGAAGG
CTTTTTATTACTGTTTTCAGTCTCCTTGTGTTGTCAGTGATCTATTAGGTTG
CTAATCTCCTTATGATTCATTTGGATGAATCAAGAAATTAATCCATCTCT
TTAGATTTCCAGCTTAATGGAATATGAGTGTTAAAGTATTTCTTTATAGC
ATCTGTATTTTTTGGCATCTGTGTAATATTCCCTGTTCTTTCTGTTA
ATCTCTTTCTTTCTTGTGGTTAGTTGGGCTAAGAGGCTCTTGGTTTTTTT
TTTTTTTTTTTTATCTTTTTTAAAGGACCAGCTCTTAGATTCAATTCCTT
TGTATTATTTTCTTGTGTTCTTTTCACTGATTTTCAATTTTAGATTTTATT
ATTTCTTGCCATCTACTGCGTTTGGGTTGGTTTGTGTTTATTTTCCAAGA
TTTTTCAGTTTCATCACTAAGTCATTCATTTGGGCTCTTTTGGGTTTCTTC
ACGAGAACCCAGTTGGGACTGTTACCTTCCCTTTTAGACCTGCTTTTAAT
GTGCCCCAGAGATTGTTACATTGTCTTTTCGATTTAACTTAGTTTCAGG
AATATTTTGATTCTTCTTTGACCCATTTCATTCGTAATGAGTTGTT
TAATCTCTAGTGAGTTTATACATTTATTAGAATTTGTTTACTGATGATT
TTAAGGTGTTGGCTTTGTTTGTGTTGTTGTTGTTGTTGTTTTCGAGACA
GGGTTTCTCTGTTGTAGCTCTGGCTTTCTCTATGTAGAACAGTCTGACCT

FIG. 3D (14)

CAAATTCACAGAGATCCACCTGCCTCTGCCACTGAAGTTCCTGGGATTAAA
GGTGTGTGCCACCACTACCTGGCTGATTTTAAAGTTTATTACATAATAGA
CAGGTAGGGTACATAGATTTTCTACATTTGTGAAGGTTTGCCTTGTTTGT
CAGCATGTAATTCTGTGTGCTGCTGAGGGAATGTATGTTGTTTGTGACAGT
TAGGTGGAAAAGTCTGTAGACATCTGTTAGATCCATTTTACATTTCAAGA
AGCCATTTAATTCTGAAGTTTCTCTGCTTATTTTTTCCCAGGTGACTTAC
CTATTGGAGAAAATAGGGTGCTAAAATCATTTACTATTATTGTTTTTTTT
AAGAAGAAAATAATTAATTTAAAAAACCTTGGAAGAAAGATACCAAATG
TGAATCATGTTTCCTGGATAGTGGGGTTATATTTGATCATTTATTTTTTCC
TCTCAAATACTGTGAGTTTTTACAATGAATAACAACATAAATATTTTTAT
GTTGCTGTGGACTTTAACTTTGCTTTGATAATATATTTGGTTTTTTGAGA
CTAATTTCTTTTTGATATTTTATTTTCTCATACTAGTTTTTAGTAACTT
TGGTTTTGTTTTGTTTTGTATTTTTTAGACTGGCCACCAACTTGCTATGTT
GTCAAGGGTGGCCTTAAAATCCACACCCAATACTTGTCTCTCTTTCTT
TCTTTCTTTTTTTTTTTTTTATTGGAACAAAATTTCTAGGTGGGAATCTCAC
TATGTTACCCAGGCTGACCTGAAACTTCTGGGCTTAAGCAAGATGGGTGC
ACATGATCAGAGACGCTGCGCTGCCCGCTCAGGCCCTGCTAGTTGGAAC
TATAGGCACAGACAGCTGTACTTCACTCATTTCATGATTTAACATTTAG
ACTATATGCAAATAAATATGAAATGTATTCACCAAGTCTCCTATGGGAG
AAACAGAGCCCTTAAGATTTTTTCCCTTTCAGCTTGCCAGTGCAACGGACA
CAGCAAATGCATCAACCAGAGTATCTGTGAGAAGTGTGAGGACCTGACCA
CGGGCAAGCACTGCGAGACCTGCATATCTGGCTTCTATGGTGACCCGACT
AATGGAGGCAAATGTCAGCGTAAGTCACACAGGTCAAGTTAGTCACAAGT
CAGGTACAATAGTACAGTACCTGCAGTTGACTTAAATATCTTAAAGGGAA
AAGGCCCTCTTGGTTTGGGATATGTCCTTCTTAAATATGTTAAATTGTTA
AAAGTTTAACTGAGGGGCTAGAAATGTGGCTCAGTTGGCTAAGAACACTG
ACTGTTCTTCTAGAGGACCGAGGTTCAATTCCCAGCACCCACATGGCAGC
TCACAAGTGCTTGTAACACCTGGGATCCAACAACCTCATAACAGACATACA
TGCATGCAAAACACTAATATACATAAAATAAATCCATTAAAAAGTGTTTG
ATGATGCTGGAAGAGGAAAAAAGGCTCAACTTGTGGGTTTGGGAGCAGTT
AGTTAAAGCAACAAACCGACAGTAAAGGAGCTAAGCTTTTATTTCTTCAG
CAGAGGCATAAACAAGGGGCCGAAGTCACTGAGGCACCAGCTGCCTTTAT
TCCATTTCCCTCCCATGGAAGCACATCAGCTCAAGTCAAGCAGAGCAGCC
TGGGATGGGAGGTCATCTCATTGGAGAAGGAGGCAGGAGGCATTGTGAGG
GGAGGGAGGACAAGGCTGGGAATGGGAAGTCTGAGCTCAGAATCAGAAT
GAGGACAAGATCTTCAGTTTCTTCTTAAATATAAAGAGGTATCACAGAGG
TCTCTATAGAAGTCTACTGGAAGCCTCACACAGGCACAAGGGTACATTTG
AAAAACTGTGACAGCCAGGGAGAGTCCCCTTCTGAAGTGTCTTCTCAG
AGACTGCAGCACCTGACTGTGCCCCAGTCTGCAAGAGGTTTGGGGAGAGC
AACTGACCTCCTGAGGACCCAGATGAATCTTTAAGATGGCCTGCTTTTG
GTTTTGGTTGGTTGGTTTTTAGACAGATCTAGGAGAGTTGGTGATGAGCT
TGAATTCTCTGTCTCTCTGCCTGACCTCCAAATGCCAGCTTCACATGGG
CTCCCATTAAGTTGTGAGTTTTCGGTGTCTGGCTCCTGCTCTCACAGCCAG
TGCAGTACATTGAGCTCCATAGAGATAGCGCCGGGGCAAATGAGAGCTGG
ACGGGCACTGGGTGACTCTGTGCTTGTGCGGGAAAATCAACTAAACATG
GGCAAAGGAGATCCTAAGAAGCGGAGAGGCAAATGTCTCATATGCACT
CTTTGTGAAAACCTGCTGGGAGGAGCACAGAAGAAGCACCCGGATGCTT
CTGTCAACTTCTCAGAGTTCTCCAAGAAGTGCTCAGAGAGGTGGAAGACC
ATGTCTGCTAAAGAAAAGGGGAAATTTGAAGATATGGCAAAGGCTGACAA
GGCTCGTTATGAAAGAGAAATGAAAACCTACATCCCCPGCCCCCAAACAG

FIG. 3D (15)

GAGACCAAACGAAGTACTAGGACCCCAATGCACCCAATGCCTTCTTCGG
CCTTCTTGTCTGTTCTGAGTACCTCCCCAAAATCAAAGGTGAGCACCCA
GCTTATCCATTGGTGATGTTGCAAAGAACTAGGAGAGATGTGAACAACG
CTGCAGCAGATGACAAGCAACCCTAGGAGAAGAAGGCTGCCAAGCTGAAG
GAAAAGTACGAGAAGGATATTGCTGCCTACAGAGCTAAAGGAAAACCTGA
TGCAGCAAAAAAAAAAAAAAGGGGGGTGGCCAAGGCTGAAAAGAGCAAGA
AAAAGAAGGAAGAGGAAGATGGGAGGAGTATGAGGAAGAGGAGGAAGAAG
AAAGATGAAGAAGAATATGATGATGATGAATAAGCTGGTTCTAGTTTTTT
TCTCATCTATAAAGCATTTAACCCCCCTGTATACAATTCACCTCTTTTAA
AGAAAAAATTGAAATGTAAGCCTGTGTTAGATTTGTTTTTAACTTTAC
AGTGTCTTTTTTTTTGTATAATTAACATACTGCCGAATATGTCTTTAGATA
GCCCTGTTCTGGTGGTATTTTCAATAGCCAGTAACCTTGCCCTGGTACAGT
CTGGGGGTGTAAATTGGCATGGAAATTTAAAGCAGGTTCTTGTGGTGC
ACAGCATAAATTAGTTATATATGGGGACAGTAGTTTGGTTTTGGTTTTAT
TTTTGGGTTTTTTTTTTTTTCATCTTCAGTCGCCCTCTGATGCAGCTTATATG
AATATGATTGTTGTTCTGTTAACTGAATACCACTCTGTAATTGAAAAAA
AAAATCGTGGCTGTCTTGACATCCTGAATGTTTCTAAGTAAATACAGTTT
TGTTTTTATTAATATTGTCCTTTCGACAGGTCTGAAAGTTTTCTTCTTGA
GGGAAAGCAGTCTTTTGCTTTTGTCCTTTTGGGTCACATGGGTTACTGC
AGTGTGTATCTTTTCATATAGTTAGCTGGAAGAAAGCTTTTGTCCACACA
CCCTGCATATTGTGGTAGGGGTAACACTTTCATCCATATTCAAAGAATCT
CCAAAATCGTGATCAGTTGGATAAGAAATATTATATAACCTACTTGGCAA
AGCAAGGTGTGATCAATTCTGTACACCATGGGATCATTAGAATCAAGCA
ATCTGAAAATCTGTCTTAAAGGACTGATAGAAAAGTATTTTCTAATCCT
TATACAAAGGCTCTCCTTTAACTGCCACTGCTATGTAATGACAGTTATGT
TTTGCAAGTTTCCCTACTAAAGAAGACCTGAGAATGTATCCCCAAAGCGT
GAGCCTAAACTACACAAGTGCAGTACTATTTGTTGACCTTAGTCCCAGCG
AAGGCTATCACGAGAATGCTAGCTATAATATAATGCCTTGCCCCCTCTAT
CTAAATATGGATTGCTCAGGAACTTGACTGCTTAAAGGTATTTTTTTCA
TATTGTTGTTCCCTCCTATAGGGTTGCAGACCCCTTTAGCTCCTTGGGTAC
TCTCTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT
TATCTCTTGTGATTTCTTTTTTCTTTTCTCTTTCTTTCTTTCTTTT
TAAGATTTATTTATTATTATTTCTAAGTACACTGTAGCTGTCTTCAGATG
CACCAGAAGAGGGGTGTCAGATCTCATTACGGATGGTTGTGAGCCACCATG
TGGTTGCTGGGCTTTGAACTCAGGACCTTAGGAAGAGCAGTCGGTGTCTCT
TAACCACTGAGCCATCTCTACAACCCCTTAAAGGTATTTTTTAAGTAGTTGA
GTCAGCTTTTAAAATTATGCCAGAAGTGTCAAAGTTCAAAGTTTAGGA
CCATCCTCTATTGAAGTACAGGGTCATCCTGGGCTACATGAGACCCTGCC
TTAAAACCAAAATCAAACAAACAGGAAAAACAAGAGTTAAGAAAGAG
AAAAAGAAGCACTTGGAACAAAGATCTGTGGAGTATGTATAGGCTTCTC
TACAACAGGTGTATGTAGGATCTTGATGGCTTTTGAGTCTATTACCCTCA
AAGAGGTACTGAGAAACCTAAATGTGATCACCGTGGTCTCTGAGGGGCAC
CTGGCAGGATTATGGGAGATAACTAAAGCTTGCTAATCACAGAGTTTAGG
GAGGGAGGACGTCTCTAAGGCAAGTTAACTGTCTGGTTTGAGATGCTTAG
GTGATGTCTGAGGAAGTAATAAGGCCTGTCCATTTTCATACACACTCAGG
CCTTAAGTCTGGGTAATGGCTACTTGAACATAAAATAGTCTCTATGAAA
GGAATAATATCTCTGTGTCAGCAGCCTTCACGGCTAATGTTAATTGTGCA
GGAACCCTGCTTCTCAGTCAGACAGAAGCTCAATCAGGCAGGGGCAGGAC
TTCTTTGCCTTTCCCATGTCCTTGTAATTTCCCTGGCTTTTCATCTTGGT
TCAAACATACTTACCTGTTAGGTAATTATAAGAACACCAAATATTACTGA

Fig. 3D(16)

ATAAAATGTGTTTATGACTTTGTGGTGACTGCCATTCAAGAATTAGATGC
CTTAGCCAGCAATGATGGCACACGCCTTTAATCCCAGCACTTGGGAGGCA
GAGATAGGCAGATTTCTGAGTTCCAGGACAGCCAGGGCTACACAGAGAAA
CCCTGTCTCGAAAAAACAAAACAAACAAAAGATTTTCGATGTCTTT
ATCACCCAAATCAAGTAACTTTCCAAAGTCTCACAGTGAGATGTAGCCTA
GTTGGGAGCCACATCTAATATATGCTGATGATCTTAACAAGTAGCCTGCT
TGTGTCTTCAGGTGACCACCCCGGTGTCTCAGCTACCTCTAGAAAGATC
ACACTTTCCTCTGTGGTCTCTGCAGGGTCCCTGTATGATTCTGGAACCTT
GCTGTACTTCTCAGAGTCCTGATTTCATAAAGCACTGAGTTTTTGTCTTGT
TGTTTTGTTTTGATACTATTGGTAAGAATATATATTGAACCTTGACATGCC
TTTTTAAATAACATTATTTTTTACAATAGTACTTTAGCCTTGATTATGTT
AACTGCTTACTGTTTCAGATGACATTCGTACATCTTTTAATCCTCAAACC
AGTCCTATGAGATGGCTAGCATCATTTGTCACATCATTTAGGCAAGGAAAC
AGGTCTTGGGTAAAGCTTCATGCTCAGAGCTCCTTGGAACACAGTGGACT
CAAGTGCAAGCAGACTGACGCGACTGGGTMTTACTAATTCAGTAAGCCTG
TACTCTATGGAGGAAGAGTTTCTGACCCTGGATGCAGTCTGATGACCTC
TGACTGTTCTGTTTGAAAGGTTCCTTTCAGTGATTTTATTTTCTCCATG
TGGACTTTTTTTCCAGCTTTTTAAATATATATATATATCTTATTCGCTTC
ACATCCTGCTCACTGTCTCTCCCTCCCTGTCATCCCTCTTACAATCCTT
CATATCCCCCTTACCTTCTGAGCAGCTGGGAGCCCTCTGGGTATCCCC
ACACTCGGGCACATCAAGTCTGTGAGGCTGGACGCATCTTCCCCACTGT
GGCCAGACAAGGCAGCCCAACTAGAACATATCCCACAGACAGGCAACAGC
TTTTAGGATAGCCCTGCTCCAGTTGTTTCAGCACCCACATGAAGACCAAG
CTGCACATCTGCTACATATGTGCAGGGAGGCCTAAGTTCAGCCCATGTAT
GTTCTTTGGTTTGTGGTTCAGTCTCTGAGAACCCCAAGGATACAAGTTAT
CTGACTCTCTTAATCTTCCCTATAGAGTTCCCTATCTCCTCTGGGGCCACG
ATTGGTGTCCCTATTGCTTCACTGGGATTCCTGCTTGGCTACACCCACTA
TGACCAAGGCAAGTCTTAGAAAAGACAACATTTAACTGGGGCTGGCTTAC
AGGTTTCAGAGGTTTCAGTTTCAGTATCATCAAGGCAGGAACATGGCCTATC
CAAGCAGGCATAGTATAGAAAAGAGCTGAGAGTTCTACAACCTTATCTGAAG
GCTGCTAGCAGAATACCGACTTCCAGGCAGCTAGGATGGGGGTCTTCAGA
CCCACACCCACAGTTGGTGTCCCTATTGCTTCACTGGGGTTCCTGCCTGG
CTACAGGAGGTAGCCTCTTCAGGTTCATATCCCCAATGCTGTGAGCCAC
AGTTAAGGTACCCACTATTGATTCTAGGGTGTCTCCCTCATCCCAGGTC
TCTTTTCATTGTGGAGATGCCCCCCTTCCCCACCCTGTGAGTTGCAGA
TTTCCATTCTCGGGACCCTCTGGCCATGCCTTCTGTTTCTCTCACACCT
GATCCCGACACCCCCGCCCCATTCTTCTCTACCTAGTTCCCTCGCTGCA
TATGCTTCTCTATGACTATTTTATTCCCCCTTCTAAGTGAGATTCAAGCAT
CCTCACTTGGGCGGCCTTCTTGTGTTTGTCTTTGGGACTGTGGAGTGT
AGCTTGGGTATCCCATTTTTTTTATGGCTAATATCTGCTTATAAGTGAGTA
CATACCATTTCGTGTCTTTTTGGGATTGAGTTACCTCACTCAGGATGGTAT
TCTTAAGTTCTATTTCATTGCTTGCAAAATTCATGATGTTTTTGTGTTTTA
GTAAGTGAATAGTAGTCCACTGTATAGATGTACCACAGTTTCTTTATCCA
TTCTTCAGTTGAGTGAAATCTAGGTTGTTTCCAGTTTCTGGCTATTACAA
ATAAAGCTGCTATGAACATAGTGGAGCATGTGTCCTTGTGGGATGGTAGA
GCATCTTTTGGGCATATGCCCAGGAGTGATGATATAGCTGAGTCTTGAAG
TAGAACTATTCTTAGTTTTCTAAAAAACACGAAATTGATTTCCAAAGTA
GTTGTACAAATTTGCACTCCCTCTAACCAAGCAAGTGAAAGATCTGTATG
ACAAGAATAACAAGTCCCTGAAGAAATAAACTGAAGAAGATATCAAAAGA
TGGAAGATCTCCCATGATCGTGAATAGGTAGGATTAACAAGGTGAAACT

FIG. 3D(17)

GGACATCTTACCAAAGCAATCTAGAGATTCAGTGCAATCCCCATCAAAA
TTCCAAACACAATTTTTCTGTAGACCTTGAAAGAGCAATTCTCAGTTTCAT
ATAGGAAAACATAAAGCCCCAGGAGAGCCAAAACAGTTCTGAGCCATAAAC
GAACCTGTGGAGGAATCACCATCCCTGACCTTAAAGCCGCACTACAGAGC
AGTCGTGATTAAAACAACAACAAAGGCTGCGCACTTTTGGTACAGAAACA
GACGTGCTGACCAATGGCATCCAATCCAAGATCCAGAAAGAAACCCACAC
ACTATAGTTTTTTTTTAAATATAAAGTTCTTCAGCTTAATGCTTCTCATT
ATTTCATGAGAGAAGAAGACTCAACAGCAAAGAAGGTGAAACAAGGGTGAC
AAGTACCACAGGGCTCTCGAGTGTCTCTTGTGATGGACTAGGGAGCCCGT
CAGTTCTGAATGCTCAGGAATGTGGTTTCACAGTGTGGCCACAGTACAGAA
GATCCCCGAGATAAGGCAGAAGACAGTCAACACAGGTCATCTCCACAGGG
CAAGGACTCAGTATATGGCATATTACTAATGCTCTTAAATATTTACTGAA
CAAAGGAACAAAATGCTGAGTCTGTACAGAGATGAAAATAGCCGTTGCT
TCAGGGGACAGCAGAAGATAGCCTTTTTTTCTCCTTGAATGGTAGTTAAT
TTAATGTTGCCTCTATATTATTAGAAATAAATTACAAGCTGAAAAATAAT
GAGTCATACGCAGTGATTTCTCTTGCTTTAGGCTGTCTTTACTACAAACC
CATTTTCAGGCTAAATGATTTTGTCTTAATCAGTCTATGGTAATCTGTC
AAGCCAGTTGTGACCTGTCTTCCCTTCCCTTCCAGCATGCAAGTGCA
ATGGGCACGCATCACTGTGCAACACCAACACCGGCAAGTGCTTCTGTACC
ACCAAAGGTGTCAAGGGGGACGAGTGCCAGCTGTGAGTACCACACACT
CTGTGTCTCCAGTGGGGGACTGGGCCTTGCAAGCTGCCTGGGCCCTGTGCG
CCACCTGCTTGCTGGGCATTGTTGCCCTTCACTCCAGGGTCTTTGAGT
GGACTAGTGTGGAGGTTTACCTTTTTTCCCTTCAGACAGGTTATCTCAGTT
ACTTTAATATTGCTCTGATAAAACATATGACCAAGGCAACTTACAAAATA
AAGCCTTTAATTGGGCTTATGACTTAAGAGCATTGGAGTCTACATTGAGT
TCCAGGGCAATAGAGCTACATAGTAAGACTGTATCAATCAATCAATAAAT
AGGACTACATAGTAAGACTGTATCAATCAATCAGTAGATGAAGAGAAAGA
AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGGAAGGAAGGAAGGAAGGA
GGAAGGAAGGAAGGAAGGGGAAGAAACAAACAAGCTTAGATAGGAAGAAC
AGGATAGAATGAATGACAAATGCTTGAAAAATGTTTGTCTTATGAGTAG
GAAGCATACTCAATCCACACAGAAGTAAAAATGTTGTTCCCTTATGAGTAG
TACCTAGCATTATTACATATGTACTTGCCTGTGTCCTTGGGCAAGTATTT
GTTTATTTGTTGTTTTTATACTGTTGCTGGTGTAATTAAGTACGAGTTA
GCAGAAACATTCCCTGCAAATGGGATAGTCTCTCTGATCTGAATAATGATA
TAGTTTATGTAAAGGATTTACTTGGTTTAAAAATAAATATAGAGTCTGT
GCTTTAAATGTCAATAGAAGATAATTTCTTTTTTCCCTAGATGTGAGGTA
GAAAATCGATACCAGGGAAACCCTCTCAAAGGAACATGCTACTGTAAAGTT
TTTGTAATTGTTTCTAGAGAGTAATTGAACAAAACGACATTGCTTTTTTT
TTTTACCATTGCTCTGAGAATGATAAATGCTTGGGGGATGAAGCAAATACT
CATAGCCATGCCCCCTGACTTGGTGAACACTGTTCTAACTGAGGCATGGTC
TCTGCTGGTCATCCAGAGCAGTTAGCAGGGGTGCTGTCTGCTGCTCCTT
GTTCACTCCCGCGGAGGCGTGCTCATTACCATTTGCCAGTGAGCTTA
TCATGTCCAATCTTCAGACAGCCAGGAAGGAGTTTCTAAGATAGAGGTGC
GTTCCACCATTTCTCTCTGCACTGATTTGTGCTCACAAACAAGTAAATAA
AACACCAAATTAATACCTTGGTGTGAAAGTGAATCTGGTAAGCTTACAGC
TTTATCATAAATATATTTTTTGTCTATGAGAATCTACATAGTAGGTTCTA
GACTATAGAACAATAAAAAAGGAATTAACATTTGGCATATGCAGCATAA
TGGTATATATAAATTGTAGAAGAAAATGGATGGTTCTAGACCTGAAAAGA
CAAGAAAATTGCTTGTGTGTAATCTGGGCAGGTCTTAAGTTGTGACCTTC
AACATCTGCTTCCCAAGCAGCTGGAACCACCAGGCCTACAGAATTCTTAG

FIG. 3D (18)

CTATGATTCTAAAGGTCATTCATCAAATATAATGTTAATGTTGATTTTAT
TAAAGTTTCAAACCTTCTATCTTTAATAATCTGCAAATGTAGCTCAGTAGA
GGAGAGCTCTCGCTGTAAGGTCCTGTGTTCTATCCCCAGCACAACAAAAC
AAGACATTTAAGAAAAAATTAAAAACAAGTTGGCTGTATTGTTCTCAGTATC
TCATCCTTGAGATAGTGAGGCAGGAGGACTTTTAGTTTGAGGCCTATGTG
GGTTATGTAGTGTGAAACCTTTCTCAAATAATATTTACACTTTTTCTTT
AAAAACAACCTTTTTCTTAATTTATGTGTTTTGCAACATGTAAGTCTGT
GCAATGTGAACATATCTGTTCCTTTGAATGCCAGAGAGGGTTTCAGTTT
TCCTGGATCTGGAGTTACCAAGGGTTGTGAGCTGCCATAGTGGGTGCTGG
TAATGAACTGAGTCCTCTGGAAGAGCAGCCAGTGCTCTTAAGTGTGAGC
CATCTCTGCTGCTAGGTACTCCCCCTTCCCCCTTAAATTTAAGACAAAG
GTCTCACTGTGTAGCCTCAGATGGTCTAGAACTCAATTTGTAGAATGGTT
GACCTTTGAACTCACAAAACCTCTGCCTGCTTCTGCCTCCTGAGTGTGAG
ATTAAAGTTGTATGTCACCACACCTGCCCTATGATTTCTATATTTAATA
AAGATCATGACTAGGATATAGAGAACACTTTTAGAACTGAAGAAGAAGAC
AGTTACAGTTAAAAGCAAAACAAAAACAAAAACAAAACCCAGAAA
AAAAAGAATGAAAACCTAGCACTGAAGAAAAAATAAATTTTAAAAATAGG
CAAAGAGTCACTATTATATTTGTGATGGATGTGTTATATGTTTAAACCAC
AAGTGAGATACAGGCCTGAAATGACTTTAATCGAAGCTACACCAGCCTGG
GGTGGTAGTTTCAAGTTGGTAAAGTTCTTGCTATGCAAGCACAAGAAGCTGG
GTTTGATGCCCAGGACCCATGCTGAAACCCAGGAGTGCTGCTGAGTGTCTT
CAGCTCTGGGGTGGCAGGGCTCACTGGCAGGAAGCCTAGGCTAAGAGAGA
CTCTGTCTCGAAAAACAAGGCCGATGGCACCTGATGAACGGCATCTCAGC
ATGACCTTTGCTCGGCATATAATGTGTACACACAAATTCATAGTTTAGTA
GAAGACAAGTATGATCTGCTTTTTCATGAAGTCTGTTGTAATACGCCTTCT
TTAGTTAACCATAGTTGCTTAAAAAAGAAAAAATCGACCTCACTGGAC
AGAAAATGGATAGAGTGTCTAATAGCCAATTCAATTCATCATCATTATC
AAAACCTATAACTTAGGGGGCTGGAGAGATGGCTCAGCGGGTAAGAGCAC
TGACTCCTCTTCTGAAGGTCCTGAGTTCAAATCCCAGCAACCAGATGGTG
GCTCACAACCATCCATAAAGAGATCTGATGCCCTCTTCTGGAGTGTCTGA
AGACAGCTACAGTGTACTTACATAAAATAAATAAATAAATCTTTAAAAAA
AAACACCTATAACTTAACTTATCAATAACTTTAACTTTCTACCCCATG
CTTCCTAGTTACCCATTCTGCTTTCTGTTTGTATGATCCFGGGTATGGCA
TCTTAATGGAAGCACAGTGTGTGACTTTGTATCTACTTAATATTAGGCAT
GATGCCTCTGACTCTCATCCCTGATATAGCACAGTTCAAATTTGCCTTTC
TTTGGTGCTGTACATATAGCTGAGCGTTTGAGTGCTTCCCTGCATGCACA
GGTTTCTGAATTCATCCCCAGCACAAAAAATGATAAAAAGAAAGCAAAA
AGGCTTATTTTTACAGCTGGACAGATCATCCTGCATTGTGCCTGTCTATG
TTTGCTTGTTTCTTCTGTCAGTGGACACTGTGTTACTTCTACCTTTTGGT
TGTTGTCAGGAATATTGTAAACATGAGTGAATATACACCCAGAAGTACAA
CTGGATGTGGTAATTCTATGAGTGTTTTGTGTTTTTGGAGGGATGGTTATTA
TTGTTTCCATACAATAAATTACATTTCCCTTACAGTTCAATTACATTTCCAA
AAGCCATGCATAGCATTTCTGTTGTTCTACATTCTTATTGACACCAGTTT
TCAATTTACATTTATTTTGTGAGTTTTTTAATTGGTAACCATCATAATGG
ACATAAAAAATAGCTCATTTGTAGTTTTTGGTATTTGTATTTTCAAGTAATGCT
TGGTGTGATTATCTTTTTATATTCTTATTAACCATTAGTGTGTATCTTTT
TTTGGAAAAACACCTCTTCAAGGGTTTTACTATGTAGCTCTGGCTGGCCT
GGAACCTGTGTCAGACCAGGCTTGCCCTCCGGTTCCCACTGTCTTAGGTAGG
TTTCCATTGCTGTGAAGAGGCACCATGACCAGAGCAACTCTTACGAAGGA
CATTTAATTGGGGCTGGCTTACAGTTTCAGAGGTTTAATCCATTATCATC

FIG. 3D(19)

ATGGCAGGAAGCATGGCAGCATCCAGGCAGATGTGGTGCTGGAGGAGCCG
AGAGAGTTCTATATCTTGATTCAAAAATAGCCAGGAAAAGACTGTCTACA
GCAGGCAACCAGGAGGAGACTGTCTTCCATATTGGGCAGAACTTGAGCAC
TAGGAGTGTTCCAAAGCCACCTACACAGTGACACAGTACATCCAAAAGG
CCACACCTATTCCAACAAGGCCACACCTCCTAATAGTTCTACTTCTCATG
GGCCAAGCATACTCAAACCACTACATCCACCTACTTCTGTCTCCCGAATG
CTGGGATTAAAGGCATATGTTGCCATTACCCAATTTTAAACCAGATTATT
ATTGTTTTTTTGTACAACAGACTTTTAAGGTTAAAGTTTGCAGCAATAGG
CATTCTTTGAAGCTGTATCACACTGATATATGTCTGTTGTTTTCTTCTT
CCTAGATTAAAATAGTACAGTATATTCAAGTTTCAATTGTCCCTTTCCAT
AAGAAGTCCTGGTTTCTGTTCATTATTAGTTTATATCTTAGTGTCTTA
AGTAAAAATACTCAGTATTTATAGATGAGTTAGATTAGAGCCAAACCCCA
ATCAGGGTATTGGTAATGAAGGTTTGCTGGATAATTCAAAGGATACTGCA
AAGATCTGGTTTCTAATGGAAGAACATGTAAGTTGGCCATTAGTGGACC
ACACATCTGTATTTCTTATTCTTTGGAACCTTGGGCAGGATAGACAGATG
AGCTAAGATTCTTCATAGCTATTGAATTTGTGAGAAAAACAATTGTGT
TTCCAGAAACCTGCTTTAGTTTGTATCAACACTTACTTTCTTCTGTGTG
TGGTGTGTGTGATGTGCCTGTACCATTTTCAAGTTTTTCTTCTTCTTTC
CATAGATACCCTTCTCATTGACTATCAGTTCACCTTTAGCCTGTCCCAGG
AAGACGACCGCTACTACACAGCCATCAACTTTGTGGCTACTCCTGATGAA
GTAAGCTTTTCTTTTAAGCTGTCTTATTTTGTGTTAAATTTTGTATAGGT
TTTTTTCTTGGTCATCCTGGACAAAAGTACTACATAGAAGCAGACAGTAT
CAGGGTGGGAATATAAAAGGCAACCAGTTTTTAAGTATTTTTTTTATTAC
TTGTTGACAGTTTTATATGATTATATAATGTGCTTGATGATATTCAACCT
GTGACCTTTTGTCTCCCTCATACTTAGTTCCTTCTCTCCCCACCAAGTCA
CCTTCACTCCCTCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
TGTGTGTGAA
AGACAGACAGACAGATAGACAGAGAGACAGAGATTGATTGATTGATTGAT
TGATTGATTGATTGATTGATTACCTACCTAGTTTACCAGCTGACTGCAG
GAGCATGCTGGGTGGGAAGTTCTTACTGGAGCATAGACACATTACAGTGA
CTACACCACTGAAGAAAGTGACTCCCTCAGGTAGTCTTCACTGCCACT
AGGTCCTCAGGGATCAAGAGAATGTTTGGAGTCTACATTTTATCTTTTTT
CCACTCAGAAGGCAAACATTACTGAATGTTTAAAGTAGTAGAATAATGT
TCATGATAGTCTGTTTAAATATTAATTAAGAATTTGTTCCCTAATTATAAA
ATTTTTAGAAGATAGACAAGAAGACAAAATTTTGAAGTTAACAGTTTGAA
AGGTTTATTTTTATTTTTATTTTTATATGTATGAATATTTTAGCTTCTTGTA
TCCCTGTGCATCATGTGTGTGCAGTGCCCTGTGGAGGCCAGAAATAGATAT
TGGATCCCTGGAAC TAGAGTGATAGATCATTGTGAGCCATCATATGGGTG
CTAGAACCAACCCAGGGTCCTCTGCAAGAGCAGTGAGTGCTCTTAACTGC
TAGGCCATTTCTTTAGCCCCCTAAATGTGAACAACCTTTTAAATAAATGTA
AGTGATCTTAAATACTCTGGAGAAAAATCTGTAGCTATACCTTACTTTTT
AAAAATTATTTTGTTTTATATTATGAGTGTTTTGCCTACATATATGTGTG
TCTGATGCCTGCAGAGGTCAGAAGAGGGTGTGATCCCTAGAACTGGG
GTTACAGATGGCTGTGAGCAGCTATGTGGTGCTTGGAGTTGAACCTGG
TTCTCTGTTAGGGCAACAACCTGCTTTTAAACCATCAACCCATCTCTTTGGC
ACATGGGTGCATTGTTGGTTTGGCTGCTTGAGTTGTGTGTGAGGGGTGTG
TGTGCATACATATGTGGGTCCATGCTTATCCAGTGAGGCCAGAGGTCAG
AGTCATGTATCTCTGTACTTTCTACCTTATGTTTTGGAAGCAAGATT
AGATAGACCCCTGGGACCTTCTGTCTTCTCCTCAGCACTAGGACTACAA
GTCCACACCTGACTTTTTACATGGGGCTTCAGATCTAACTCAGTCCCAAC

FIG. 3D (20)

ACTTGTTCATTTCCTTAGCACCTTGGCTAGATTCTTAGGATTTTAGAAG
GAGCTTATAGCAAAATACCACAAGTGAAATTTACTACTGCCTTAGTCATA
AGCAAATATTGAAGGCTCAGTCTTTAAGGGTATAATTGATAGTGTCTTT
TTTTTTTTTAAGTAAACAAATAGCCTGTCATGGTAACTATCGCTGTAGTCC
CATTACTTGTGAGAGATGTCAGCTCAAGGCCAGCCTCCGCTACATAAGTA
AGGGAAGACCAGCCTGAGCTATATGGGACTCTATCAAAACAAATAAACAT
TGTAGAATTTTTGTAATACTTATTAGAAGGTAGCTGATGATCATGAGAGT
CTTTAGACATTTCTTCATTCCACTGTTTTGTGTGTGTGTGTGTGTGTGT
GATTTCTTACTAGATTTATCTCTTTGTGTGTGTGTGTGTGTGTGTGT
TTACAAAATGACAAAGATTTTAGTCCTTCTCGTGGAAGTAGTTGCTAGT
GGTCAGCAGATACTTGCTAGTATAAATAAATGAGCATAGATCTGCGCTTG
CAAAGGAAGACAAAGGGAAAAAAGGTTTTCTTGAACATAATTCCTACTTT
GTGAAAGAACTTCTCATTGTGGAATTACATTTTGAAAATAGGTATFGTG
AATGTTTTCCATTGTGGTTTGTGGTATAACTATCAAATAACACTTTTTTAA
AAAGAAAAATCTTAATTTTCTAAGATTTTAAATACCCTTTTAAATGAG
CATTTCCAGCATGGTTTGATTAATTTGTAAAATGTAAGAATATAGTATCT
AAGGCTACAGAAATGACTCAGTGGTTAAGAGCACTGGCTGCTTTACAGAG
GACCCAGGTTCCATCCCCAGCACCTCATGACAGTTCACAGCCATCTGTA
TTTCTAGTTCCAGGGCATCTGATGCCCTTCTCTGATTTTCTCCAGTACTA
GTGACACACAGCATACATTTGAACAAAACCACTGATACACATAAAATAAA
TTGTTTTTCAAGAAACAATATAGCATCTAATTAGCTTACAAAACATAATTAT
TTGTTTCTGTACTAATTACGTTTCTATTGGCATGACTAAGGCAACTTATA
AGAGAAAGCATTTAATTTGGGGTTTACACTTCTAGTGCCTTAGATTCTAT
GAGCATCATGGTAGGGAGTGTGGCAGTAGGCAGGCAGGCATGGTGCTGGA
GCAGAGGCTGAGAGCTCACATTTGATTTTCTACTAGAAGACACAGAGAGA
GCTAACTGGAAAAGGCATGGGCTTTTCAAACCTCAAAGCCCCCTCTAGG
AACACACACCTCCACCAAGGCCATACCTCCTAATCAAACAGTCCTACCAA
CTGAGGACTAACCATTTCAGAGATAGATGAGTCTATGGAGGCCATTGTCAT
CCAAACCACCACAGGCCCAAGAAAGATTTGTTAGTGAAATTTTCACTGAA
AACTAAAACAGCATTAGAATTTACCTGGCATAGCCAGCAATGATCTCTTC
TGTTCACTGCCACAGATTTCTTTGAGTTAAAACCTCAGTTGTTAAAACCAA
AAATCAAATGTAATTGGCACTTTAAATTGCTATAAGGGGAAACAAGGTT
TTCAAAGCCATGAAACCATATTCAGAATAATTTTAGCGAGAGAAATATTT
TTTCTTTTTTTTGTTCGTTTTCTTTTTTTTCTTGGAGAGAAATATTTTTAT
ATTTTATATTATTTTAATTACATATTTAATTATTAACCATTCTGACAGA
GGGCAAAAGGTGAGGATCTTCATGGAACATAATCTGATAAAGCACCAAA
TTCTTCCCAACTCTGGGATGCAAATGACAGTTCAACTTCAGTTTATTGCT
TGTATTGAAGAAAATTGACAAGAAATGTCATGTCTTAACATAAGCATGGA
TTTCTTTTAAGATGTAGAATAGTCTATAATTAATGTTTTTTGAGACTAGTA
AGACCTGATTATTGTTGTATCTTAAATCTAGAAGGTACTAACAATTTTC
TAATGTGTATTTTTTTTTTTCATCAGCAAAACAGGGATTGAGACATGTTCA
TCAATGCCTCCAAAAACTTCAACCTCAACATCACCTGGGCCACCAGCTTC
CCAGGTACAGACACACCTAGAGAGATGGATTGGCAAGTTTAGTGTAGGAG
TTGGGGAAGGAGGCTCTGAAGGCTGGTGAGTGAGTTCAGAGCCCACCTCT
GCCTCTTAGTAGCCATGGCACCTTGAACAAGCCATGCTTGAACAAGCATG
TACAATTCCCTCTCTACCTTAGGCTACTCAGAGTGAGGAGTCACAGCTCT
TGCTTCCAGCGTTGCTGGTTTCAAGTTGGTGGATGGCTGCTCCCTGCTTT
GCCACCACCTTCCAGCACTATGACTATCTCTATGTTTGTGCTTCACAGGG
GAAAACTAAAGTGACTCATAGTTTTAAGAAATGAAAACCTTTAAGGGA
AGGGGGATAACTCTAATATGTAGAGGTATTCATACTTTGGGATAACTCT

FIG. 3D (21)

AAAAGTACAGCTTTTCCATTCTTGTATTATCTTATAGTGACTATAAAATTC
TGATGGCCCTAATGTAGCAGTTACTATAAATAACCACTCCATAACTTGAT
AGCCCTGAAGATAGACCTAGGTTTGAATTTACCTGCACGGTGTGAACAA
GTTACTGAAGCTTTCTTTTCTTTGTTTTTTAAGTTTGTATTTTATGT
GTGTGTTTGCCTTTGCCTGTATGTGTATAAGTGTACCATGTATGTGCAGT
GCTTGAGAAGGTCAGAAGAGGACATCAGCTCCCCACCCTCAACGAGTTAC
AGACAATTATGAACTACTATATCTGTGCTGGCAACAGAACCCAGGTCTTC
TGAAAGAGCAACCAGTGCTCTTAAGTGTGAGCCATCTCTCTAGCCCC
CAAGTTACCTAACTTTCTGATCCAGTTTCTTTCTTTATAAAATGATACA
GTGAAAATAGCTTTGCTATGTACAGAGATATTCCTAACTTTTAAATATTAC
AACATGACATCTACAAATATGTTAGCCCTCATTCATAATCTTGCCTGAAT
TGATAGAGTGTGCAAGGAATAAATGAAATAAAGGAGGTACTTATTATAGA
GTTTGAGGTTTGCCTTCATGCATAAAGAGAAGCTTTTTTGTAGTCTGTACT
ACTCATGTTCTTAGCCAATGGAGTATATAAAATATGGTAGAACCATTTAG
AAATGGAGTCTCACTGGGTACAGGCCTGAATGCAGTGGTAGCAGGTAGCA
GAAAGAAGGCCTGAGTGGCTGCTTGAGCACCTTCTCCATCAAGACTTGAG
GACCTTTCTGCTTAGGAAGTGTAGAGCGAGTAAGTGTCCCTGAACAGGAG
CCTTGAGCATATTCTACAGTGTGAAGCAGAAATACAAAGGAGTTGAGGTA
TCATGTGCAAAATGAATGCAGTGTCTGTTTTATATGTATGATTGTTTTAC
ATACATGTATGTCTGTGCATCGCTTATATATCTGGAGCCTCTGAGACAGA
TTACTTAATCTATTGGGACTTGAGTTTTTCCAATCTGTAGATGGAGATAG
GAAGGTGTTGTGTGGGTTAGAGACTGAAGCTCATAAGGCTATATTCTTTT
GACACTGTAAGTGCTCAATAAACTTTTACCCTCATTACTAGTGCAGCAAG
ATTCTTTCTGATTGGCATAACCCGCCTCCCAAGTCTTTATTTTTATTCTTG
CTTCTTTCTAGCCGGAACCCAGACTGGAGAAGAGGTGCCTGTTGTTTCAA
AAACCAACATCAAGGAATACAAAGATAGCTTCTCTAATGAGAAATTTGAT
TTTCGCAACCATCCAACATCACTTTCTTTGTTTTATGTACAGTAATTTTCA
TTGGCCCATCAAAATTCAGGTAAGAACTGCTTTTTTAACCTTCATTCCCGTA
AAGATGGTGACATCTCTTTAGTGGAGACTAACTTCACTCATTTGGAATCT
GTGGTGACTGAAAGATAGTGTGCTTTGCCTTTGAGGGATCTTTGCCATA
GACTGAGTAGCAGGTGAGTGTGCTTTGCCTTTGAGGGATCTTTGCCATA
GTGGAGTGCTTGCTACACAAGCCTGAGGACATGCAGTTCATCTGCAGCCT
CTCATACAAAGCGGGACACGCGGGTGTGCCTGTACCTCAGCACTGGAC
ATGCAGTGTGTGCCTGTACCCCGACACAGGACACGCGAGGGTGTGCCTGT
CACCTCAGCACTGGACATGCAGTGTGTGCCTGTACCCCGACACAGGACA
CGCAGTGTGTGCCTGTACCCCGACACTGGACACGCGAGTGTGTGCCTGT
ACCCCGCACTGGGAAGCAGGGGACAGAAAGATCTTGCTTGCTGGCCAGC
CACTCAAAGCTGGATCTGTGAGTTCTAGATTAGATTAGAGACCTGTCTC
AAGTAAATAAGGTAGAGAGGAATTGAGGAAGACACCTGATTACCTCTGG
CTTCTGTATGCATGTGCACATATATATACCTTCACACATATACACTCA
GAGAAAAAATTCTGAGAGTGTATATCACTTGTGAAGAAAGTTTTAAAGC
ACTTTTAAAGCAAGATGAAAGCTATGCAAGGTATGCAAGGTAGTATACT
TTTGTAATCCCAGGATGTGGAAGACCAATGCAGGAGGATCACCTGAGTT
TGAGGCCATAGGAAGACCCTGCCTCAAAGGAGGGAAGGAGGGAGGGAGG
GAGAGAGAGAAAGAGAAAGAGAAAGAGAGAGAGAAAGAGAGAAAAA
GAAAGAAAGAAAGAAAGAAAGGAAGGAAGGAGAAAGAAATCAAATTGATT
GGCATATAGTTATGTGTTTTATTTTTTGAGTAATTGCTATGTAAAAGCCTT
TAGAAATACACAGTTTTAATTATGGAATTGAGTATAAATAAACAAGTAC
ATGTTTGTAACCAATAAAGTATAAATAATGACACATAAGATGTCAAAGTGG
TATGATGGCTATAATGTGGAGTCCATAGAGGAAGCAGTAGGCAGTATGAG

Fig. 3D (22)

GTACTGTGTAAAAACACATAGCTTTACTATTGCACAGACAAGTGTGGATT
CTTGTTCTGTGTGTGGTTCATGGAGGCTCTCCAGTTTGCAGATTCTCTGT
GCATGTGTCTGAAGGATTGGTCTTCCTGCTATGACCTCTGGTGTATTATA
GCCTGAAGTGAAGTCTTAAGGAGACAGGTAGTGGAAATGTTTGTATTGCAA
AGACAGTATGGGTAGTTGTTTTTAGAAACAGGAGTTCAACAGAATTGATA
GAACTTGTGATCAAGAAGCTAACAGCTGGACTGGGATGTAGCTCAGTTGA
AAGAACGCTTGTCTAACATTAAGAAGCCCTGGGTACCATCACTACCACAG
CATAAACTGAGAGTAGTGACAGACTCATGTGTCCAGCACTGGGAAGGTA
GAGGTAGGAGGATCAGAGGCTGCCCAGGGAGGTTGAGAGTGAAGTACGCT
AGGAGATAGATCTAAAAATGAAAAGGAAAAAGAACTTGGTAGCTGCTAGA
GCTACCATGAAGAGAGTGGAGCTTAAGGATTCAGCTGAAGAATGTAAACT
GCCTTCTGATGACAACTGAGAGTCGCTGAGTTATTTAAAGTCAGGAAGTG
AACAAAGATCAGTGTTCAGAAAGACCTCTGTGGCAACAGTATTGACTAG
AAGTAGCCCCCTCCTATGTTCAGGTACTGGTTTAGACTGTATTTGGAAGTGT
CCTCTTCTTGATGGCCCTCAGACACCTTTCATGGCCACTCCTCTGCATT
TGTACCCCATAGCCACACACTTGATGGTTCCTTTATTACATAAATAGCTCC
TTATAGGCAATGATAGATTTTATATTTTGTATAATTTTAAGATAAACTCT
ATGTCATTGCATAGAATTTAGTAGTTGTAGGTACTCAGTAAATGTATATA
GGATGAATACAAAAGCTTTAGGGTAACAGTATTTTGTGTTCTTCCCCCG
CATTTTAACTATCTCATAGTAGCACAGACTAACCATAACTGACCATGA
AGCCAAGGATGACCTTGAACCTCTGTACCTTCTACCTCTTCCCCGAAAGT
GCTGAAGTTACTGGCATGTGCTGCTCACCCAACTAATAGCAAGTTTTTCT
TATAAAGGTGCTGATGCCCTTTCCCTGTTTGTGTTAATTGCTGACACTTA
AAAGCTCTTTATCCCAACCCACAGTGTAAAGAGTTTAGTTAAATTTTGT
GGAAATTTTGTCCCAAATGAAGTGGTTGATGGCAGGCCTGGTGGCTCCTT
CCTATAATTCCAACACTCAGGAGACAGAGTCAGGACGATGGCCAAGAATT
CAAGGCCTTGGGCCTACAGAGTAGAAGAGAGAAGAATGAGGATTGGAACA
CCTGATTAAATAGATACCATTTCTGCTACCAACCTGTGCCTTAGCTACT
CTTCTATTGCCGTGACAAAACATCATACCCAAAGGCAGCTTATAAAAGAAA
GCATTTATTAGGACTCACAGTTTCAAGGGTTATACTCCAAAACCATCATG
GCCGGGAGCAGGCAGCAGGACAGGAACATCTGCTGTGAGGAAGAGCTGAGA
GCTCACTTCTTTATCCACAAATAGGAGGCAGAGAGAAAGCTAACTAGGAA
TAGAATGAGCTTTGCAGACCTCAAAGCCCACCTCCTTCCCAAACATTTCC
ACCAATTGGGAACATAAGTATTCTAATCTGTGAGCCTCTGGAGGCCCATTC
TTATTTAACTACCACTTTATAAGTTAATACTACATGTGATGAGGAAA
CTGGTATGGGAATTCTGAAAAGTAGTTTACAGGAGTGGGAGGGGCTGAAC
GTGAGTAGATGCTAGCATGTGTGTGTCAGGAGTGAAGTGTTCAGAGCATTGC
CTGGTTTGACTTCTCTCCAGAGCTGAGGTGAACATGCTTTGTGCCAATAC
AAACCCGTATTAAAGCGGTGGTAGTTACTGAAAATCAGTGCAGGGCTGTG
GTCTCAACACAATGTTTGA AAAAGAAAACAGGGCATCCACATCAGGCAGT
GTACAGCTGCTTATAATTCCAGTCCCTCTGGCCTCTGCTCACATGCACATA
CCCCCCCATACATACACATGATTAAACATAATGAAAAATTAAAAATTA
ATGCTATAAAAAATGGAAAGAGCCGGGCGTGGTGGTGCATGCCCTTAATCC
CAGCACTTGGGAGGCAGAGGCAGGCGGATTTCTGAGTTTCGAGGCCAGCCT
GATCTACAGAGTGAGTTCCAGTACAGCTAGGGCTACACAGAGAAACCCCTG
TCTCGAAAAACAAAAACAAAAACAAAAACAAAAAAGTGGAAAGAAA
GGTTCAGTGTTCACAGGAAACTCTGAGAGGTGATAATCAATCCAGT
TTAAATATACTCCATAGTGCACACAGCCTCTCCCATCCTTGGCAACTGA
GGCCTGTGAGAAGACTCAGTCCCTCTCCTGGCTTCCAACCTTACAGTGTTC
AAAACCTCTTCTGCAAGATCCACATGGTCCCTACCAAGACCCTGAAGGTCAG

FIG. 3D (23)

GCATGCTGATTAGGCTGTCTCTGGGCCTGAAGTGAAAGGTAAACACTTCC
GAGATCTCCAAAGCCTTGGGAAGATTCTGAAATGTATGGGTGTTGGTTCA
GGTAGACTCTCAGCCTTGGTGAAGCTGCCCCCGGAGCTGTAGGGTTATCT
GCAGAAAGTCAGCCAGGTGCACCTTACCCTGGAATCCTCTCCCATTACAG
ACACCTCCCTGAGGCTTTGTGGCTTCACCTCACTGTGCAGCTAGCTCCTG
TTTTACATGCTTATATAATGAATGGTCTTGGTAAAGAAGATGATAAAGGC
AAGCTAGAGGCCTTTTTTTTCCCCTCTTCAAATTTTGATTGGCCTTTCCC
TACTGTTACACTGTCTACTCAAGGTTTGTAGCATTTACTTTGTGTACATA
GTAAAAGCAAAGTACATATTTTTAAGTAGAAAAGAAAGCATCTGTGGTCT
TTGATATAGGTGCTTTTCTTTATTTTAATAGTAATACTTATCCATGCTT
GTTAAGAAATTCATTACAGCGTGTTTTCATAGAGACTTTCTCTATAGAG
ATATATAGAAATCTAGACATGAGGACAGCCCACTAACCCTCTTCAGAC
ACTAGCTGCTTCTCTTAGAGCCCTGGGCTCTCACCCCTTGGAGGACAGCC
ATCCTCACTCATATGTGACAAGCTTAGACACAGAATAATCACAGAGACTC
CAGCCTCCCCACAAACCCACAATGCCAATATCCCATATCCCAGGAAGT
TTTAATAAGCCATCCACTCTAATACTCCATCTCTTATCTCAGGCATAGGC
CCTGGTTTGTGGTTTGTCTCAGAGTACTGCCTTTTCTCTACCAGCCCTTC
CCACTCTTGTCTGACCCTCCAGAGATGTCAATTTCAAATGAAGGGGTTT
TTGGTCTGTGGGTGTTTGTTTTTCAGTGCAGTTCTTAAGTCTATTC
AGGGGACGGAGCAGGCAAACAGATCTCTAACTTCTGAGGCCTGTGAAGA
GAAGCATCAGAACCTCCCAGGGGAGCTGTAGGAGCAGGAGTCAGGCCTAG
ATATGACTGTGAGAGAGTGGGGACCATTACCAGTGTCTTACAAATGAGGG
GAAGGACTACCGTGCTGGGCCCTGAAAGATAAGGAGGACCAGGCTTCAGG
AAGGTAGGACACATTCTGCTGACTGTCTGGGATTGAGGACAGTAACACAA
CTACTTAGACATACTTTGAATGAAGGACAGACTTAGTGCTTCAGAACTGT
AAATCCATTATATCTTTCCCAAGTCTTAGGCTAGCCAAGTTTCTCAACAT
TTATCTACCTCATCCCAAAGGGTTCCCAGGACAAATATTTCTTACTCAA
CATTTGATGGGAGTTGGAATCAGGTTGAGGAAATGCAGGGGTGTAGATTT
TAGATTTCTGGGAATATGTATAGATAGCTACCTTCTGTTGGATAGAAAAT
GAGATTGTAAGTTTTTTCAGTGTTTTTTTTACACGAGTTTGTGTGCCCATGT
ATGCACATGTGGAGGCCACGGGTCTACCTTAGGTGTCTTCTTCAGGAACC
AGCCATCTTATTTTTTAAGATGATCTCTCTCCAGACCTCAGGGCTATCAAC
ACACCTCAGGGATCCATCCTCCTGACTGTATGTCCCTAGCATTGTTGGTTA
CTGTACCACCATGCTCAGGTCTTTGTGTAGGTCTTGGGGATCACAGTTAG
GTTCTCATACTGCAGGGCAAGCACTTTGTAAACAACATATCTCCCCTGCAT
ATGGAAGTATTACCACTAAATTACAACAAGATTTTCTTCTATTAAAATTA
TATTTTAGAAGCTGGATATAGTAATGCGTTGGGGCAAAGGAGGGAGGGA
AATGAAGAGGATAGGAAGAGGGGGAGGAGAAGGGAAAGAGTGGAGGCGG
GATCAGAAGTCCAATGTTATTCAAGGGCAGCCTGACCTAGATAAATCCCT
ATTAAGAAAGTTTTTCAGTATAGAACTTCTCATCACCTTCATTATCAGAAA
AGCCCCATAATTCAGAACACTTTTTTAATCTTAATTAGTTGACAATTTTCAT
AAATGTATTATTTATATATATGAATAACATTTTCTCCTACCTTTTTTTTC
CCTTCCCCCTCTGATGATTCCCATCCTCCCAACCAAGCCCCCTTCTGCAT
TTGTTTGTGTGCTTTAATGACCCACTGAGTTCCATTGGGCTCACTTCCATG
AGTGTGACTAGAAGAGCTATTTATCAGAATGTGGGCAACTTACCAGTAGT
GACACTGATGAAGAAAGTGTTCCTCTTACCCAGTAACCATTAAATGGCC
AGGAGCTCCTGGGAGGGGTGGGCGCCTTATGAGCCCCCTTCTCCAAAATGC
TTTCAAAGTGTGACCAGCTATATTTAATGTTTTTATTATGCCTGTGTATC
CATGTGGGACAAGAAAGCTTGAGAGTATCATAGCATGCATGTGGAGGTCA
AGAACAAGTGTGTAAAGTCAGATCTCACTTCCCACCTTCACATGGGCTC

FIG. 3D(24)

TGGCACTGAACTCATGTCAGTGACCTGAGAGGCACCTTATCCTCTAACAC
GCACCCTGTGCCCAGCCTAAAATTTGACCTTTGCAAGGTTTAGTGTTGT
TATCTGACTGTCTGAGTAAGGATGACAAAATGAAACCAAACCTTATGGGAT
AAAGCTTGGTGGTTGTATCAGTACATTTTTATTGTTGTGATAAACATTA
TGACCAAGACAGCTTATAGAAGAGTTTATTTGGGTGTATAGTTCCAGAGA
GGTAAGAGTCTGTCTTGACAAGGAAGCTGTGGCAGCAAGTGGCAGGTATG
GCTACAGGAGCAGGAAGCAGAAAGAGCAAACCTAGAAACAGTTGAGGTTTT
TTAATAGGAAAGCCCCTCCCTAATGATGTCCTTCCCCTAGCAGACCAC
AAGTCCTAACCCCTCCCTACACAGCACCACCAGCTGGGGAGTTCAAATGTC
TGGGACTGCAGGGGACATCTCATTCAGACCACCTCAGTGGGAGAATGCTT
GCCTTCATAGTATGTGCAAGGCCCTAGGTTCAATTCCTAGCCAAGAAAAGA
GAACATGAGGAAAGAAAAGAAGGTGGGAGAGAGTAGAGAAAAGAAGAGAAG
AAGAGGAAAAAGGAAGGGAAGGGGGAGACAGAGGAAAGCAGGGAAGCAGA
GGAGAGGAGAAGAGAAAAGAAAAGATTAACCAGCCTGGTTTTTAATAGCAC
CCCTCCCCTCTCAGTAGTTCCCAATTTGAGCATTAAGTTCAAGACTGAT
AGATATTTCTGGGTGGGTGACCAGTGTGGTCATAAACATGGTGACTTTTG
CTCTCCGTACAACCTTGTGATTATGAACTTGTTAGATGATCAGCTTCAACA
GGAGAGGGCCTCCTTTAGTCTCAGGTGCCCCCTCCAGCCACCCTGGGACT
CGCAGCCTCTCTGTGATGAGACACAGGACATTAAGTGGTATGGTTCTGCT
TTGCCAAAACGTCAGTCCATGGTTGAACCTCTCCACAATGAGAAAAGAAGCT
TTGAGAATCATTACATGGCATCAGGCAAGCCAGGACTGATGGAGCCTGAG
AAAGGGCCAGGAGCATCCGCAGGTTTTTGGCACCCAGTACTAACTAGTAAA
AGCACCTCATAGGTTTCTTTAAAATGCAAACACTAAGGAAAATCTAACTT
TTTTTTATTTATTAAGGCCATTCATTTTATTTTATAAGTATTTTGCCTGT
ATACATATGTACCACATGCATACAAGGTCAAAGATAGTATTTGGGTCTTC
GAACTGGAGGTACAGATGATTGTGAGCTGCCATGTGGATCCTCGAAATTG
AACCTAGGTTCGTCTACAAGAGCAGGAAGTGCTCTTAACCTTCTGAGCCATC
TCTCCAGCTCCAGAAAAGCTACTCATAAAAGTCAAATCTAAGCCATGTGT
CTGGTGATGTACACCTTTAATTGTAGCACATGGAAGGCGGAAGTAGGCGG
ATTGTTATTCATCCAAGGCCAGTCTTCTCTTAACAGTGACAAAAACAAAA
CCAAACCCGAAACCTGTTACTTTGCACTTTAGAGTATAAGTGATAGAGAA
AAGACACAGAAATTTAGAACTCTATACCTTAAAATACCTTATGGCTTATA
TGATACTGTTGGGACCATATTTACTTATGGAATGCAAAAAAAAAAAAAA
AAAAAAGATGGGGGGGGAGCTGAAGGTCTCCTTTCTATTCTGTGTGTAA
TCTAGCTATAAAAAGAGTAAGAGGCATGAGTGTGTCTCAGTGGTAGAGCA
CCTGCTTAGCTTGTGTGGGATTGAATGATCCTCAGCACACAGAAGAAGG
GTGGGGCAATAAATTTAGGAAAATAAGATGCTAATCATTGACTTTCTTGA
TTTTTTTAAAAAAGTTATTATTTTATGTTTATTGTATATGTTTATATTT
TCTATGTGTGTTTTTGATGTGTGCTGGAGGGATGGGGGCCACTTGCTGAA
CTTCCCAATTGTTATCATAACTACCATCTTTAGTGAACAGTTAGCATCT
ACTTAGTAATTGTTTTCATTTCGAATAGATACTGAACACTCTTAATCTGAAA
CTAATGCTCAGAAAGTTCCACTTTGCCAAGCAAGCAGGATAATGTAAGCC
TATAATTTTAGCACTGGGAGGGTGAGGCAGAATTGTGAGCTCAAGGGCAC
CCTGAGCTTTTGAGATCCTGTCTCAAATAAAATTAAATTTATATAGATATC
AGATTTTCAGAAATAGGTGTGTTTCAGCTGCTGAATAAATCTAAGCAAATAT
CCCCAAAGAACCCTGAAATCTGAAAGGTATTAGTTCTAAGCCCTATGTTG
TGT
TAAGATAGATTCTCACTATGTAACCCCTAGCTTGCCCTGGATCTTGCTATAT
AGAGAGACCAGGCATATGCTATCGTGCCCTGGGAGTCCCAAACGTTTTAGA
TGAAAGATTTCAGTTGTACCATTATCTTCCCTAATGAGGGCTCTGGTCTAG

FIG. 3D (25)

TGAGGCAGGTGACATTAGGCCAGTAGTAAGTATTAGGAATTGGTGATGAC
GGTCAATTCTGAGACACACAGTAGATACATCTAATCTACCAATACAACCA
ATGATTTAGAAAGAATTAGGCCATAGTTAAATTTGCAGTGTTTTCTTCT
CCACAAAATAATGTTACTTCTTTTCAGTTCTTAGTTCAAATACAGTAGGAA
TTTTTTATATTCTTGGTGCTAAACACTATTATTTTATAGTAAAGTTAGTA
AGATAGAAATGACGCCCTGTGGGTGTCTGGTCTGTAGTCTGTAGCTGAGG
CCATTTTGCTGAGAAGCAGCGTAGGCTGTCAGTGGCTTTGTCAACCATAT
TTCTGTATTTTTGCTGCAGATTGCCTTCTCCCAGCACAGCAACTTCATG
GACCTGGTACAGTTCTTCGTGACTTTCTTCAGGTAATTTCTCTATGCTAA
TTGTACACATTCCATCGAGACAGTCCCTTAAGTGCAGCTTGCTTTGTATA
TCCCTACAAAGCTGCTTTTCACTCACAGTGATGTAAATTTAGTCTGATGT
GATAAACTCTCCGTTTGTATGATTCGGCTCTTTGCATGGGGAGAGGTTT
GGGCTCAAGCAGTTATTAATAATATAGCTACTGCTGTGAGCTACATGTCT
TAATCTGTCTTAATCAAGATATGACTGTGATTTTCCATAGGGAAAGGTAA
GGTTTACTTGCAAACCTCCTGGGGTTCTCCTTTTTTATAGTTTCTTATT
AGTAGGGTTTTTTTTTTTTTTGAGAATACTATGCAGAAATGATTGAAAG
AACAAATTAGTCATTGCATATTGGTAAGAGAAGCAGCAAGAGCCACCTCA
CCTCCCTCTGCTCTCCCCAAATAGAACTGCTCTGCTGTGCTGCTTCTCT
ACCTTCACACCAATGCTCGGCCTGCCAACTCAGTTATCTTTCCTTTCTCT
TTAAGATAGGGTCTCTCCTTATAGTAGTTATGACTGTCCTGGAATTCTAA
ATAGAAGAGGTGGCTTTCAAATCACAGATCCTCCTGCCTCTGCCTTCTG
AGTACTGGAAGTATGGTGTATGCCACCGTGCCACAGCTAACTCAGTTATT
TTTTGGTGTCTATAACTGCCTTACATACATACAGACCAGGTACACACAA
AATTCCTTTCCATTAAATTTAATAGTTATATCACAATGCATTGACCAACTA
AAAAATCCTAAATTGACTTATGATTCTACTTGCTCATGTTTTAAAGGAAA
GGTTACTCTTTGCTTATCTTAAATGTAATATTTTTCCTTTGCAGTTGCTG
TTTAAATTTTCCCTATAAGTCGACCCCAAATTTACATCTATAATCTGGCA
AAACAAAAGACCTCTAGTGATGGTTGTCTCTTAGCTTTAGTCTCTCTTG
GACTCCATTCCCTCCACCCATAATGTTCCATCCTCTGTCTTAAGTGTA
TAGTCTCCAAGGCCTGCTATGTGGTTGTCAATTGTTGTAGTTACTTTCTA
TGTGTGACAAAGCACCCTGACAGTGGCAATTTAGAAAGCATATAATTG
AGGATCACAGTTCCTGGTTAGAATCCATGACCATCTTAGCAAAGGCAGAC
AGGCAGGCCTGGCACTGAACAAGTAGCTGAGATCGTCCATCTGGTCCACA
AGCATAAGGCAGAGAAGCTAATTGGGAATGGCATGGGCTTTGGAAACCTC
AGAGTCCACTCTTAGTGATACCTCCTTATCCTTCCAAACAGTATTACACA
TTCAAACCTTCAAATGTGTGAGCCTCTGGGGACCACTCTCATTTAAACCAC
CACAGTGATCTTGGCAACTTCTTTTGTGTTTCGTCCCATGCCACAGTCTTT
CCATGTATTTCTCCTTTTGTGCTGGAACTTTTTCCCTCGAAGGTTCTTGAGG
AAAGAAACATAGATAACTTTTGTATGTACTTCTACAACCTGAAAGTATCTT
AATTTTGGCCCTAACAAATTTTGTGTTGCTTACTTGCTTGCTTACTTGAT
TCTGCGTGCATGCATTTATTTGTTGTTGTTGTTGTTGTTGTTGTTGAGAC
AAGATCTCTCTTTGTAGTTCTGGCTGCCTCAAACCTCAGAGAGATTCTCT
GCCTCTGCCTCCAGAATGCTGGGATAAAGGCATGCTCCACCATACTTAAT
CCAACCTCACAAATTTTTTAAGTGTGTATTTATATGTGTGTGTGGTATATG
TAAAGGTGTGTGTGTTTCATGCACACATGTGCAGAGATCAGAGGAGTCAGG
TTTTCTCATCTATCACTCTCTGCCTTATTATTTTGGAGACAGGGTCTCTTG
TTCGATATTACATATACTAGGTGAGATAGCCCAGGAGCTTGTAAGGAATTC
TCTCCCATTTCTACCTTCCAAATGTGTGCTACTGCATCTGGCTTTAAGCA
AGTTCTGGGAATCTGAGGTGAGGTCTTACACCTATGTAGCAACTCTGCC
TACTGAGTCATCTTACTAGTATTCACAAGGTCAAAGGTTGGGACCAACAG

FIG. 3D (26)

CCAAGGTTGTCCTCAGATCTCCACACAGATGTACCCACAATTATACAAAC
ACTCAACATAAACCTATTTACACACCCACATCACACGCACACACATACAT
GCACATACAAAAAATGCTTTTTTGAAAGAAGTAGAGAATGCTAGATATGG
TATTACACGTATATAATCCAAGCCACTCTGGAAGCTGAGGCAGGAGGATT
TCAAGTTTGAAACCAGCTTGACCACATAATTATACCATGCCTCAAAAATT
GTATAGAGAATAAGAATGAATATGAATGAGACTAAAGTCATATCTCAGTT
ACTTTTCTATTGCTGTGGCAAAACACCATGACAAAGGTAATTTACAGAAG
AGATTATTGGGGCATATAGTTTCAGAGGGTGAGTCCATGACAATTATGAT
ATGGCACTGAAGTAATAGCTGAGAGCTTAAATCTGGTCCACAACATTAGG
CAGACAGAGAGCTAACTGGAAATAGCCATGAGATTTTGAAACCTCAAGCC
CCACTCCTAGTGATGTCCACACCTCCTAATCCTTCCCAAACAGTTCCAT
CAGCTGGGAACAAGATATTCAACATATAAGCCTATGGGGGTCATTCTCAT
TCAAACCACCAGTAGTAATTATTAGAGCCAGCAAAGAAGGAAGGGATAG
AAAGAAATGATTGATGGGAACTGGGGTGAAGTCTGATACAGAGAGATCTT
TATGTACTGCAGCGTAGCTCAGGAAGATAACTATGGTTAAGGACAATTAG
CTAAGTGATTAGTAGAGAGGATTTTAATATTTCCAATACAAAGAAATGCT
GCAGGCCTGAAATAGGGTACGTTTCAGTGACCCAGATCTGATTATTACAA
CTCATACACTTGTACCAACCACATAAATATGTACAATAATTGTGTCAGTT
TTATATTAAATAAAAAATGTGGAGCAAGTTAAAAAATGCCGTGTTTTAACT
GATCACAGTTATATGCCAGCTTTTCTTTGCTGTGACAAAATACCATAGGG
AGTAGTTTATAAGGAAAGAGATTTCTCCTCAGCTCATAATTCAGAAATTTT
CAGTCTAGAGTCAGTTAGTTCTATCATATTGGGCCCACAGCTAGACCAA
TACAATGATGGGGAGAAATGTGGTAAAGAAAAGTATTTACCTCAGAGTGGT
CAGGAGGAACACAAGACAAAATATACATTTTCAGTCCCATACCTCCAGTGA
CTTGCTTCATCCAAACAGACGCCACCATCCAATAGCCATTAATAATACAAG
TCAACCAGTTGATTGACATCCATTGATCTTAGTCATATCCCTAAATTCAA
CCTCTAAGCTCTGATGCTCTGGGGGCCAAGCCTCTATTGCATAAATCTCT
GGAGCATATTTTATAATATGAAATATTAACAGGCTCTCAGGAGCTGTT
TGGTAGACTTAGTTGTTTTTTTTTTTTTTTTTTGTTTAAGGTTTTTTTGGTT
GGGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTT
TTCGAGACCGGGTTTCTCTGTATAGCCCTGGGGGTCCTGGAACCTACTTG
TAGACCAGGCTGGCCTCGGACTCAGAAATTTACCTGCCTCCTCCTCCCAA
GTGCTGGGATTAAAGGTGTGCGACACCACTGCCTGGCCTAGACTTATTTT
TTAATCAGATTTGAGTCTTTGCCTCTGGAATCACAGTAGCTTTTCCCAT
TCAACACCTAGTTTACAGAAGAAAGAAAACCCAATTTTTTTTTTTTATAAT
CATTAGACAACCTAGAAGTTTTCCCTCCTATTAAGAAAACATATTAACGGG
CTGGCGAGATGGCTCAGTGGGTAAGAGCAGCCGACTGCTCTTCCCAAGGT
CCAGAGTTCAAATCCCAGCAACCACATGGTGGCTCACAACCATCCGTAAC
GAGATCTGACTCCCTCTTCTGGAGTGTCTGAAGACAGCTACAGTGTACTT
ACATATAATCAATAAATAAATCTTTTTTAAAAAAGAAAAAAGA
AAAAGAAAACATATTAACAGTATTGAGAAAACCTGTPGGCTTAAATTTGAT
GATTTGAATTTTATTTTACTAATAAATGCATGTATTGCTGGGCATGGCAG
CACATCCCAGCACTCAGGATTCCGAGATAAGAGATCATAAGTCCACGCTA
GCTGGAATAGCAAAAATAAATCTTTTTTTAAAAAATATACATACATACAT
ACATACATACATACATACATACACACACACACACTTTTCTCAGT
AGTACGGCCAATTAGTTGACTTGTCTAACGGAGGGAGGAAGAGGAGGCAG
AGAGCATGCTGTTTCAAGTACAGTTCTCTTTTGCATTCAAGTCTGGGACCCC
AGCCCATAGTGTGGTGTGCTGCCACATTGATTATTGGTATTCAAGTTAACC
AGTGTAGAACTCTCTCAGAGACATGCCAGATGCTTGCCTCATAACCAC
TGTGTATGTATATATGCTTACAGAAAATATACTCATCATTACACATAAAT

FIG. 3D (27)

TTCATCCACTTACCTCTTATGAAAAGTTGATTATTTACTGAGATTTTCT
CATTCTGAAAATCCATAAAGTCTACCACATTGATTAAATTACTTGTCTT
TACCTGTTATTGCTCATGTTAGAATTGCTTTTCTTATTTGGGGTAAGCTG
TCGTTGGCCACTGTGAGGGGCTTATCAAGAAGTCAGAAATGGGAACACCT
TCTAGGAAGTCAGGACTGGAAGCTTAGCTGAGCCAGCAAGTGTCTTCAC
ACTGCACTTCTGTGAGCCTACCTGTGCGGCATCAGGAAGTGGAGTTGGG
ACCTTGAGGATTGTTCCCTGGAGGCAGGGGTGGAGTCAGGCAGGGGTGAA
GCTGACTCACAAGATGGTCTTGCCCTTTCAGTTGTTTCTCTCGCTGCTTC
TGGTGGCTGCAGTGGTCTGGAAGATCAAGCAGAGCTGTTGGGCATCCAGG
CGGAGAGAGGTAAGCCCAAGTAGACAAACTCCACATAAAACTCATTTTTT
TCCTTCTTTCTAGGCAGATCACTTTTACCTGTTGAGTGATGATAATATT
CATATGAGAAGCATGCTGTTTAAACCTGCATTCTGTGGTCCACTATGTGC
CATCAGTAGATTTTAATTATTCTTGCATAAAGTGTCAATAGTTTGGCCAC
TGCTTGATTCAAGTCTTCTAAGAGTCTTTCCTAAGAATATGAGTGTAGA
GACAAGTTCAGCTCAGTGACAGAGCACTTGCCCTGGCATAAACTGAGTCCC
TGGATTCTAGTCTCAGCACCTCTAATAGCACAACTAGAGACAAAGCT
TCTAACCTGTGGGTCTTGGGCAGCAGGTAGGGGAGGGGGATTAAAAAAC
AAAAACAAACCTCTAGCTGTAGCCTGTGTCAATTTGTTATGACTAAGCACT
AGAGTGGGTACTAGTAGACATGCCATGTGGACATTGAGCATCTCTCCATC
CCAGGCACTGATCCAGGTGGTCTGCTTTATCTTCATCTCCACCCTAGGA
TATAAGGGAGGCTACGTAACATCCCATCACACAGATGCTGAGGTACA
GAACTGAGGGGTAACTAGTGCCTCTGCCTTCACAGCACAGGTTCTTAAAC
ACGTTTTCTACAAACACTTCATTTGTTCTAGTCTGTTCATTTAAGAATCT
CATGTTCTGACTGAATGAGCTAGACAACTCACCTTAGACTATACATTTA
AAGAAGGGCAACAAGGCAGTTTTGTTACTGTTGAGAAGAAAACAAAGTTA
TTTCCGTATGAGTTATTGAGATAGAATAGTAGAGATTTGTCTGAATACAA
AATAGAAAGTATATAAAAGTATATAAGTGGATCATAAAGAAAGCAACAAT
CAACTGGAAAATATTTGCAGTATCATGAGAGAGAGAAAACCTAGAAGATGA
ACCCCTCAAAAAAGGATTTTTTAAATATGCTTAGACTGTATTCAGTCAG
CTAATAAACTTTTTTTTACCTTTATTTGGAATTTACGAATAGCACTGAACC
TGACCATTGTAAATGCACGAGGTCAGGCATGACTTGTTCAGTAGGAAG
TTGTTTTTAGTTCTTGCTGTGGCCTGGGTCTGATGGAAGTTCTTTACCC
ACCTTATCTCCTGTCTCTTGCCAGAGGTTCTAGAATAGTGCTGTGATGG
GGTAGCAACTGTCTTCTGTGACCTGCACCTAGATTATTACAGAACCCA
GACTGGGTTTGCTGAGTTAATGGAAATCTTTCTAGGTTCACTAGAGAGA
TGTGCTGACACATACTAGGCCATCTAGTTTTTTCAGTAATGCTCAGAGACC
GCAATAGGATATGTAAACAGCAACAAAATTTTTAACATAAAATTTCCCTTC
TAAACAGAGTGATGATTTATGTAGCTTCAGGATCCTGCCTCCTAGAAGA
TGGTTTGAAGCAAGGCCAGTTTGTCTTCCCTAGCATAACCTCAGAAGACC
TCTCATATTATTGATGGTATAGGAATGAATGCCACATTCGTATTTGAG
ATGTGTGCTATAGTATCTCATCTGACCCAACATGAAAACATTTCAAGCCA
TGTGTGCTTGGGTAAGGTAGGAGTTCAAAGTCATCCAGTGAGTTCAAGGC
CAGCCTGGGCTGCATGAGACACTGTCTCATAAACAGACACTTGAATCTCA
TTTAAAGAAGACATTGAAGACTTGATACTTTGAACACCTATCCTAACGTA
TCCACCCCCAAATCCAGAGTCCTTCATGTTCTTGTCTCTGCAGTTCCAC
TTTCATTGTGTTCTCAGCAGCAGCTCTCTCCGAGGAGAGTTGTCTCCCAT
CCTATCAGCCATCTTTTTTATTGTTGTGCTCTGACAATGTCTGGTTTCAG
GTTTTAACACAAAGCAAGCTAGAGTGATTTTAAATCTAGCAACAAAATAT
AAAAAGGTAAGTTTTTGCCCTTTTATATATTCAATCAACAGATATCATAG
CATTATATCCTCCACTTTAACTTTTATTCTTACTGGTAAGGGCTTTTTTA

FIG. 3D(28)

TAAAAATATAATAGTGTTACACATGTAACAAAATTTGATACCTTGTGCT
ACCTAGCACCTTGTTCATGTCCAGTTTTCCTCAGCTGTACAGAAAGCGACA
CTGCATCTGATCAGTTTGAATCAGAGAGAGTGATGATGTCTAATATCTA
GTATTCACCTAATAAAATCTCAGTACTAAGCATATTAATAATACTATATTA
TTCATTAGCAACTTCTTCGGGAGATGCAACAGATGGCCAGCCGCCCCCTT
GCTTCTGTAAACGTTGCCCTTGGAAACAGATGAAGAACCCTCTGATCTCAT
TGGGGGAAGTATAAAGGTGAGAAGTGGCTCAAAGGTCCATATAGCTTTTC
AGAACTCAGGCCTCAGTTTGTCTAGGCTACAGACAGCAAGCGCTCTGTGTG
TCACTCCTGTCTCCTCTCTAACAGTTAGTTCAGCAGAAAGCAACCCCGAGCG
ACCGTAAGGGGCTCTGTGTGTGGCTTTACTTTTCGAGTTGTTGCATGTCA
GATTTTAACATGCAAATTAAGCTTGTATTCTTACTTTGTGGCATAATAC
TTTATAGTTTTTATTTTGGAAATATCTAATCTGGGCTAGGTGTGATGGTGC
ACATCTTTAATCTCAGTTCAGAGGAGGCAGAGACAGAGGCAGGCAGGATC
TCCTTGAGTTCTAGAACAGCTGGTCTACATAATGAGACCTATATGTTAG
AAAAAAGAAAGAGGGGGTGGGGGAAGGCAGCTAACTTTAACCATTAAAT
GAACCAACACACACACATTTTGTTCAGAGCCCCAGTACTCAATTAAGC
CAGGCAGGCATGGTAACAGTACTTAGGGAGTCAGAAACAGGATTTCCAGA
GTAAGCAGTCTGACTAGGCTAGCAGGAAATGGTGAGTTTCAGGTTTCAGCA
AGAGGCCCTGCCCTCAGTAAGTAAATTTGAAGAACAACCTGAGGGAGACTTGC
ATGTGCACCTTGTGCATGCACCCACACATGCACCTTGCACACATACCATATG
TCACCATGCTTAGACTATAAAATGTAGTCACTACTGGCAGCACATGCCCTA
CAATACAGATGCAGGAGAATCACTGCAAATTTGAGATCAGCCTGGGCTAC
TGGACAAGATTTTGTCTCAAGAAACTAAACAATACAAAAGTGTACTGG
GGGGGTATTCTAATGCCAGTGTATTATGACAGCACATTCAGAACTGACAG
TAAAGGCAATCAAGGACTGTCAGTGGTGGGTATATACATAGGCAGAGGAG
CAACTGCTACTAGAACTGTTTATCCTTTAAAGACTAATGTATGCTGCA
GCATAGACAAACGTTAAGTTGTGTTAAGTAAAAGATGCTGTATCATTTCCA
CTTACCCATCGAGAATAATCAAATACAAAGACAGAGTAAATAGTGAAGTGC
TAGAGGCTTAAAGAAAGAACAGGGGGTGGGGAAAGGGAGGGAAGGAAG
TGGGAGAGGGAGGAAGGGAGAGAGGGAGGGAGGGAGGCCAGACTTTGTGGC
TTACAGCATCAAGAGGCTGAGGCAGAAGGGTTACAAATTCAAGGCCCTAC
TGGGCTACATAGTGAGAAGTAGGATTTCTTGTAGCTGTCTTTCTAGGTCA
TAATCTCTCATTTGGGGGAAGTCAGGGCAGGGACTTGAGGCAGAAACCATG
GGGAATGCTATTTGCTGGCTCCTTCCCAGGCTCCTCTCTAGCTTTGTTTT
CTCATTTTGTTTTTTACTGTCTATGGGTGTTTTTACCTGCTTGTTTTTCTGT
GTACCATATACATGCCCTGCTACCCACAGAGGCAGTATGCTGGAAGTGG
AGTTACAGATGGTTGCAGGCTGCCCTGTGAGTGTGTTGGAAGTAACTGGG
GTCTCTACATGAGCAAGTGTCTTAAACCATTGAGCCATCTCTCCAGCCT
ATAAAATTCTTTTTTTAAAAATAAAGTCTGCAACAGAAAAATGAATATTTTC
TAGAGCTGAAGCATTCATGAGTGGATAAAGAATCCATTTGATGAGCTAT
CTACCTTTTACAAGCTCTTAAACCCCTACAGACTCAGGACTTAGTGGCTGG
AAGATGAATGTAAACAGGTAGCTCTCTCCATAATATCTGGTCTGTTTGT
GCCAGGTGTGCAGAACTGTGCAACAGGTCAACATACAAACCGGCGTGGGC
CTTTCCTGACACTCACACAGCTCTCGGGACAGTGCCGGGTGGGGACCTCTT
ATTGACCTTATAAGCACCTGACTGTGTCAGTGTAGCAGGGAGTTAAGGTGC
TTCTGTTTTTCTTCTCCAGACCGTTCTTAAGCCCATTTGCCCTGGAGCCCT
GCTTTGGTAACAAAGCCGAGTCTCTCTGTATTTCGTGAGGCTCCCTCGA
GGACTGGGAGGAATCCCTCCTCCTGGTTCAGTCAGGTGAGTAGACAGGAGA
CAATGACAGATATTGGTCTGTGAAGGACTGAGTCTTAGACACTTCTTCTG
GTATAGAACCTGGGTCTGGGCACAGTGTCTTAGTGGTACAGAGCTTTGGTG

FIG. 3D (39)

GAACAATTCTATAGTCCCCAACTGTGTTCTGAGCACTGACATTCCTGTC
CTGGGGTGGGAAGTTCAGGACCTTCCTCACGGTGCACAGCGTCCCTCAGACA
TTCATGCTCTGGTCCCCCTTGACTCTATTGATCCCTGCTTTCTTTTTTTTT
TTAACCCTTGTTCTTATCTCAAATTTAGGCTTTTCTTCTTCTGATACAA
GCTCCTATTTCATCTCCATGCCTCTGGCTTCCAGCCATGTCCTCAAAGCTT
GTGTTGCCAAGTACAGAGTTCTAGTCATGCTCCACATCTTCTTAAGGTCT
TGCTATGCAGCCTTAGCTGGACGAGTGCTCGTTATAGGCCAGGCAGTGGT
GGTACACGCCTTATGTCCTAGCACTGAGGAGGCAGAGGCAGGCAGATCTC
TGAGTTCAAGACCACCTGGTCTACAGAGTAAATTCCAGGACAACCAGAG
CTACATAGGGAAACCCTGTCTCAAAAAAATAAAAAACAACAGGAACAA
CCCCAAAACCTCATTATATTGCCAGGCTGGCTTCAAACCTCATAGTTATC
CTCCTACTTCAGCCTCCAAAGTGCTGGGATTATGGGTGTGACCCTTCATG
CCCAGATTGTCTTAAATATGAGGCATGAAGAAGTATTATGAAAACATAAA
GGATATTTTGAAAATTATAATTCTACTGGGTAAATGCAGATCCATTTTCA
TTTCATTGAAATAATGATACAGCCTTTGGAGGTTAGGGGAGCCTCTCCTG
TTTTCAAACCTGACTTTGAACTTCTGATCATCCCGCCACCACCGCCACCTC
CTCCTCCTCCTCCTCCCCAGTGCTGAGATACATCACTACTCCTGGTT
TATGTGGCACAGAGGCTCAAACCCAGGGCCTCATGCATGCTAGGCAGACA
CTCTACCAGCCAACCTACCCACAGCTCCTAGATGTGCACCGTATTACAAA
CATTTATTTCTTCAGCATGTTTTTTTTTTTTTTTTCTTAAAAATCATCTCTA
CAGGAAACAAGTACCAGTGGTGTTTTAGGGCAGGAATAGGAAGAAAATAT
TTTTACTATATACTCTTTTTTTTTTAATCATTTTTTTAGATTTTATTTATT
TAAAAATTTATTTACTATTATAAAGTACACTGTAGCTGTCTTCAGACA
ACCCAGCAGAGGGCATCAGATCTCATTACGGATGGTTGTGAGCCACCACG
TAGTTGCTGGGATTTGAACTCAGGACCTTTGGAAGAGCAGTCAGTGCTCT
TAACTGGTGAGCCATCTCTCCAGCCCCCTACTATATACTCTTTTAAATGAC
TTATTTGCTTTTTATTTTTATGTGCAATTGGTAATCTGCCTGCATGTATGTC
TCTGAGAGAGGATCAGATTCCCTTGGAAATTTGAGTTACCTTGTGGGTGCTG
GGAATTTGAACCCAGGTCTCTGGAAGAACAGCCAGTGCTCATAACTGCTG
AGCCGTCTCTGCAGCCCCCTACTATATACTTTTTTTTATAGTTTTGAATTTT
TTTTCTTTTTTGGGTATTGCTAAGGATCAAATATAGATCTACTATTTATT
TTTTATAACATCCATTAGTATTTTTATAACTTACTACATAGTTTGCCAAT
TCTTTTTATACATGTCCATCAAACATGTAAGTCATAATTTATATAAACCTT
GTGTTAAAGCTGGAGGCACAGAAGGAAGATTGCTACAGAGTGAAGTCTAG
ACTAGCCAGGGCTATATAGTGGGACCTGTTGCAAAGAAAAAGTTCTCTC
TTTAAACACAAAGGCAGTATGAAAAGACATACCTTGATTCTGAAGCTGTG
CATAGGAATGCCTCACACAGTGTCTGCTCAGGACTATACTCAGATGCAG
TGGTCTGAGGGACTTGGTGGTGTCTCAGCCAAAATAACCTGGAGTTTAGT
AGGAAAGTCTCCTTTATCCGTGTCCAGTCTTGAAGGGAAGCCTTATTTAT
GTATGATGAGTCAGGACCCATTGTCTTCATCTTACTTGGCATCCCCCAG
CACTGAGTCTCTGAGTTAGCCTTACTTGGACAGAGTGACTCTCTGGGCAC
TCTGGACAGCATCTCCTGCTTCAAAGGGCAAGATCTTTAGAAGACACAG
AGATGGAGCAGGTCTTACATGGAGATATAGCAGCTTTTCTTCTGACCC
TGACCCAAATGCTTCTTTGGAAATCCTCATGAAACCCTGCTCCTTTCTGG
AGACCCACCCACAGCAGGGTTATCCATGCCAAGCTTCTGTACTTTCTC
TTTTTGAGGAAGCACATACACAAAGTTTTAGTAGCTCGCACATCTCAC
TGTGAAGTAGTGATACTTTCATTGCTATCTTCTGGAAACAGGCAGGAGTA
GGCACACGCTCAGAGCATAGCTGCACTCTCATTCACTTGCCACCCTGAGG
CAGAGCACACGACTTTGTGATCTGCTATGGAGGAGAGAGAAATGAGTAGT
TAGGTGTGTATAAATAAGCTAACACCATCACCCCTTATCTTTCACTAGG

FIG. 3D (30)

GAAATGTAAAAAGAAATCTGAAATTATTTTGTAAAAAAGTAAGCTGCTTC
ATGACACATGTCCCTCTTGTGGGTCTTCCAAGGTCTCGCTGTGGCCAG
TGCCCTGGTGGACATTTCTCAGCAGATGCCAATAGTGTACAAGGAGAAGT
CAGGAGCTGTAAGAAACCGGAAGCAGCAGCCGCCCTGCACAGCCTGGAACC
TGCATTTGATACTGGGGCAGGAATTCGCCCTCACAGAGGGCGTGTGGTCC
ACGAAGCTGTCTACAGGGGAGGCTGCAGGCAGGAAGCAGGCGTGGGGCAG
AAGACTGGGGACCCCTTGAAGCGTCCAACCTCATGTGCATGATCATGCAAGC
TGTTTTTCATGGCTCACCCCTCTGTGTCCAGCATCTAACCTTTTACTTCTG
TGTAGGAAATAATTTAATTACAAGTCCAGGAATGGTCTGCTCTACTCATG
GGTGGAGGAGACCAGTGCCGACCCCGTGAGAGCTGAAGGTGATGCTGAGG
TCCCTTGTGGAAGCCTCTCTTGGGAATCTCAACTGCAGAGGAGCTGCCCT
CTGTCAGCAGCTCTCCAGCATGGTCTCTGACACTCCTCAGATGAACTGT
TCTCATCGGAAGCTTGCTGTCTTTTTTACAAGATGAGCTTTTACTCTCTTC
CAGGAAGTAGCTTTTTTTCTAGCTGAGAATTAATAATGGTCTTTCTCTTT
GGAAGTCATATCAAAGTATAAATTGATGGGGGCCTTGTTTTGTGTTTT
GGTTTTTGGAGACAGGGTCTCACTGTGTAGTCTTAGCTGGCCTGGAACCTC
ACTATGTAGATCAGGCTGGACTGAACTCACAAAGATCCACCTGCCTCTGC
CTCACAAATGCTGGGATAAAAAGCATGAACCACCAGGCCAGCAAAGAGG
GCTATTCTAAATGTCAAGGTCAATGGAGTTAGAATATATATAAAAAAATG
CAATTGATAATTCTCTATAGAACTTGATTAATTTTAATCCATTCTTTCC
TTCTCTTTCTCTCACTCTGTCTTACACACATGCACACATACACACACT
AAGTGCCTAGACTTTGAATAGATCTAGCAATTGGACATTAGTAAGCCTAA
GTTTTTACATGATTGCATTCTTACATTCTTGTAACCTTTAAGTAACCTACC
ATTGCAGTTTGTTCTTTTTTTTAAAGTCTAATTTGCAGCCAAGAACGAGTA
ATTCTCACCCCAAGCAACATCTAATAGGGACTGAGTGACCCCAAGCCAGC
CTAGTGTCACTTTAGGCCTGACGTTTGAGCAACCCTCGGCTCTTGCCAAG
GCACCACAGAATGCACTTGCTCATGCCCTGTGCCCTCTTGAGCAGAAAAGA
GCACTGACAACCTGGGACACCTGGCTCTGTCTTCTTACAGCTGCTCGCACT
GACCTGTGGGAACCTGTGGGTCTATCCCCAGGCTGAATGGAGTACACACTA
GAAGAGGGATGATGCCTAGCATTTGGGGCAGCATCTGCTCAGCACATGGAA
AGGGACCTGGTTCCATCTCCCCCTGGGCAGGAGTTGGTCCAGCCTCCTCCC
AGACCCAGCTGGTGGCTGTGAGGAGGTGGGGAATGCTAATGAGAATGAAA
AGCACATGGGTGATGGGAAGGGACAAGATTACCACGTTAGGAGGGTGAG
CAGCCCTCTGCTATGTGCCAGGACCCTGCCTGGACATTGCATTTCCCCA
TTTATGGTGCTCCGTATTTCTGGCATTATGCAGCAGCCTCACACACCTGTC
CTCTCCTTCTTCATGTCTTACAGTTCTGCTATCACCTGACTAGAATAGCC
CTCTAGGCAACAGTGCTCAAATGTATGAGTTTGAGAGAAGTTAACAATCAG
AAGAACAAAACTGTAGTGTTCACCTTTAAATGCAGTGTGTAAGAGGGA
GCCTTTCTCTAAGCCCTGCACTAACCCTCTCTCCCAAGACTCTTGTGGA
GTGACAGTTCCAAGCTGAACCATAAATCACTGATGCACAAAACACTGCTA
GAAGGCTCACCTCTCAAAACACGACTCTTTGCATCACTATTAAAGAGCAG
AAAGTTCTAGAAATGATCCCAGCCTCATCCCCTATACAGTTAGGAGCTCC
CCACATCTCTACCAAAACCAGCACATAAGTATCTGCGTGGTCTAGCCTT
TCATCTCCGTAACAAGCCAGGGGACTCTTGCCCAAAGAAAGAAAGGGAA
GTTGCACTAGGGCTTGTCCGTCCATAAGGAATTCCCCTCTGCTTTGCTCA
AAGGACCAAATTTCTTTGGCCAAAGAAGTTGCTTCTATGTTAGTCCCAT
CCCTGAAGTAATATGTACCATGGCTCCACCTACCTGTTTATGCTCTCCC
TGCCCCCAGGGAACTGTTTATTCTTTCAAAAGAAGCAAACAGCGTTTCAT
TTCTGCTCCTGTAATGGAGAAACAGCCAGCTCCCCCTGCATCCCTTACAGC
CAACAGCTCCCTTCAGGCTTAGAGCAGGGGGAATGGCAGGGATTAAAGAGC

FIG. 3D (31)

TCAGCTCAGAGCCAGTTACCAAGATGGAATGGAGTTGTGACCCAGTAACT
GTGTACGAGAGACCATGTATATAAAATAGTCATGACGACACTGACCTCT
TGCACTTGTACATAACTATACTGTAGTGTCCAGAATGTTTACAGACATTCAG
GGTGACATAAACAGAAGAGTATCATAATGTATTTTATTAAACACTAAC
ATCTGAGTTTACCTAATCTGTTTCTGTGCCATATACTGGGTATCCAAGC
TCTGGGAAGTTATCCTACCAGGCCCTGATCTGTTGATAAGGCACTATACA
CCATGCTGGTGTGTTCTGTAGCCTTGTGCCCATTAGGTAACGAACAATG
ATTGAGCTCTTAGAATACCTAGGAAGACAGCAAGCAGGGTGACACACGGC
TGTGATCTAAGCATTTCAGAAGACAGAGGCAGGAAGAAAATTCAAAATGG
GGCTGGAGAGATGGCTCAGTGGTTAAAAGCACTGGCTGCTCTTGGTCAGG
ACACTAGTTCAGTTCCCAGTACCCACATGGTGGCTCACAACCTTCTGTGA
CTACAGTTCCAGATAACCTGACACCCTCCTCTGGCCTCCTCGGGTGCCTG
TGGTGGTCCACCTGGTGCACAGACAAACACCCAATACACACAAAACAAA
GTAACCTCAAGAATAGCCTGGGCTACATAGCAAGAGCCTGTCTCAAAACAA
ACGAACCTATGAAGAGCCAGGCAGTCTATCTATTTACATGGCAGTATACT
AGAGAACTCAGGAAGCAAGAGTGTTCATCACTGTTGTAATTTCAAATGC
TCCTTGTGATTTCTGGCATCTCTGTGGGGTGAGGTGTTCTGTTACTCTTC
ACATTCAAAGACTGTCACCCATGAACGTCAGACTTTGCAAAGGGGCTCTC
TAAGCTGCACTGTTGTGGCTTTGTCTAAAATTTTAATGACGTTTCTGAGA
ACCATGTTCTTTTATACTAAAATCTGGGGATGGGAGGGCTCATTTGTTG
ATAAATAGCACTATTTTCCACACCTCAGCCTCCTGTCCCCGTCTGGTC
TTCCCTACACAGTCTGGAGAGGGCTCTGAAAGGTCCACAGAGTTTGACAG
ACACGAAAGCAACCCATTGCCCCGTTGACCTGACCTGGAAGAAGACTGTC
AGCAAAAGGAAAATACCAGAATATCTGGAAAGCTTGAAGTGTAAGATGGG
ATCTCGTTGGGGAATTGGATGAAGAAAAGCAGAGCGCCTCTGGTAGGTGA
CTCTGCAGCCTGCCAGCGCCCCCTCTTTCTACACAGCAGAGTGTGCAT
GGCAAGGAAATGAGTCACCTCCTTGGGGGATGGTGTCTGTTTTTATGAAAA
CCTCTGATCCTTGGTGTCTTTAATTGATCTGTTCAACAAATATTTACTA
AACACTTCTAAGCTAACATTAGGGCAGTGAAGTGGAAACCCAGCTC
TTTAGACAGCTGTCATCCTAGGATAGCTTCTGGAAGCAGAACCAAGAAG
CCAGAAGGTTCTTCTAGGGTGGCCTTGGCTCCCTGAAGGAATCTGAAAT
GCTGACCCTGTCACAACCTCCCAGCACAGCTTTGGAATGAGACATCAGCC
TGGCCTCCAGCAGAGCAGAGGCTCTGGAGCTCCACATCCTGCCTGCAGGG
AGCCCTCAGGGTGGCCTCCAGAGTACAGGGAGAACTAAAGGCAATAACA
GAAGCTGCTCTCAGAGCCTGACTGTGACACAAAACACTAGTGAAGCCTGCT
GAACTAATTCTGCCTCTGGAAATCTTTTCTGGTTCTTTACAGTTTGTGTG
TTTGTTTTGTATCCAAGCTTAGTTTGTACTATGTGTGATTTAGCATCTGT
CGCACTTGTGTAAATATGGAGTAAGTATTGTAACTATTTAATTGCTGCG
ATTGTTGGGTATACATACATTTAGGACTGCAATTTTTTGGTATTTTTTG
TATTGTAAATAACAGCTAATTTTCATCAGGAACAAGAGAATTAAGGGGGT
CTGCATTTTAAATGCAGATGTGAAGCACTTGTATATAAATAAAAGTAAAT
ACTATAATACAAAGTTCCTTCTGAAATAAAAGTAGATCTGGTAAAAATGT
GCGTGCGTTTTCGTTCTGAATGTTCAATGCTAATTTTGTTTTATTTATAT
TTACATTTTAGTCCTTATTTTAGCAGTGAGGAGACAGGCACAGCAGTGCA
TTCTCACCTTGGCAGCTGAGGAATCCCCTAGAGTAGACTGCAACTCAAGA
CTCTTGGCTTCCACACTGAAAAGAGTTTCAGTTTATGAAGCAGAGTTAG
GAAGTTTAGTGAGGAATTTAAGGACTTCTTTAATGTTTGTGTCTACATA
TGTGGGTACATATATGACACAGCATGCATGTGGAAGGCAAAACACCTT
AATGGAAGTGGCCTGAAGAACAACTCAGGACTTCAATCTTGGCAGCATA
AACCTTTACCTAATGAGTCATCTCCAGTCTATACGGGGTGTGTGTGTGAA

FIG. 3D (32)

CACATGTGCAACAGCACACAGTGGAGGTCAGCACAACCTCTTGCGAGTCAA
TTCTCCCTTACCTTGTAAGACCTAGAATTCCACATTGCCCAGGCTCTGAA
AGTTAGGTTGGGTCCACACTGGGCCATGGCTGATGAAATGTTGGAAAAGT
GATAACACCAAACCTTTTGCACAGAAAATATTTTCATCTGGGGCCTTCCCT
GGAGTTCACAGGCTAAAGTGTTGGAAGGAACATGGGTCCCTGAGCCACCA
CTTTCACAAAACTACCTGATCAAGAAGAACTATTCTGGGTTTCTGTTGC
TAAAATTCCCTTCCCAGAGAGAAATGTAAGCAATGTCTGCCCCCTTCAAGGG
TCCCAGCAAGAAACCAAGGCACAATTCCACCAAAGTTCAGTAGAAAACCA
GTGAGTTTATTGGGCTTCCGTGCAGAACATACATGAGGGGTACTTAGAG
AAGTGTGGATACTCCTCCCCCTAACAATCCACACCCTGAAAAAGCCTTAC
CCAGCAGGGATGAGGGCTTCCCCAGACCCACATTGATGGTGCTCCCATTC
CATTTTTCCCTGGCATGCAAAGAGATAGACAGAAAAATAGATTATATATA
ATATACACATAAATTAGAAAAATAGATTATATAATATACACATAAATTAT
ATATTATATATATAATATATAATACACAGATAGATTATATATGATATATA
AAACACACAGAAATAGGGTATATATAATATATAATACACAACTACTCAG
CTATTA AAAACAGTGGATTTCATGAAATTCTTAGGCAAATGGATGGAAC TA
GAAAATATTCTGAGTGAGGTAACCCAATCACAAAAGAACACACATGGTAT
GCACTCACTGATAAGTGGATATTAGCCCAAGCTTGGAATACCCAAGAT
ACCATTACACAGACCACATGAAGCTCAAGAAAGGAAGATCAACGTGTGGGT
GCTTCTGTTCTTCTTAGAGGAACACCCTCATAAAGTAGTGGTGGGGGGTG
GGGGGAGACAGAATAGGTGGTTTCCAGGAGAGGAGGAAAACAGGAAAGGG
AATAAATAACATTTGAAATGTAAATAAAGAAAATACCCAATAATAAAGA
AAAAGAATTTTGAAACAGAGGGTAAAAAATAATACACAAACCAGGTAGAT
AGATTATATATAATATATATAACACAGAGATAGATAGATAGATAGATA
TAGATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGGTCAACTGCTC
GCCCCCTCCACTAGGTAACATGCAGTTAAGGCAGAGCTGCATACAACAGAT
GTTAGGGATACTCAGGTGAGAATCTCAGGCTTTGCTCCATCCATCTATGC
TGGGGTGTAAGCTGTCAACAAGTTTAGCTGGGATGATGCTTTGCAAGAGG
GCACAGCTGAATGCCCTAAGATGGTAGATGCTTGGCTCAAAGGAGACACT
ACAGCTCTGCATCAAGGCAAACCTAAGTGAAGATGAGGGCCTTTATTTTCCA
GATCTGTATCCTGGAGCATCATTACCTGTTACTACACTGAAAACATTTG
GTGTTGGTTTTCATGGCAGATGACAGGCAGTGAGAGAAGTACAGCAGCGGA
CTGCTAGAGGTGGGGGTTCTGTCAAGGACGTGGGAGGCTGTTTGGTTAGTA
ACTTGGAAGCAACAAGTTTTTAGCTAGAGGGAGAAAAGCTGGAGATAAC
TGTA CTTGCTTGATTCTTAAATATCAAATTTTATTTTATGCATATGGGT
ATTTTGCTTGCATGTATGGCTATACACTACATGCTTGTTGGTGCCACAGA
GACCAGAGGAAGTAGTGTGAGCCTCTGAAACTGAAGTTACAGACATTACG
ACTTGAGTGCCCTGAAACTGAACCTTGGTCCTCTGGAAGAACAGCCAGGGC
TCCTAACCCTGAGCTATCTCTCCAGCCCTGACAGAACATCATGTACTCC
AGGCTGGTCTCAAATTTGCTTTATAGCCAAGAACGGTCTTAAATTTCTGAT
CCTCCTGTTCTCTCAAGTAGTGGGGTTACAGGTCTACACTGCCGTTTCT
TGAGCAAATCATTACAAATTGAGTTCTAAGCCAGGTGTAATAGTTTCATGT
AGTAACAATCTGGAATTTTGGTCTCTTAAAAAAACAAATATTATAAGAAT
GTATTTTCATTTTAATCCCAGGTGTATGGCATATATCGAACTGCTTTGGA
CTGACTACAGCAGCTATGATTTTTTCTTGTTCCTAGCAGAGGTATGGTTTT
GCCAGCTACAGATAGTTTTCTGTGATTGTGTGACATTTGGAATTTCTGGA
CTTTTCAGATGGTATATAAATATTAGAGCCCCAATAGGCAGAGTTGATGA
TTGTTGGTCATTCAGGGGTATTGGTTGTGGTTAGTAGTCTTGCTTGAAGA
AGAAACAAGAACAATTAGATTCAGAGATCTCTATATCTCTCTATCTT
CCTTTCTGTCTATCTAGTAATAGGGGGTAAAACAGGATGATAAAGGGT

FIG. 3D (33)

TGGGGGAACCCACAAAGTAACAAAGACTGGCTACAAGTGGCACCCAACTT
GGAAC TCAAAATTGCCATAGAGGAAGCAGCAGGGGATGAAGGAATGGATT
GTGGCTGTTGTTGCTGGGATATTCCTCACTTTGCTCCCAGAGGGGATTTT
TCTGAGGTTTGTGTTGTTTGTCTTTGCTTTGCTTTGCTTTGCTTTTCTTCTACATA
TTCTGTTT TTAAGTAAGTTGAAATAATAGCCGAGAAGCTGGAAAAGTTT
GGTGTGGAAATGGAGCAGCCTGAGAAACAAACAATGTATGAAATGGGAAA
ACTAAAGGGGCCACTCTTCTCTCTTTTCTGAAAGGCTTGCAGACTTGGTG
GTGCACCTGGAGAGTTTATGGATGGAGATGGAAGCTCTTAGGAGACAAGA
AGCATGGAAAAAGAGAACAAAGGCTCAGTCCCAGTGACTGAAGAGAGCAG
GAGTTTTC AAGAAGGTGCATGGGAGGGCCACTGGTCAGAAAAAAAAGG
CTGAAAAATACCAAAGGACAATGTGCTGAAATAGCCCATTTC AAGAGAAA
GGGTTCA TCTCAAACCAGCATTCTGACAGAGTGGAAGGAGGGGTGGCTCA
GGGTTATGAGATCACCATCAGCTTTTCCAGTTTTC CATATAGCATATGC
CTGCTAATGGTATGGAACAAGAGTAAGGCAAAATAGGATGGTGTCCTATA
GAAATGATAGCTCTAAGGTGTTTTTAAAAGGCCTTGATTTCATATGGAAT
GCACTCTCCTTATGTGGAACGGATATTAAATAACCGGGGTACACAACTA
GAATCCCTTCCCAAGATTGGAAGGGATTGGTAACAGCTGTACTAGAGACT
GTCAGCCGTTGCAATGGTTAACATGCTGGAGGAAAGAAGCTGTGAACATT
GAACAGTAAACAGAGCAAGGGGTATTAATATAGTGAACGAAACAGCTGCT
AGGTGAAGGGCGGTACTCTAGTGTACAAGCACAGACTCGGTGTCATGAAA
CTACTATAGAACAAGGTTGCCTCAGTGGCTATAACACCTTGGGACAAAGG
AGGAGCCAGGAAAAAGTCCAGTTTCA TTTACAAAGATTATATAAGGCTCTG
GAGAAGCCTTCACTGATTTTTTTTTTTTACAAAGATTAGTCTCAGCTATGA
ACAAAGCCATATCAGACCCTGACACAAGGCAGGTGTTGATAGACCTTG
GTGTATGACAATGCAAATACCAAATATAAAAATGTCATTAGACTTTAAA
GGCACAAGTAATGCCTATGGATGAGTGGATAAGGGATAAGACCAATATTA
GTTCTAATGTGTACTGTGCTAATATCATTGATCAAGCTATAGCTAGAGAT
CTCTGATGTCAAATGCCTTGTGCTTCAGTTGCAGCAAATACAGTAATTT
GCAAGGAGTCATTGTGGCCAAACTAAAGGTCTCAGATCTCAAATGCCT
GATGCTTTGTGGGAAATAGGGTCATTGCAACAAAAATGTGAACAAGACA
TCTTTAAGGGCAATGGTTTCTTAAATATAAACCAGAAAGACGGCCTAGG
CTTCCAAGGTTGTGCTGGCGATGTGGCCAGGGTTGCCACTGGACCAATGA
GTGTAGGTCCAAAAGAGATATTCAAGGTAACGTATTACCATCATGAAATG
GTCTTGGGGGCCCTATCTTGAGGGCCCTGCAGCAAAGAGTATGAGCCATTCC
AACCAGAGAGTGGCATGGAGACTCAAACCTTCACTGGGCACTGGAGATT
TAATGCACACTAGCTATTGCAGGCAGCATGGCTCTAGACTTGGCCACAGA
TAAACATCTTGCTCTATCCCCCAAATTCAAAGTTATAACATAGCTACTG
GAGTGTATGGTCTTTTCCCTCAGGGACAGTAAGGATAATCTTGGGAAGG
AGTGGATTGACTTCCTAAGAATTCAGTGTGCATCAGGAAGTATAGATGAA
TATTTCAAAGGAGAAATTAAAATTGTGGCATATGTAAAGGTAGAGCTGCA
ACTTAACACAGGCGATAGGGTTGCTCAGCTGCTGCTGTTTCCCTATATCA
AAGGCAAAGCAACTGCAGCAGAAAGAGGAGAGGCCTGAAAACCTTGGGCA
CTGACACAAAAATTGCTTATTTCA TTGAAAATGTCGTGTTTATAACTTCCC
ACTATACAGCACAAACAGGAGGGGGCTTAAAACATAATGGGGAAAATGTCA
CAATTCTGCAATTTTGTGTTTCCCTTAAAAAAAACACACACAGAATTTTA
ATAATGTGTTCTCATCTTAATCCCGGGTGTGGGAATTAGGGCTGCTTTGG
ACCATTTCCAGCAGCTGACTATGATTGCTCATGCTCTAGCAGAAGTAT
GATTTTTGCCACCTGCAGATAGTTTCTGGGATTGTGTGACATTGGAATT
TTGGGAAC TTTCTGAAGGTATATAAATGCTAAGGCCCTGGTGGGGAGGG
TTGGTGGTTGGTGGTCATT CAGGGGGGTGGTTGTGGTTAGTGGTCTTGCT

FIG. 3D (34)

CAAAGAACAAACAAGAAAGTCATTTGATTTCAGATGTATCTTTCTTCCTTC
CCCCACTCTTTCTCTCCTCCCCCGGCACCCTGCCCCCTGCCCCGACCTC
TACCCTTCTTTTCTATCTAGTGACAAGGATGAAACCAGGGGGATAAAGG
GTGGGAAAAAGAAGAGCCCACAAAGTAACTCAGGTTGGCTACAAGTTTCAT
GCCAAGAATCCTAGGACCTTGTTGTTTAAAGGCTTGTTTATTTTGTGAA
CATGAATGTTAAATGTACATACATGTTAAGTGTATGTATGTACACCATAT
GCATGCATACAGAATCCAGAAGAAAGTACATTATACCCTGGAATGGAACT
TAGAGTTGTGAGACAGCATGAGGATGCTGGGAACTGAACCCAGTTTCTCC
ACAAGAGGAGTAGTTGCTCTTCACTGCTTAACCTTTCTCCAGCCCCAAT
CCTAGCATTTTGGAGGCTGATGTAGGAAGATTATCCCAAGTGTGAGGTCA
TCTTGGGCTCCATAATAAGTTTAAGACCAATCTCAGCTCCAGAGTAGGAC
CCTGCCTCAAAAACACACAGGTGGAAAGATGGGTCCGCAATGAAGAGCAC
ACACTGTGCCTCCAGGGGACCCAAGCTTGGGTCCAAGCACCCCTTGTTGGG
CAGCTCACAACTGCCTGTAACCTCCACCTCCAGAGGATCCTAAGCCACCTT
CTGGCTTGGCTTCATGGAGGGAAACAGGTATGTGGGTATCTGAGTGTGACG
AATGAGCAGCAAGTGAGTCTCGCTGTGGCTAGCACAAAGTATGGGCTGAA
GAGCAGGAGGACAGCTGAAAAGTGGCCTTTCCTGGTGACTAAGTTGGTCT
GAGCAGCTGAGTCAGTTTCTTCTTGGCTGCTTGGCTGGTCTCAGTGCTTA
TAAGCTGCTCACTTGTAAGTCTTTTCTTAGGAGCCCAGCTTGCTTAGGGG
TTGTCTTTGCAACTGGCCTTGCTCTGACAGTGACTTTCAGCAGTCTTAGCT
GCTTATATACACAGTCTTAGGAAAGAAGGCTGGTGAATCTGATCCATTTT
AGGAACCTTCTGAAGCTATTCTGAATTTACTTTACAAGCTTACCTGCAGG
ATAGAGGATCTCAGCTCTTTATAAACATCCTGTCTTAAACACCCCTGTTG
TTCTCTTCTCTTTTACATCCTGTGTCTTGAGAAGTTTGCCTCCAGGATG
GAAGTTGTTCAATTTCAGAGGACACTGTTGACACAAGCTCCCAGCACCCACA
TGTGAGCTCAGTGCTCTCCTTGGCTCTAGCTCTGCCCTATGAGGTTTTTT
ATTTTGTATCATAATCTTTTCTTATATCCTTCTTGTCTGGGAACTCA
TCTGGTTTCAATTTTTTGGCATTTTGAGAAAAGCTCTCACTATACAAATCA
GGCTGCCCTCCAAATCATCTTTTGGCCTTAACCTCCTCAGTACCAAGATCA
CGAGTGGATCTTAACACTTGACTGACTCGTTTAAGTGTGAGGAAATGTGG
ACCAATAAGAGAGCCCAGGAAAGCCCAGGAGAATCTGTAGCCCCATGGCT
GTTGTGTGAGAACCCAGAGTTTGTCAACAGAATTTGGTTCTTAATTTCT
CCACTTTATAAAAACGAGTGAGAGAAACAGGAACCTATTTCAGATCTGGGG
TCTGAGCAATCAGTGGGTGAACATCTAGAGATCTGTTCTGCATCTCCTCG
CCAGCTGGCAGAGCATGCGTAAGGCGGGAGGGAACAAGGGCAATCACTCA
CTCTGGGGCTCAGGCTTGCCCCCTTGGGTGAGGTGTTTCTGAGAGAGCTGA
TGTCTGCTTCTCTTGTTACCATCCCTCATCCTCTCCCCTCCTTCTGTCCC
CTACTTACCAATTTCACTGGCCAGTGTCATATTTCTTGCAAAGGCGATT
TGGTTTAATGAGCTTGACTATGCCCCGACTCCTTTAGGGAGGGTGGGGAAA
GGGCAACGAGGGCAGTAAGTGGTTTCCACAACCACTTTGCACCCGGCTGC
TGGGCCCCAAGCCAGAGGAACGTGCATGAGCCATGAAGTTTCCACTGATA
AATCCACAGATGCTTCTAGCACCTGCCTTTCTGACTCAGCCTCACCGTGC
CGCCTGCCAGCTGTGAAATCAGTGCCCAACAACAGGTAACCGAGACCCAGG
CGCAGGGCCAGGACAGCTGTCTGACACTTCCAGACAGGATGTGGAGGCTG
ACAGTTGTGATGGAGAGGAGATGGGGAGGACAGAGACGGGCTCAGCTTTA
AGACACCGAGCCACAGAGCACCAAAACAAAAGCCAGGGCCTTCTGAGGTAG
AAGTAACAGAAACCAACAGGCAATTTCTACTAGTTTCTTGGGACTGTTTG
CTGCATTTGCCAATCTTGGTAGTTTAAAAAACAACAGTTTGTCTC
AGCACTGGCAGAGCTTTCTCTCTGGAGGCTCCAGGGGTCCAGACTCTC
CTCTGTGGTACACTGGCTTCAGACATATCTCTGCCCTATGGCTGCCTCAC

FIG. 3D (35)

TCTAAACTCTGCCTGTCCTTGAATTACCTCTCTCTGCACTGGCTTTATAA
AGGAAACATGAGATTGTGTTTAGGGCTGTTTGGGTGACCTCCTCAGGAT
CTATAACATAATCACATCTCTACCGTATGAAGTGACGCTTCCGTCCCAGT
GTGTAATACATTTGCCGGCGCCTGTCTTAGGACAGTGACCACCACCAAC
TGTGGAACCTTGACTATGTCCACGTCATCTTCTACTAGCTTTAGAAGGCT
TATACCCACACTTTCTATCCAGAATTGTATTTTATTTAGAAATCATTCCT
ACTTTTAAAAAAGTCTCTGTGGTTAAAAGCATTGCAGAGGGCTTGGGTTT
TGGTCCCCAGGACCCACATCAAGTGGCTCACAGTGTCTTGGAACTCTTGT
TCCAATACCTCTTCTGGTCTCCATAGGCACTACATACATATGGCACATA
TATGTATACTCAGGCACACGTGTAAATTTAATGTCTACTTTTATGCTA
AATATCAAAGTCACTCGAGCAGTGGAGTTGAGCACACTCACATAAGGAAA
TCATCAGACAGACACTTCATCCTGTGTGGAGCCACTTTGTGGCTGGAGT
AAGCAGGGCAGAGTGATGTTTTCATTACTCTCTGGCCCCAGCACCCCTG
CCTCTCCCCACCCATTCTGTCATGCAGGTGGGGAAGAGAATTCTCTTTGT
GAAATTGGAAGTTTGGACCCAGCTTCACTCTTACTCTGCCCAGTACCTCC
TGTGAGAAACCTCCTATCCCAGGTGACCTGCTGGCTGTGACTCTCCTCA
GAAAAGGCCCGTGACCCACACTGCGCCACTAATGTATCATCCCCAAATG
CTGAAAAGGAAGCGTGTCTTCTCTCTCTCTCTTTTCTTTTGGTCTTTT
TGAGACAGAGTTTCTCTGTATAGCCCTGGCTGTCTTGGAACTCACTTTGT
AGACCAGGCTGGCCTCGAACTCAGAATCCGCTGCTCTGCCTCCCAG
TGCTGGGATTAAAGGCGTGCATCACCAGTCCCGGCTGCGTGTCTTTCTC
TTAGCGGTCTCTGTGGAGATGCTGAGTATGAAGCTCATCCTACCCACCT
TCAGTGGGGCCTTTTCTAGCTACTGAGCAGCTGTGTGAGGACTCGTGATC
ACAAGGTCTTTGAACCCTTGAGACAGATGTGCCTGAGCCCAGTTTGACC
TGACAAAAGCCTAGAGCTCACTGATAATGCCAGCAAACACCATCTTTGAG
TTTGCAAAGGAATCGCAACACATGCATTCACTTTCCGTTGCTGGCTGCTG
CTCCAGAGATGGCTATATTCACTCTCAGGTACTCAGACTCAAGAGTAGTT
CTGGCCACACAGGTCTCCACATTTTCGAGGTCAAATGACAGAAAACCAGGT
TGGTCTCAGTGCACATGGGTTTATTGAGCCACTGCAGGTGCTGGGGAAAC
CATGGCAGGGAGATCCTGGGAAGCCAGTGGGGTGCTGAGCAGGAGGGACC
TCAGTCTCTCCTTAATGTCTACACACTGTGTCTATAGGTGACAAGCCACGT
CAGTGTCTGTGACACGGGTAAAGCTTAATGGTGAGTAATGGCTAAGTGGGAG
GGTATTTAGGCAGCCTTGTCTGTGACGCTGTTTCAATATGATCTCCTTAGTG
CCTTGTCTCTTTGGAAAAGGACAGTTCCAAATTTCTAGGAGCGGGGGCTAG
TCTCTGTCTCTGTCTGTAAAGCCAGGGGACCCAATGAGGCCTCATCTATG
GGTGTCTCAGCTCTAGGATGGGGAAGAAAATGGACAAGATGCCTACTGACG
GGAACACAGGCTTTTCAGTCAAGCCCTAGCCTCCAGCCCCCAATCCAGAG
GACAGCCACACAGGGGTCCAGGCCTGCAAAGGGCAGCAGACCTGAGGGCA
AGGGAGTTTCAGCTCAGTGAGCAGTCATCGGGAGACATGGCAGTCAGCTG
TGTCGTCCACGGTTTCATGTTCTAATCAGAGCAGGGCCTGGAGAGCCAGG
GCAGTGAGTGACATACAGCCAGGACACCTTGGGCGTTAGGACAAAACAAGG
ACTGTTTCTGCCTCCAGCTCTTCTCAGGCCACTCGTGCCTTGCCTAGGAA
GGGTAAGAGAGCACAGATGGGAAGGATTTCGAAACTGTCAACTCCCTGTC
CTCTCCCCATACCTACCCGCGGGAAACAGCACCCAGCAGTCTGGTCTCTGC
AGAAGTGTATGGCTGCAAGCTGTCAAAGGCTTGTATGGCACCATCTGCGGA
GTGCAGAGATCCAGAGAAGGCTTGGCCAGGAAACCCTAGAAACTACCCCA
CTCCCTTGGGACAAAAAATAAGACACCCTGGAACCTGCAAGGCATGGCCT
GAGATGGAAGGTCACTGTGCTAAGAATGACCCACAACTGCTAGTGAGGT
TGACAAGGGCTGCCCCCTCTCCCTTTACAGGTGAACACAATCGGGATTAA
TAAGAGTTTAACTCTCAGCTACTAAGTGGCAGAGACAGGCTTCAAACAGA

FIG. 3D(36)

CCCCCAGAAATCTGGAAGTGGAGCCATTCCACCCAGAGGCAAGAACAGCAG
AGGTAAGTTGGGCACACATGGAAGAAAGGGCCACCCATTAGTGTCAAAA
GGGAGGCCAACTTCAGGCCATTGGACACGTTTAAACGCTGACTTCCACCC
ATGTACCATGGCATGTGCACACTGTCCATCGCCACACCAAACATGATGC
GACGTAAATAAGACCCACGGGCCAGGCAGCTTGGATTGGGCCACAGACAT

Fig. 3D (37)

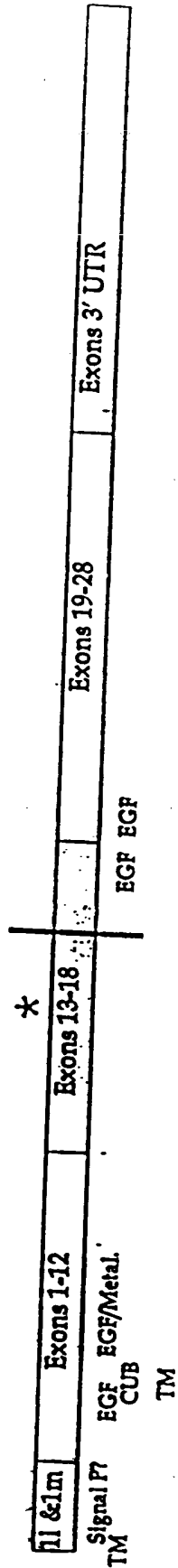


FIG. 4

Exon 1	CelegE106	TCTCCTAGTTGTAGTACATGCTGTTG
	CelegE108	AGGTCCTGTCTCAAGAAATAGCAATAAC
Exon2	CelegE33	TTTGAAGGCCCTGAAGTCAGAG
	CelegE36	TTGAGTCCCCATCATAAACATATAAATGG
	CelegE37 CelegE40	TTCTAGGCCAAATAGAATAATGAGACTTC AGAACTAATTCCATGAGATGAGTGTG
Exon 3	CelegE41	TGAAGTTGCTGTAATCTGGTCTGTG
	CelegE44	AAGGAGCCTGACTAGAAGCCTC
Exon4	CelegE69	TAAACTCCCTACAGTTCCTAACTCAG
	CelegE72	AGCGCTGTTGAGTGTGAATGTTCTG
	CelegE73 CelegE76	AAAGCCACAGTTGTCTGTACAGTGAG AGGTCTGCATTAGTTGCAATGTTGC
Exon5	CelegE77	TATACACCCCCTTATATACACTCAG
	CelegE80	AGAGCCTCTCATAAAGCTGTGGTC
	CelegE81 CelegE84	TTGAACATATATCCGCCAACAACCC CTTGGAATACTATAAACTTTCAGGCTGC
Exon6	CelegE101	TAAAGCAACAGGAAGAGTTGAACTTCTTG
	CelegE104	TGCACCCTGTGTGCACATGG
Exon7	CelegE109	TTACGGTGTCTTAATAATAAGGGCAG
	CelegE111	AATCATGGGTATTGTTAACTCCGAAAGC
	CelegE114 CelegE116	TGTAACAATGTGTGCCGAGTGTCC TCTCTCTCCAGCCCTAGAGTTG
Exon8	CelegE86	AGAAGAGGAGCCTGCAACATTGAC
	CelegE88	TTTGTTGGCGCTGAAAGCCTTG
	CelegE89 CelegE91	TGGCCACAGTAGTGTATTATGATGAC TTAATCAATTGCTCTGCAGATTCTAG
Exon9	CelegE93	TGGCTTACGTATAGGGGGAAATCAAG
	CelegE95	TTGTGTGTGTTCCTCCAAACACC

FIG. 5(1)

Exon10	CelegE98 CelegE100	GGACCATTCTTAAGGACAGCCGAT ACATAGTGATCTTTCCATCAGCAAAG
	CelegE117 CelegE120	TGAATGCACAGAGACCCTCCTG CCTCTTACCATTGAGATACTGTTAGG
Exon11	CelegE121 CelegE124	AGCAACAACCTCAAACCAGCCCTAC TTCTTCAGTTGCCAACTCCCAGG
	CelegE125 CelegE128	AAGCTGCTTGTGTGGCAGCAG AGTAAGGTGAACAGGAAAGTACAGAG
Exon12	CelegE130 CelegE132	TACATAAGAGAGGGCTGCCGCATAG CCCTACACTCACACTCATCTAGC
<hr/>		
Exon13	CelegE30 CelegE32	CCCTGTGTTCCAGATCTCCATTG TTCCTAGGTCCACCTTGATCTGAG
	CelegE14 CelegE15	AGCACCTGAATTCAAATCAGGATGAG AAACCAAAGTTCTGAACACATTAACCTCAC
Exon15	CelegE17 CelegE20	CTGGTTGCATTCATAGCTGTGTTTC ACAGAAGCCAGCATCACTGGG
	CelegE21 CelegE24	TTACTGGTGCTGGGAGGATATGTC ATAAGTACTTCATCACCTCAGCGCTC
Exon16	CelegE1 CelegE4	TTGATCTTAGCTGACCAGTGTCTC TCTGCATGGACTTGAGCAGAAAGTC
Exon17	CelegE6 CelegE8	CAAATCTTGTGATAGTGAATTACAAGTTGG TTTATAGCTGCCCTCAATACATTTTCC
	CelegE9 CelegE12	TGTACCTGCAGCCATTGCTTGG GGATCTGGGCTCTAGTTTATGTACG
Exon18	CelegE25 CelegE27	TTGAACTATAGGCACAGACAGCTG AACTTGACCTGTGTGACTTACGC
Exon19	CelegE193 CelegE194	TCACAGTCTATGGTAATCTGTCAAGC AAGGGCAACAATGCCCTGGCAA

Fig. 5(2)

Exon20	CelegE195 CelegE196	TTCCTGCAAATGGGATAGTCTCTCTG ATCCCCCAAGCATTTATCATTCTCAG
Exon21	CelegE197 CelegE198	TGTGTTTCCAGAAACCTGCTTTAGTTTG TAGTACTTTTGTCCAGGATGACCAAG
Exon22	CelegE199 CelegE200	TGACAAGAAATGTCATGTCTTAACATAAGC TTCAGAGCCTCCTTCCCCAACT
Exon23		
Exon24	CelegE203 CelegE204	TAGTCTGTAGCTGAGGCCATTTTGC AAGCAAGCTGCAGTTAAGGGACTGT
Exon25	CelegE205 CelegE206	TTGGGACCTTGAGGATTGTTCCC CACTCAACAGGTAAAAGTGATCTGCC
Exon26	CelegE207 CelegE208	TGCATCTGATCAGTTTGAATCAGAGAG AAACTGAGGCCTGAGTTCTGAAAAGC
Exon27	CelegE181 CelegE182	CACCAAAGCTCTGTACCACTAAGC TGACTGTGCAGTGATGCAGGG
Exon28 'UTR?	CelegE171 CelegE172	TTGACCTTGACATTTAGAATAGCCCTC GCTGAGAATTAATAATGGTCTTTCTCTTG
	CelegE173 CelegE174	TACACAGTGAGACCCTGTCTCC TAGCTGAGGTCCCTTGTGGAAG
	CelegE175 C.elegE176	AGTGTGAGAGGACCATGCTGG CTTGAAGCGTCCAACATCATGTGC
	CelegE161 CelegE162	AACTCATACATTTGAGCACTGTTGCC TGAGGAGGTGGGGAATGCTAATG
	CelegE163 CelegE164	ACATAGCAGAGGGCTGCTCAC ACTGACCTGTGGGAACCTGTG
	CelegE165 CelegE166	AATGCTAGGCATCATCCCTCTTCTAG AACATCTAATAGGGACTGAGTGACCC
	CelegE167 CelegE168	TTCTGTGGTGCCTTGGCAAGAG CACACATACACACACTAAGTGCC

FIG. 5(3)

CelegE169	TGGTAGTTACTTAAAGTTTACAAGAATGTAGG
CelegE170	AAATGCTGGGATAAAAAGCATGAACCAC
C.elegE145	TTCAGTTACCTAATGGGCACAAGGC
CelegE148	ACGACACTGACCTCTTGCACTTG
CelegE150	TGTACACCCTGAATGTCTGAACATTC
CelegE152	GCGTTCATTTCTGCTCCTGTAATGG
CelegE153	TGAGCTCTTAATCCCTGCCATTCC
CelegE154	TAGGGCTTGTCCGTCCATAAGG
CelegE157	TGTTACGGAGATGAAAGGCTAGACC
CelegE158	TAAGCCCTGCACTAACCCTACTC
CelegE159	TGTTTTGAGAGGTGAGCCTTCTAGC
CelegE160	CATGTCCTACAGTTCTGCTATCACC
CelegE141	CTTTTCTTCATCCAATTCCCCACGAG
CelegE144	TCTCTAAGCTGCACTGTTGTGGCT
C.elegE129	TGGAAGCCAAGAGTCTTGAGTTGC
CelegE132	GTCTGCATTTTAAATGCAGATGTGAAGC
CelegE134	CGAAACGCACGCACATTTTTACCAG
CelegE136	GTGTGATTTAGCATCTGTCGCACTTG
CelegE137	TGTATGTATAACCCAACAATCGCTGC
CelegE140	TCCAGAGTACAGGGAGAACTAAAGG

F14.5(4)

AGCGCTATTCAGCTGTGCCTCCTTTGCTGTCTTGGCTCCTCCTGGAGCACTAT
ATGCACCCATGTCCTTACCAGGCCTTTCACAGACGCTGCCATTGAGAGGGT
TGATGCAGGTTGCAGCCTTTAATCCCCGAGTACTAGGCTCTGACAAGATCCCA
CAGAAGCCAGCATCACTGGGCTCAGATGGCATCCACTGCAGCAAACCTATTTG
TGAATGGAGACATATCC

FIG. 6

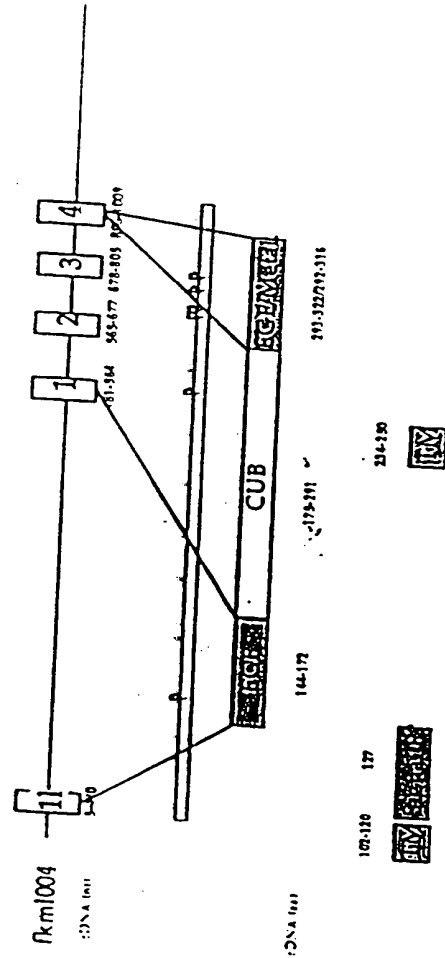
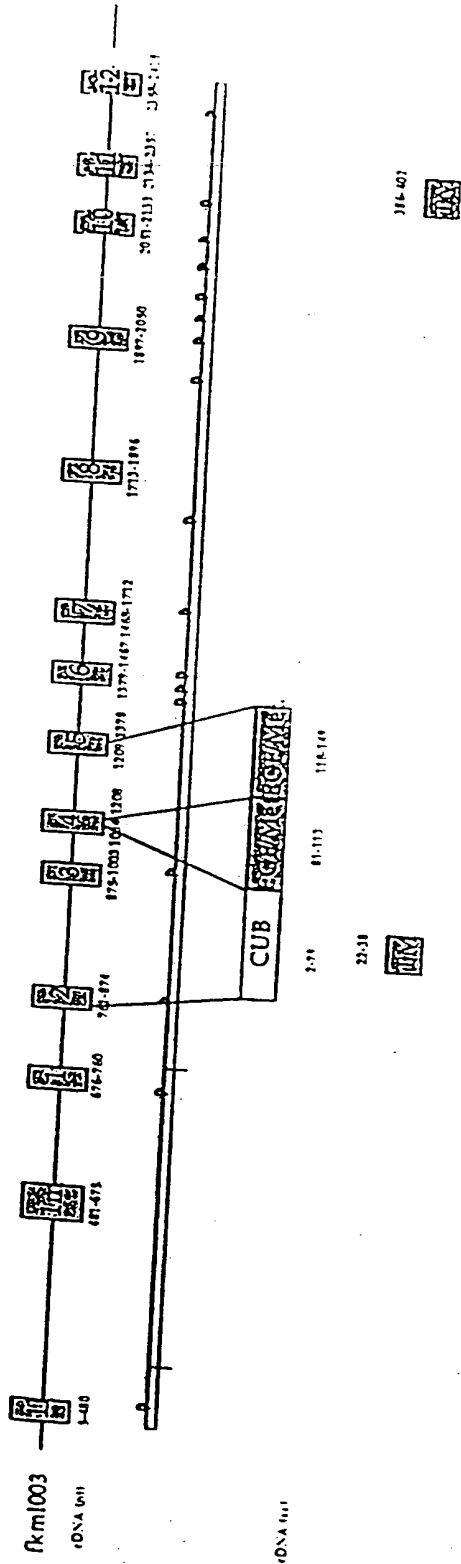


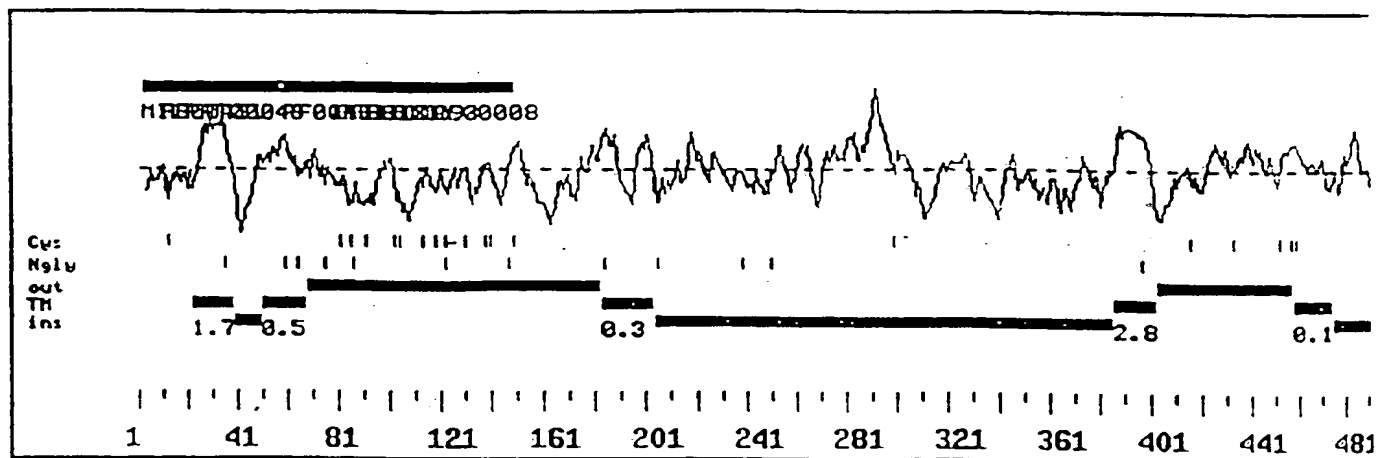
Fig. 7

GAATTCGGGGCGAAGGGGAGCCGGCGTGCGGGGTGTGTATGTGTTGGCTGGGCGCCGGCTCAGCCCCAGGAAGATGGTG
GCGGTGGCGGGCGGGCGGCGACTGAGGCGCGGCTGAGGGGGAGCACGAGGACGACAGCAGCGCCTGCGGGCAGGAAGG
GCAGGCAGCACCGACCCCTGCACCGGACAGGGGCTGGAGGCGGGACCGCGCGCCCGGCTGTGTCTCCCGCGGGTGCT
GTGCGGGGCGCTGCCCCCGCCGCGCTGTGCGCGTGTCTTTTCGCTGTGCTGTGCTGCGCGTGCCTCGGAGGCGAG
GCGCTGTGCGGTGGCGGGCGGGGTGTCCGGCTCGGCCGACGCGAGGCCAAGGAATGTGACCGGCGGTGTGTCAACGGCG
GCGCTGTCAACCCCTGGCACCGGCCAGTGCCTGTGCCCCACGGGCTGGGTGGGCGAGCAATGCCAGCACTGCGGGGGGCG
CTTCAGGACATCTGTCTCACGCCTATAATCACAGCTGTTCGGAAGGTGAGGCTGGAGGAACAGTTGAGGCAAGCTTCG
GCTACAGAATAAGTTCAAGAGTAACCTGGGGCAACTTGGGCTTGTCTCCAAAACAAAATGAGCGAAAAAGGAGCAAGCT
AGAGTCTTTTGGGAAAATTTTAGCTGACTAATTTTTCACCGAGAATAACTGGCTCTTCTGGATTGTGAACAGATGGAC
CTGGGAATTATAAATATAAGACGAAGTGCACATGGCTCATTGAAGGACAGCCAAATAGAATAATGAGACTTCGCTTCAA
CCATTTTGCTACAGAATGTAGCTGGGACCATTATATGTTTATGATGGGGACTCAATCTACGCACCTCTGATTGCTGCC
TTTAGTGGCCTCATTGTTCTCTGAAAGAGATGGCAATGAGACGGCTCCTGAGGTCACTGTCACTTCAGGTTATGCACTGC
TGCATTTTTCAGTGATGCTGCTTATAATCTGACTGGATTAAATATCACTTACAATTTTGACATGTGTGCGAATAATTG
CTCAGGCCGAGGAGAGTGTAAAGAGCAGTAACAGCAGCAGCGCTGTTGAGTGTGAATGTTCTGAAAACGGAAGGGGAG
TCGTGTGACATTCTCACTGTACAGACAACCTGTGGCTTCTCTACCGAGGCATCTGTAATGCAAGCGATACCAGAGGT
GCTCCTGCTTTCTCACTGGCAGGGTCTGGATGTTCAATTCCTGTGCCAGCTAACCACTCTTTTGGACTGAGAGAAGA
ATATTCTGATTTAAAGCTTCCCAGAGCCTCTCATAAAGCTGTGGTCAATGGAAATATAATGTGGGTGTGTTGGCGGATAT
ATGTTCAACCATTCAAGATTACAGCATGGTTTTAGCGTATGACCTGACTTCTAGGGAATGGCTTCCACTAAACCATTCGT
TGAACAGTGTGGTTGTAAGATATGGTCATTCTTTGGCATTACATAAGGATAAAAATCTACATGTATGGAGGAAAAATTGA
TTCAACAGGGAACGTGACCAATGAGCTGAGAGTATTTTATATTCATAATGAATCATGGGTATTGTTAACTCCGAAAGCT
AAGGATCAGTATGCAGTGGTTGGACACTCAGCACACATTGTTACACTGGCATCTGGCCGTGTGGTCATGTTGGTCATCT
TCGGTCATTGCCCACTCTATGGATATATAAGCGTTGTGTCAGGAATATGACTTGGAAAAGAACACATGGAGTATATTACA
TACTCAGGGTGTCTTGTGCAAGGGGGTTATGGCCACAGTAGTGTGTTATGATGACAGGACCAAGGCTCTGTACGTTTAT
GGTGGCTACAAGGCTTTTCAGCGCCAACAAATACCGGCTTGAGATGACCTCTACAGATACGATGTGGATACTCAGATGT
GGACCATTTCTTAAGGACAGCCGATTTTTCGGTTACTTGATACAGCTGTGATAGTGTGAGTGGAAOCATGCTGGTGTGTTGG
AGGGAACACACCAATGACACTTCCATGAGCCACGGTGCCAAATGCTTCTCCTCGGACTTCATGGCTTATGACATTGCT
TGTGACCGATGGTCAGTGCTTCCCAGACCTGAGCTCCATCATGATGTCAACAGATTGCGCCATTACAGCAGTCTTGTACA
ACAGCACCATGTATGTGTTCCGGCGGCTTCAACAGCCTCCTCCTCAGTGACGCTCTTGGTCTTTAAGCTGGAGCAGTGCGA
TGCACACCGCAGTGAAGCTGCTTGTGTGGCAGCAGGACCTGGTATCCGGTGTCTGTGGGACACACAGTGGTCTGATGT
ACCTCCTGGGAGTTGGCAACTGAAGAACAAGCAGAAAAGTTAAATCAGAGTGTGTTTTCTAAAAGAACCTTGACCATG
ACAGATGTGACCAGCACACAGATTGTTACAGCTGCACAGCCAATAGCAA

FIG. 8A

MRLRFNHFATECSWDHLYVYDGDSDIYAPLIAAFSGLIVPERDGNETAPEVTVTSGYALLHFFSDAAYNLTGFNITYNFD
MCPNNCSGRGECKSSNSSSAVECECSENWKGESCDIPHCTDNCGFPHRGICNASDTRGCSCFPHWQGPCCSIPVPANQS
FWTREEYSCLKLPRASHKAVVNGNIMWVVGGMFNHSDYSMLAYDLTSREWLPLNHSVNSVVVRYGHSALHKKDIYM
YGGKIDSTGNVTNELRVFHIHNESWVLLTPKAKDQYAVVGHSIHVTLASGRVVMLVIFGHCPLYGYISVVQEYDLEFN
TWSILHTQGALVQGGYGHSSVYDDRTKALYVHGGYKAFSANKYRLADDLYRYDVTQMWITLKDSRFFRYLHTAVIVSG
TMLVFGGNTIHNDTSMHGAKECFSSDFMAYDIACDRWSVLPPELHHDVNRFGHSAVLYNSTMYVFGGFNSLLLSDVLVF
TSEQDAHRSEAACVAAGPGIRCLWDTQSSRCTSWELATEEQAEKLKSECFSKRTLHDHRCDOHTDCYSCTANTX

FIG. 8B



Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
22	38	out-->ins	1.7
50	67	ins-->out	0.5
183	203	out-->ins	0.3
386	402	ins-->out	2.8
458	474	out-->ins	0.1

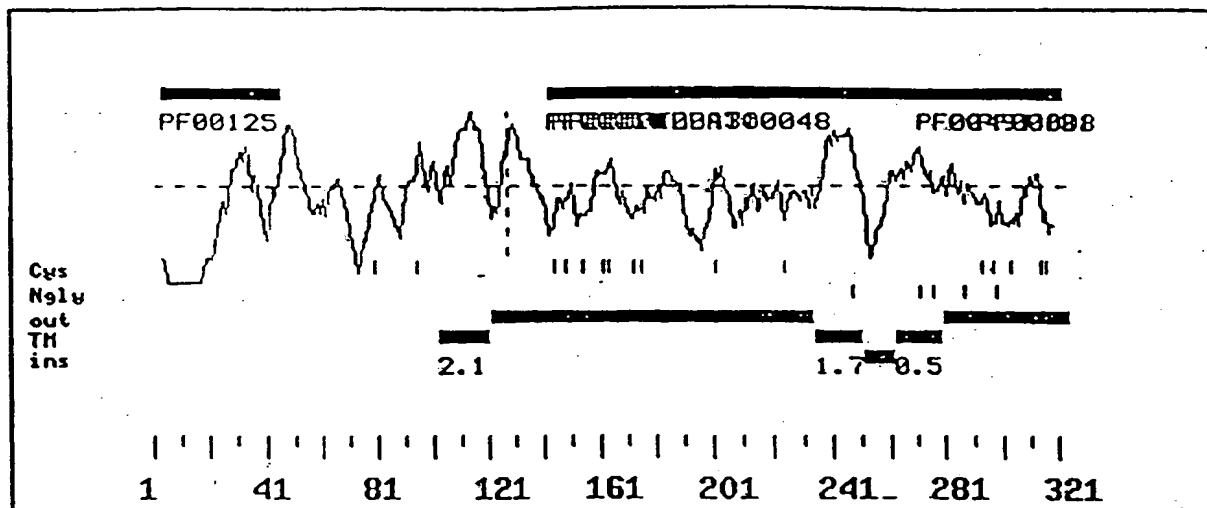
Signal Peptide Predictions

Method	Predict	Score	Mat@
SignalP (eukaryote)	NO		

FIG. 8C

FIG. 9A

FIG. 9B



Signal Peptide Predictions

Method	Predict	Score	Mat@
SignalP (eukaryote)	MAYBE		127

Transmembrane Segments Predicted by MEMSAT

Start	End	Orient	Score
102	120	ins-->out	2.1
234	250	out-->ins	1.7
262	279	ins-->out	0.5

Fig. 9C

ATGTACTACTGTAAACAAGAAGACCAGCTGCAGGAGCTGTGCCCTGGACCAGAACTGCCAGTGGGAGCCCCGGAATCAGG
AGTGCAATTGCCCTGCCCGAAAAATATCTGTGGCATTGGCTGGCATTGGTTGGAACTCATGTTTGAAAAATTACTACTGC
CAAGGAGAATTATGACAATGCTAAATTGTTCTGTAGGAACCACAATGCCCTTTTGGCTTCTCTTACAACCCAGAAGAAG
GTAGAATTTGTCTTAAGCAGCTGCGAATAATGCAGTCATCTCAGAGCATGTCCAAGCTCACCTTAACCCCATGGGTGCG
GGCCTTCGGGAAGGTYCAATGTGTCTACTKGGTGCTGGGGAAGGATATGRTCCCATTTTACAAATAGTTTACTACA
GTGGGATGSCCGTCTGTAGGCCCCAGTGTGTGCTTGGRATTCTGTGGGAATTTT:ATTCAGGAACCCAGTTACTTCGGGGA
CTGAAGGCTGCAACCTGCATTCAACCCACTYMAATGGTAGTGTCTGTGAAAGGCCCTGCAAAACCACAGTGCTAAGGCAGT
CCCCGACACCATGTGCCTTGAGGACAGCATGTGGAGATTGCACCAGCGGCAGCTCTGAGTG:CATGTGGTGCAGCAACA
TGAAG: CAGTGTGTGGACTCCAATGCCTATGTGGCCTCCTTCCCTTTTGG:CCAGTGTATGGAATGGTATACGATGAGC
ACCTGCCCCCTGAAAAATTGTTCAAGGCTACTGTACCTGTAGTCAATTGCTTGGAGCAACAGGCTGTGGCTGGTGTACTG
ATCCCAGCAATACTGGCAAAGGGAAATGCATAGAGGGTTCCTATAAAGGACCAGTGAAGATGCCTTCGCAAGCCCCCTAC
AGGAAATTTCTATCCACAGCCCCCTGCTCAATTCCAGCATGTGTCTAGAGGACAGCAGATACAAGTGGTCTTTTCATTAC
TGTCCAGCTTGCCAATGCAACGGCCACAGTAAATGCATCAATCAGAGCATCTGTGAGAAGTGTGAGAACCCTGACCACAG
GCAAGCACTGCGAGACCTGCATATCTGGCTTCTACGGTGATCCCAACCAATGGAGGGAAATGTGAGCCATGCAAGTGCAA
TGGGCACGCGTCTCTGTGCAACACCAACACGGGCAAGTGCTTCTGCACCACCAAGGGCGTCAAGGGGGACGAGTGCCAG
CTATGTGAGGTAGAAAAATCGATACCAAGGAAACCTCTCAGAGGAACATGTTATTATACTCTTCTTATTGACTATCAGT
TCACCTTTAGTCTATCCCAGGAAGATGATCGCTATTACACAGCTATCAATTTTGTGGCTACTCCTGACGAACAAAACAG
GGATTGGACATGTTCAATGCCTCCAAGAATTTCAACCTCAACATCACCTGGGCTGCCAGTTTCTCAGCTGGAACC
CAGGCTGGAGAAGAGATGCCTGTTGTTTCAAAAACCAACATTAAGGAGTACAAAGATAGTTTCTCTAATGAGAAGTTTG
ATTTTCGCAACCAACCAATATCACTTTCTTTGTTTATGTGAGTAATTTACCTGGCCCATCAAAATTCAGATTGCCTT
CTCTCAGCACAGCAATTTTATGGACCTGGTACAGTTCTTCTGTGACTTTCTTCAGTTGTTTCTCTCTTTGCTCTGGTG
GCTGCTGTGGTTTGGAAAGATCAAACAAAGTTGTTGGGCCCTCCAGACGTAGAGAGCAACTTCTTCGAGAGATGCAACAGA
TGGCCAGCCGTCCTTTGCTCTGTAAATGTGCGCTTGGAAACAGATGAGGAGCCTCCTGATCTTATTGGGGGGAGTAT
AAAGACTGTTCCCAACCCATTGCACTGGAGCCGTGTTTTGGCAACAAAGCCGCTGTCTCTGTGTTGTGAGGCTC
CCTCGAGGCCCTGGGTGGCATCCCTCCTCTGGGCAGTCAGGCTTGTCTGTGGCCAGCGCCCTGGTGGACATTTCTCAGC
AGATGCCGATAGTGTAAGGAGAAGTCAGGAGCCGTGAGAAACCGGAAGCAGCAGCCCCCTGCACAGCCTGGGACCTG
CATCTGATGCTGGGGCCAGGGACTCTCCCAACGACAGCTAGTGAGTGGCACACCAGAGCCATCTGCAGGGAAGGGCGT
GGCGGGGAAATGGCTGTGCGGTGCGGACGGAAGACTGGAAACCTCAAGCATCTGACTCACCTGCATGATCACAAGC
TTTCTTTGACGGTTTCTCCCATCCGTGTTCCAGCATCTAACCTTTTACTTTTGCCATAGGAAATACTTGATTAAATTACA
GGTCCAGGGATGAGCTGATGGTTGCTGGAGGAGGCCAGTGTAGAGCCAGTGAGAGAACTAGGAATGACACTCAGGTTCA
CTGTGGAAAACTGTTCTTGGGACTGTCTCAACTGTGCAAAAAACAAAGATGGAGTGTTTACAAGTAGACATTCTGTCAT
CAGTTGTTCTTGAACATGGTCTTTTAAAACTAGTCAGATGAATTAACCTTGTTTTCTATCTGAAGCCTGCTATCTTTTTT
AAAAGATGTGCTATTTATTCTTGACGATTTAGGCAATTATCTCTCTCCAGGGAGTACCTTTTTTCTAGTTGAGAAT
TAATAATGGTCCATCTCTTTTGATCATATCAAGCTAGGATAGAAGGGGGCTATTTTAAATGTCAAGGTCAGCAGTGT
ACTTTGAATGTAACTGGTATAATAGGTAGTTTCTATAGTAACCTTGATTAAATTTAGTCTTAATCCATTGAACTCTC
TCTTCTTTCTCTGCTGCTGCTCTCTCTCTCTCCATCTCACCTCCCTCTCTCACATACACACAAACACATACA
CACAACACTAAGTGCTAGACTTAAATAGATCTAGCAATTGGAAGTTAGTAAGCCTAAGTTTTTACATAATTGCATT

FIG. 10A(1)

CCTACATTCTTGTA AAAATTTAAATAGCTACCATTTGGCAATCTGCTTTTTTTCTAAAACTGATTTGCAGCCAGGAAAAGA
ATTTTCTCACCCAAGGAACATTTGATCTAGCAGCAGGGATGAGAGGAAAGCAGAAATGAATGAACTGTGAAAGCTCCTG
TTTTTATTATCAAAAAGGACACTGTCAAGAAGGCGCCCCCTGCCCCACCCCCGTGTACCCCTAGGCCTGATAAGCGAT
CAGAGGAAAGGACTCATTCATGTACGCTTCCTTGAGCAGAAAAGAGCACTGAGAGCACTTGGGACCCCTGGATCAGAG
AGCATCTGTGTGTCTGTCAGCCTCCTCTGAACCTGTGTGTTTCTATTCTCAGGCTGGGGTGGACTCAGATGCCAGGAAAGGG
ACAGCCTCCCATTTGTTCAGGCAGAAAGCTGCCCAAAGCCTGGGAGAAGGACTTGTMTGCCCTCTTTCCCCCAGGAGGGGCTC
GACCCACCCACCCCTCCCTCTCAGACCAAGGTGGTGGCTGTGAGGAGGGCAGCAAATGCTGACAAAGGATGAAAAGCACAT
GGAAAAAATGGACGAGGAGGGAAAACTCTGCCAAATGGAAAAATGACCAAATTTAAGAGGGTGGGACAGTCCCCCTGCTC
CTCTCCAGAGGGGCACTGCTTGGAAATTTGTGTTTTCCCATTTATGGTGTCTGTATTCTGGCATTATGTCAGCAGCCTC
CCAGAACTCTCTTCTGCTTCAAAAACCTGGGATCTCTGGCATTACCTATTGGGATGGACCGCTGGACAGCAATGCTCG
AGTTTGTGAATTTGGAGAGATACTCAAAAGAGCTAAACTGCAGCATTTTACCTTTAAATGCAGTGCCTAGAGAGAGAG
TATTGTCTCTTCCCCAACACTAACCCCACTCCCATGAAGAATTGCCTGGAAAGATGTTTTCAAGGAATTTGAACCATAA
AACACTATCTGATGCACAGAACACCTCTACTTTGAGACTCACCTCTCATAAAGCTTCTTTTTCACATTACTGTTAAAGA
CCAGACGTTCTAGAAAAGACCCCTCCTCTCATGAGCTCCCCCATCCCTGCTACAGAACACAGCACCCATGGCGCCTGCA
GTGGACTGGCCCCCTTAATTCCACAGGCCCCCCCAGCAAGGCCAAAGGGAGGCGCTGGGTATGTCTCTCTACAAGGA
AGATCCTCTTTGTTTGTTCAAAGGACCAGTTTTCTTAGGCCAAAGAAGTCTCTTCCCCATGTTAGTCTATGCCTTGAA
ATATCATGCACCATGACCCACAGCCATCTGGTTATGTCTTATTTTTTCTCTAAAAGATAATGTTTATTTTTTAAAAGGA
AGGAAGAAGCAAGTGAAGTTTCAATTCTGCTCCAGCGGTGGGGAAGCCGCTGAATCCACCTGCTTCTCTCTTTGCAACCGA
CAGCAAACAGCTTTCTCCGGCCTCAGGGCAGAAAAAGGGAATGGCAGGGAGTAAGAGGCGCTGGGCTGGGAGCCTGTTT
CCAAGAAGGAATTTGGTTGTCTATCTGGCAGTGTGCGCGTCACAAGAGAGCCTGTATATAAATTTAAATAGTCAAGACAA
CACTGACCTTGCACTTGTACATAACTATACAGTAGTGTCCAGAATGTTTCAGACATTCCGGAGTGTACATAAAACAGAAAA
AATCTTCATGTATTTTTTATTAAATATAACAATGTCTGAGTTTCACCTAAGATGTTTTTGTGCCATATGCTGGATATCCA
GGTTCTCGCCAGGCCCCGATACATGAATAACAAACCCAAGAAACGCATCCCCATTGTGTGATGTGTTTCAGATGCATCTG
GCACCAATTAGGTATTTCTTAAACAGGACTCATCTGTCTAGAGTGCACATGAAAAATCAGGCAGGGAATCGAAACGACA
GCGCTGGAGGAGACTCAGGAAGCAGAGGCGTCCCTGCCGCTGCCCTTGGCCCTGCAAGCACATCATGACCCCTTTCTGGC
AGCCTCTTGGTGCTCTGGGTAGTGAGGGATGACAGTCTTGTCTTGAGAAATGTTTCTCTTAGTCTTTAAGTTCAAAGA
CTAACCTGTAGCAATCAGACTTTCCAAAAGGGGGTTCTCCATTTTTTGTAGTTTTGTCTAAATTTTTTAATGAOCATTTT
CTGGAATCAGTTTATTATACTGAAAACTGGGGGTGGGAGTAGGGAGCTAGTTTGTGTGATAAATAGTTCCCATTTCCCGG
TGGAGAATTTGACATACCCCTGGACTCCTGTGTGCTCTCTGCCATCCCTGCACACAGCCTGGGGAGAGGCTGTGCTCC
CCGTGTGGAGAGAAGGCAACCCAGATCCGCTGAGCTAAGCCGGAGGAAAGGCAGTCTGGACAGAAAGACTGTTCAGCAG
AAGGAAAGTACTGGACTACCCGTGGGTAACTCCTGCCATTCAAGACTGGAGACAGCTGGGAAATAAAAAGAGCAGGGCA
CTGCTGGTGGGAAGAGGCATTTTACCTTCCAGTGCAAAATCCTGCTCCTTTGATTTAATGGGGTGTACTGGGGCCAGGGG
CTGATTCACTTCTTGGGAGATGGTGGTGTTTTTCATGAACATCTTTGATGCTTCCATTTTCATTTATTCATCATCATCATT
CAACAAGTATTTGCTAAACACTAACTTAAGCTAATGCTAGGGTAGTGACTGAGATGTAAAAATAGATTTTAGAATTAA
ACAAAATCCAAGTCTCTACACCCCTGTCTATCCAGGAGATCTTTCTTGTGGTGGTTTCTGTGAGAATTGGGCATCCTG
AGGACACAGCCAGGACGGCAGAGGCCCTCTGGCCTCAGGGCATGGCCTGCCCTACCTTCTGAAATGTTTACCCCATTTGAC
CAAACCTGGCTCCAGCCATTGCGGTGGTTTCTAGATAGCCAGGGCCACCAAGAGATATTGCCCTTGTATGAGAGTCAAA
CACCCCTGCCTACAAGGAGATGTTTTGAAATGGAGAGGAAAAATGGCAGCTCATCTTTTAAAGGCAGTAATGGAATGAT
TTTCAGTAACCTGAATTTGTGCAAAAAATTTCTAAACACTAGTGAAGCTGTTTCGTTGAACATAATCTGGCTCTGGAA
ATGTTTTTGTTTTATAGTTATTTACGATTTCGTTTGTGTTTGGATTCAAGCTTAGTTTCTTAATATGTATAATTTAGCATC

FIG. 10A(2)

TATTACACTCATGTAAATATGGAGTAAGTATTGTAACTATTTTCATTGCGGGGATTGTGGGTGTTATACATACATTTAG
GACTGCAATTTTTTGGTATTTTTTGTATTGTAAAATAACAGCTAATTTAAGCAGGAACAAGAGAACTAAGGGAGGTCTG
TGCATTTTAAACACAAATGTGAAGAACTTGTATATAAACAAAAGTAAATACTATAATACAACTTCCTTCTGAAATAAA
AGTAGATCTGGTAAAAAAAAAAAAAGAAAAAAAAAAAAAAGGGCGGCCGC

FIG. 10A(3)

MYCNRKTSRSCALDQNCQWEPRNQECIALPENICGIGWHLVGNSCLKITTAKENYDNAKLFERNHNALLASLTQKK
VEFVLKQLRIMQSSQSMKLTLTWPVGP SGRXNVSYXVLGKDMXPILQIVLLQWDXRLEAQCCCLXFCGNFXSGTQLLRG
LKAATCIQPTXHVVSVKGLQTTVLROCRTPCALRTACGDCTSGSSEKHVVQHEXSVWTPMPMWPPSLXQCMWYTM
TCPPENC SGYCTCSHCLEQPGCGWCTDP SNTGKGKCI EGSYKGPVKMP SQAPTGNFYQPPLLNSSMCLEDSRYNWSFIH
CPACQCNGH SKCINQSICEKCNLTGKH CETCISGFYGDPTNGGKQCPCKCNGHASLCNTNTGKCFCTTKGVKGDECO
LCEVENRYQGNPLRGTCYYTLLIDYQFTFSLSQEDDRYYTAINFVATPDEQNRDLDMFINASKNTNNTIWAASF SAGT
QAGEEMPVVS KTNIEYKDSFSNEKFDFRNHPNITFFVYVSNFTWPIKIQIAFSQHSNFM DLVQFFVTFPSCFLSLLV
AAVWVKIKQSCWASRRREQLLREMQQMASRPFASVNVALETDEEPPDLIGGSIKTVPKPIALEPCFGNKA AVL SVFVRL
PRGLGGIPPPGQSGLAVASALVDISQOMP IVYKEKSGAVRN RKQPPAQP GTCI

FIG. 10B

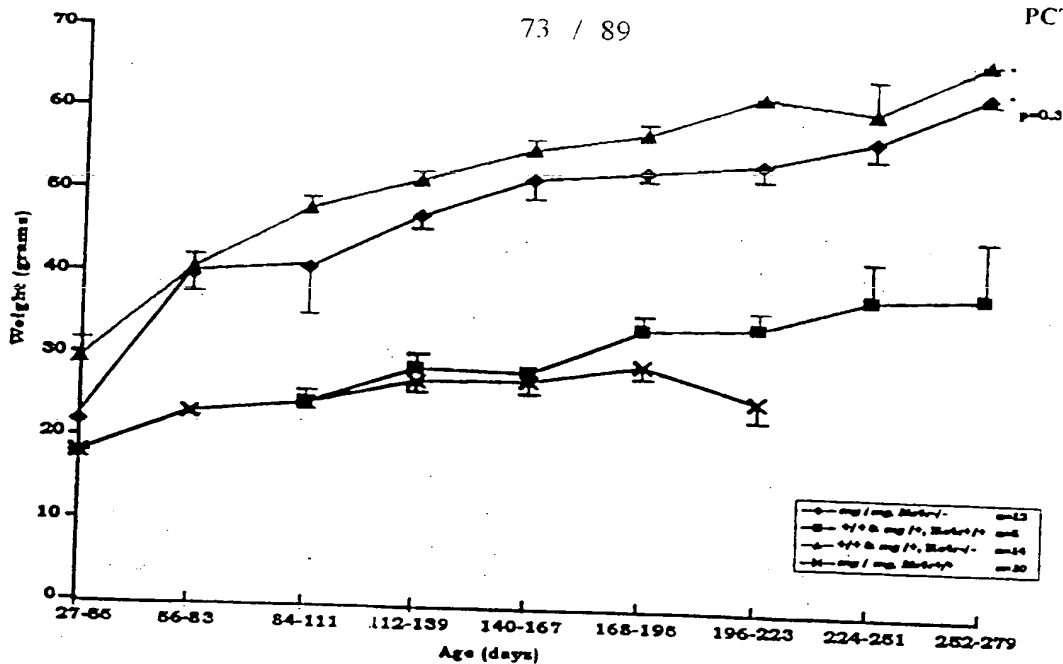


FIG. 11A

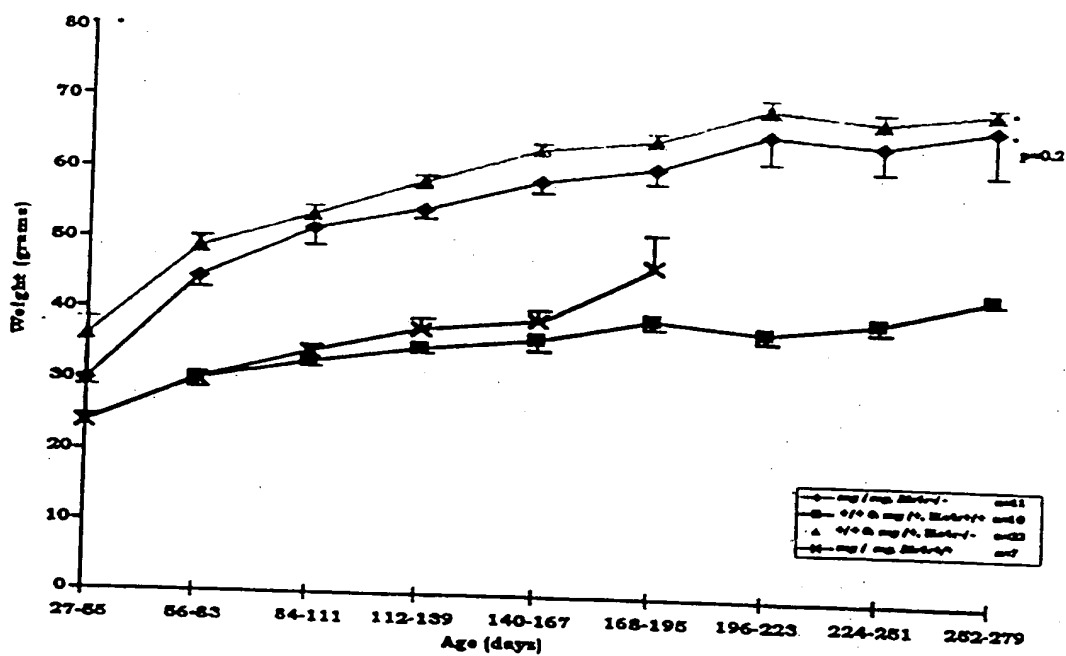


FIG. 11B

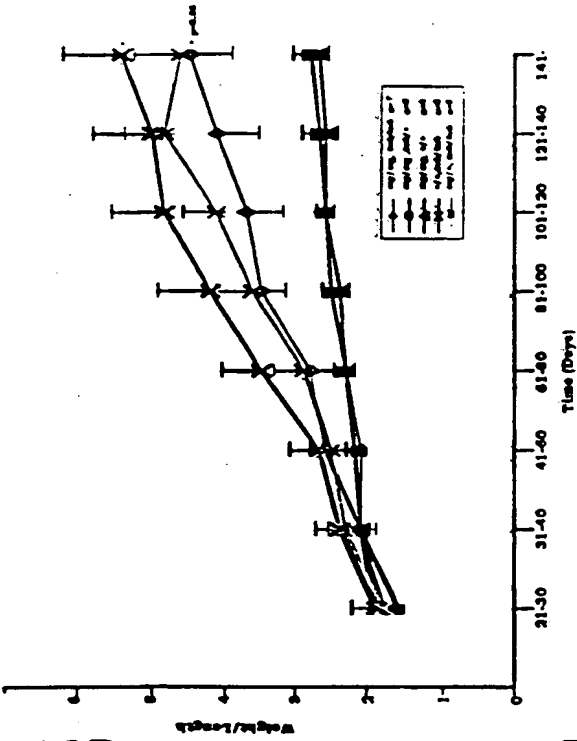


FIG. 12B

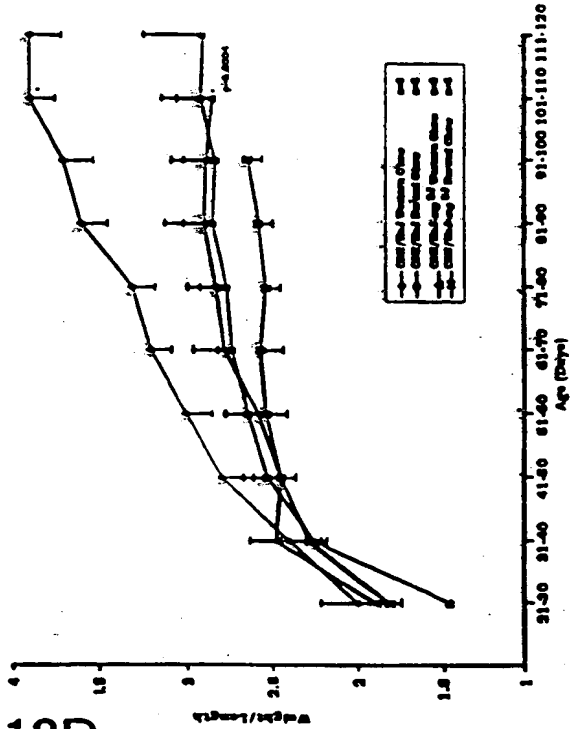


FIG. 12D

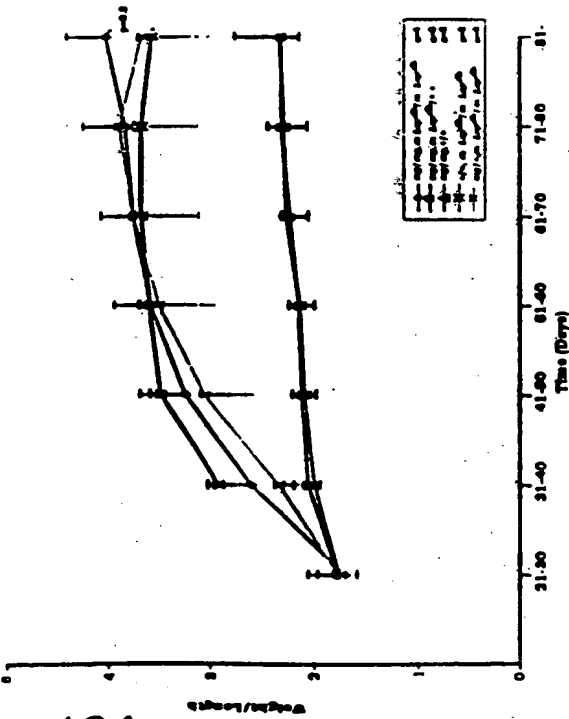


FIG. 12A

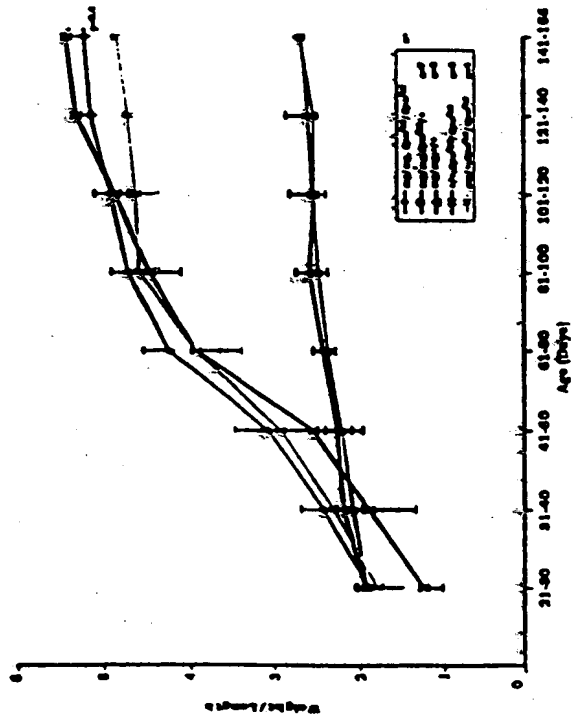
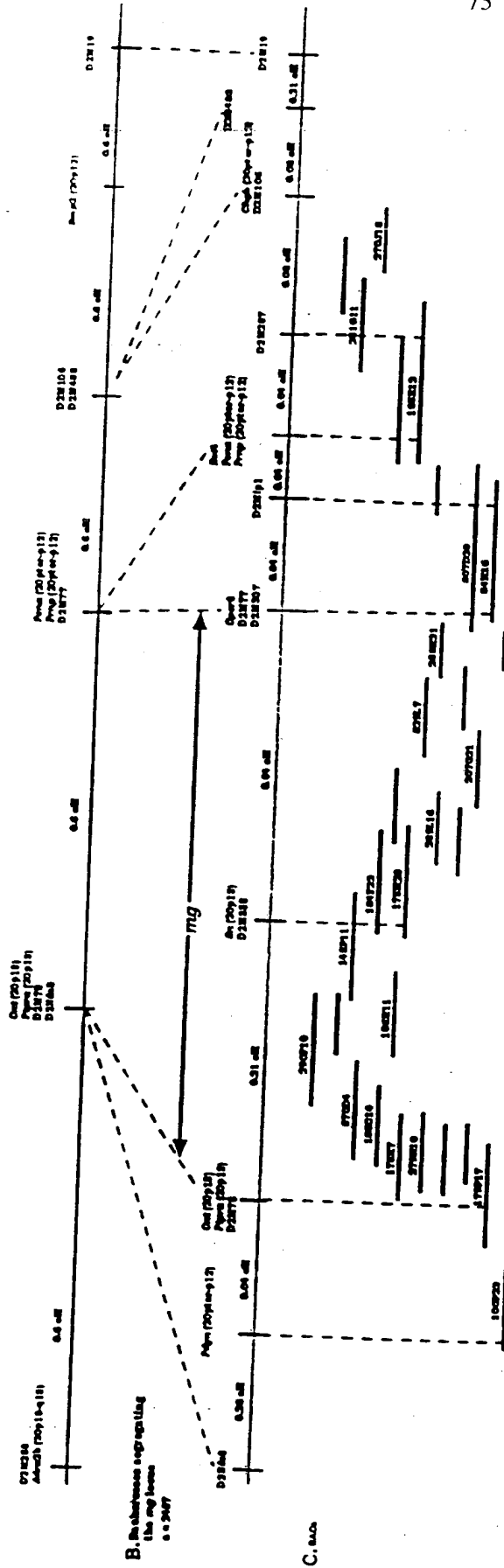


FIG. 12C

A. (CSTN/BJ 2 878/BJ) 2 C878/BJ
a. 10m



B. Distances separating
the mg from
a. 2407

C. 600

D. Prescriptions Data

FIG. 13

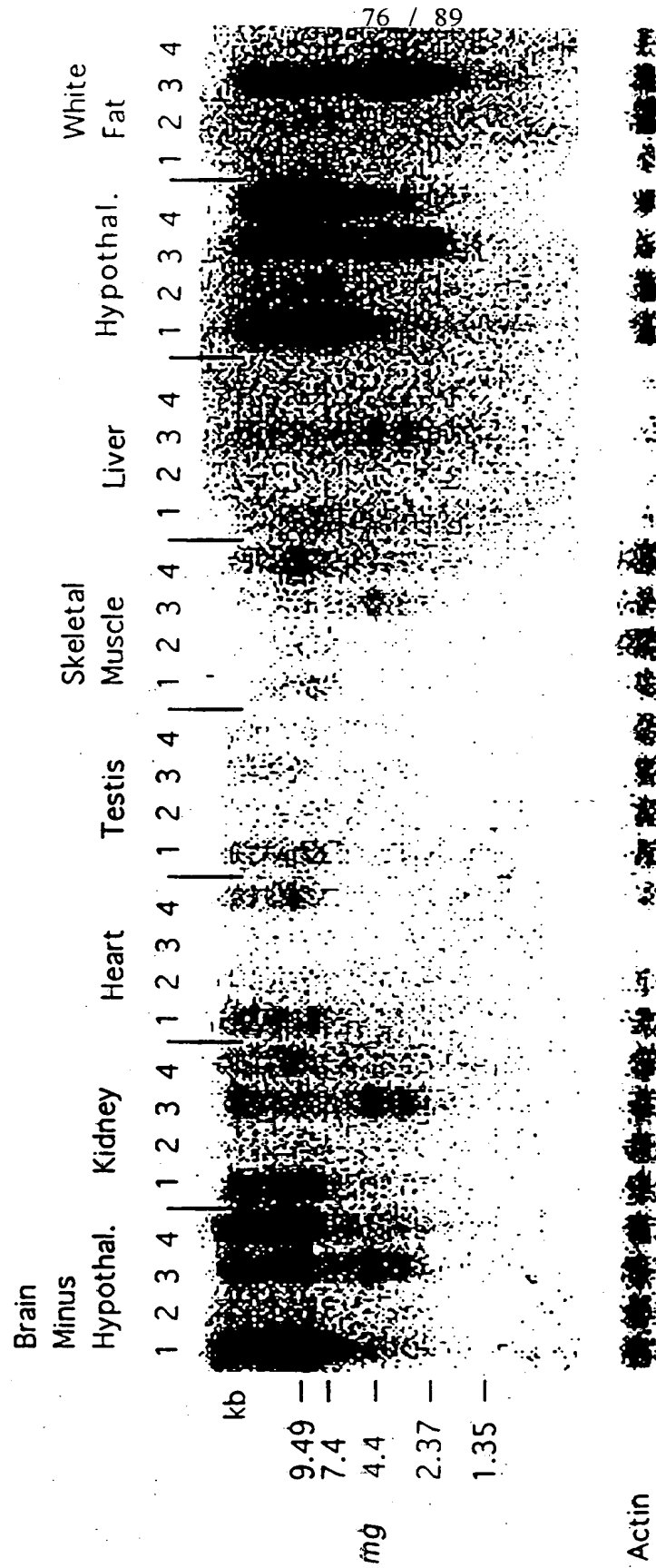
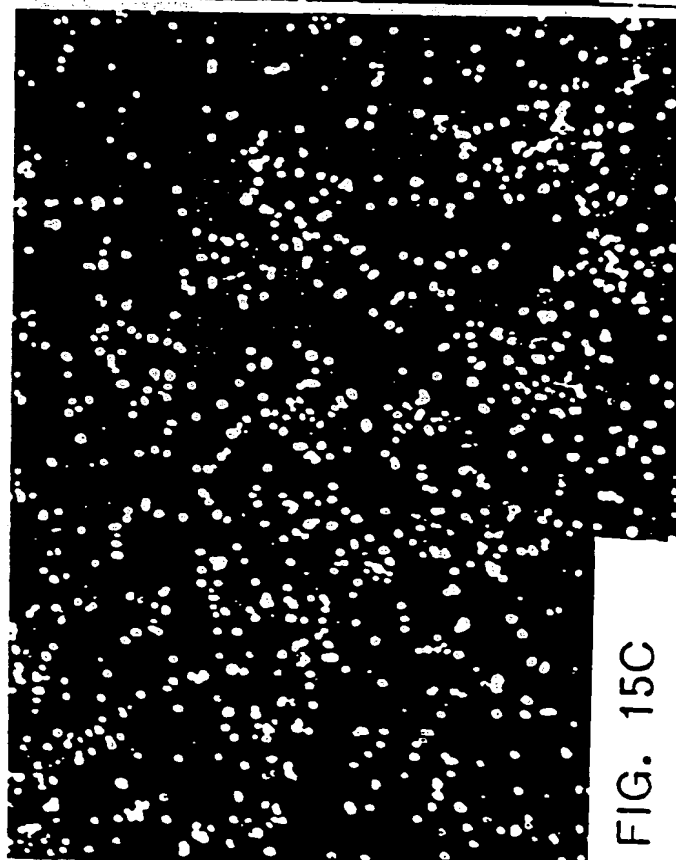
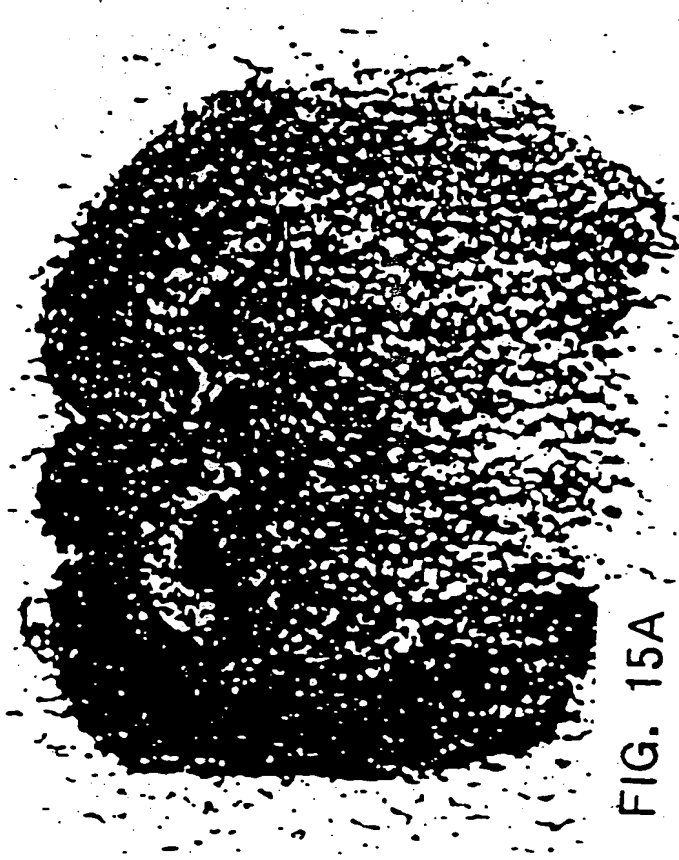
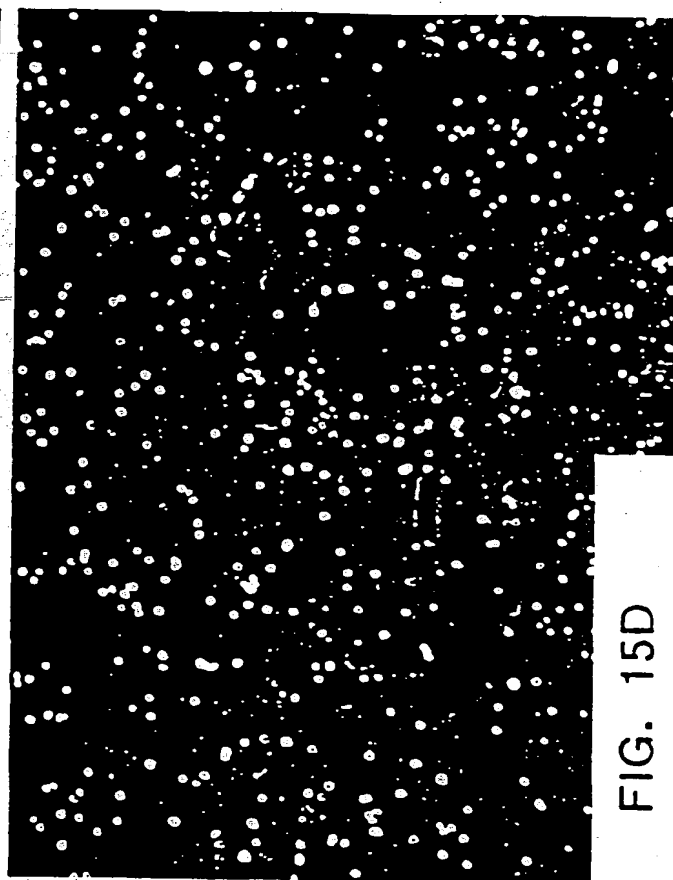
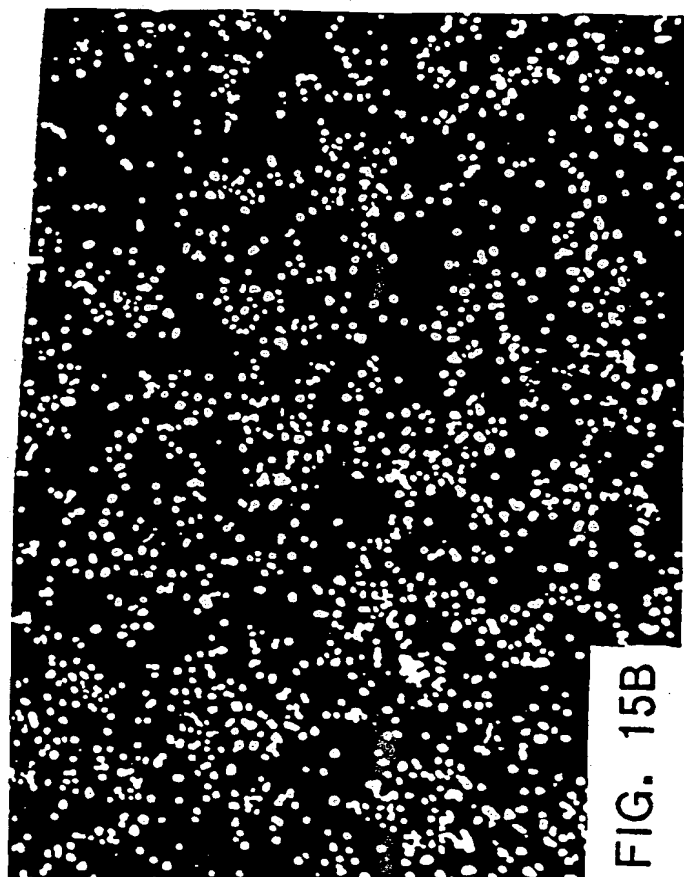


FIG. 14



obe2
KIAA0534
YC81_CAEEL
MEGF8

FRNHNITFTVVSNTWP-----IKIQIAFSQHSNFMDLVQFFVTFTSCFLSLLVA
FRSNPNITFTVVSNTWP-----IKIQIAFSQHNITMDLVQFFVTFTSCFLSLLVA
FGPDSNTFTFVRVNTWP-----VQIVVSEFAQSPPIN-WVLEFVIFAACFTIVLLVVA
LKSSRFYLLLLGVGDPSGPGANGSADSQGLLFFRQDQAHIDLFFVFSVFFSCFLEFLSLC

obe2
KIAA0534
YC81_CAEEL
MEGF8

AVVWKIKQSCWASRRREQLLREMQQMASRPFASVETLEPNR-----
AVVWKIKQTCWASRRREQLLRRQQMASRPFASVDVALEVGAEQTEFLRQPLEGAPKPIA
GLLWMIKVRIEAYRRNQRRIDEIEHMASRPFASKWELSMLSQFSSAG-----
VLLWKAQALDQREQRRHLQEMTKASRPFASKVTVCFFPDPTAPASAWKP-AGLPPP-A

Transmembrane
Site

FIG. 16A

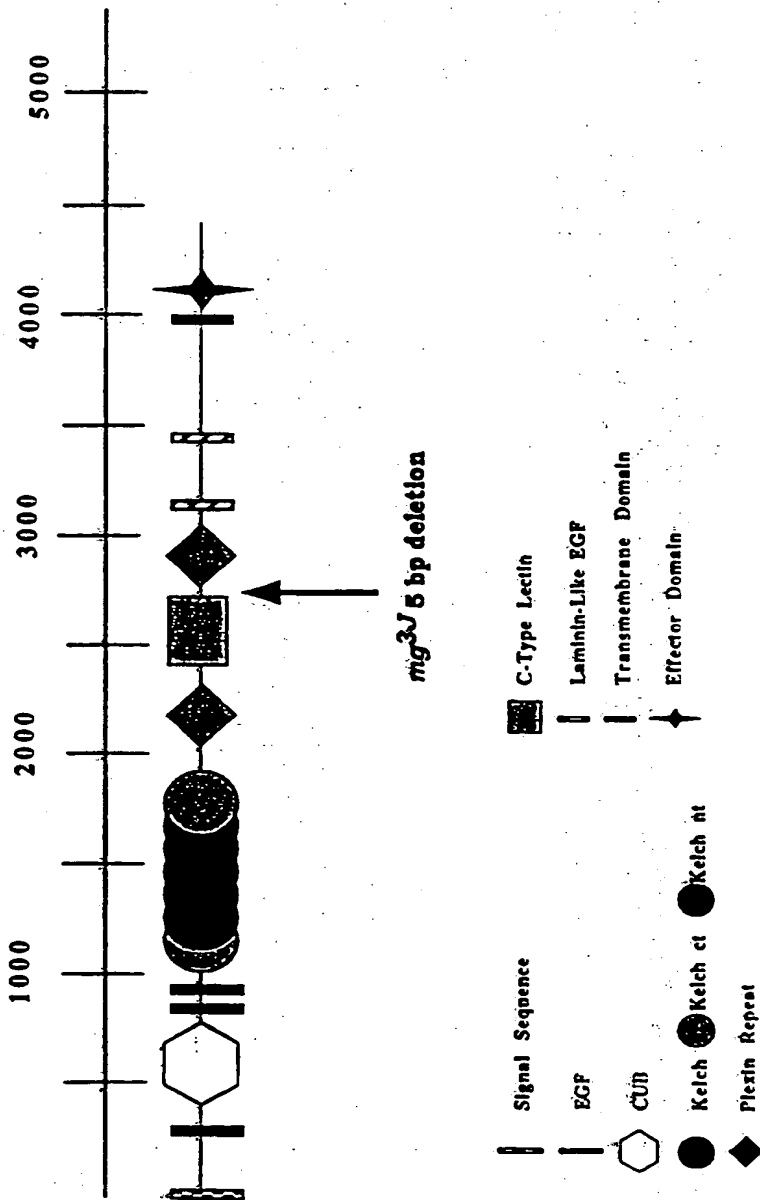


FIG. 16B

[illegible]

FIG. 17A

FIG. 17B

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```
inputs NLTTGKHCETCISGFYGDPTNGGKCOBCKCNHASLCNTNTGKCFCTTKGVKGDECQLCE
.....
NLTTGKHCETCISGFYGDPTNGGKQPCCKCNHASLCNTNTGKCFCTTKGVKGDECQLCE
1010      1020      1030      1040      1050      1060

      1150      1160      1170      1180      1190      1200
inputs VENRYQGNPLRGTCYYTLLIDYQFTFSLSQEDDRYYTAINFVATPDEQNRDLDMFINASK
.....
VENRYQGNPLRGTCYYTLLIDYQFTFSLSQEDDRYYTAINFVATPDEQNRDLDMFINASK
1070      1080      1090      1100      1110      1120

      1210      1220      1230      1240      1250      1260
inputs NFNLNITWAASF SAGTQAGEEMPVVSKTNIKEYKDSFSNEKFDFRNHPNITFFVYVSNFT
.....
NFNLNITWAASF SAGTQAGEEMPVVSKTNIKEYKDSFSNEKFDFRNHPNITFFVYVSNFT
1130      1140      1150      1160      1170      1180

      1270      1280      1290      1300      1310      1320
inputs WPIKIQIAFSQHSNFMJLVQFFVTFSCFLSLLLVAAVVWKIKQSCWASRRREQLLEMQ
.....
WPIKIQV-----QT-----EQ-----
1190

      1330      1340      1350      1360      1370      1380
inputs QMASRPFASVNVALETDEEPPDLIGGSIKTVPKPIALEPCFGNKA AVL SVFVRLPRGLGG
-----

      1390      1400      1410      1420
inputs IPPPGQSGLAVASALVDISQQMPIVYKEKSGAVRNRKQOPPAQPGTCIN
-----
```

FIG. 17C

ATGGTGGCGGTGGCCGAGCGGCGGCAACTGAGGCAAGGCTGAGGAGGAGGAGCGGCGGACGGCAGCGCTCGCGGGCAGGAGCGGCGGGCC
GCACCGACCCTGCACCGGACAGGGGCTGGAGGCCGGGACCGGCGGCGCGGCTGTGTCTCCCGCGGGTGCTGTGCGGGGGGCTGCCCGGGC
CGCCGCTGCTGCCGCTGCTCTTTTCGCTGCTGCTGCTGCGGCTGCCCGGGAGGCCGAGGCCGCTGCGGTGGCGGCGGCGGTGTCCGGCTCG
GCCGAGCCGAGGCCAAGGAATGTGACCGGCCGTGTGTCAACGGCGGTGCTGCAACCTGGCAGCGGECAGTGCGTCTGCCCGCGCGGCTG
GGTGGGCGAGCAATGCCAGCACTGCGGGGGCGGCTTCAGACTAACTGGATCTTCTGGGTGTGTGACAGATGGACCTGGAAATTATAAATACA
AAACGAAGTGACGCTGGCTCATTGAAGGACAGCCAAATAGAATAATGAGACTTCGTTTCAATCATTGTGCTACAGAGTGTAGTTGGGACCAT
TTATATGTTTATGATGGGGACTCAATTTATGCACCGCTAGTTGCTGCATTTAGTGGCCTCATTGTTCTGAGAGAGATGGCAATGAGACTGT
CCCTGAGGTTGTTGCCACATCAGGTTATGCCCTTGCTGCATTTTTTAGTGATGCTGCTTATAATTTGACTGGATTTAATATTACTTACAGTT
TTGATATGTGTCCAAATACTGCTCAGGCCGAGGAGAGTGAAGATCAGTAATAGCAGCGATACTGTTGAATGTGAATGTTCTGAAAACCTGG
AAAGGTGAAGCATGTGACATTCTCAGTGTACAGACAACCTGTGGTTTTCTCATCGAGGCATCTGCAATTCAAGTGATGTGAGAGGATGCTC
CTGCTTCTCAGACTGGCAGGGTCTGGATGTTGAGTTCCTGTACCAGCTAACAGTCATTTTGACTGAGAGGAATATTCTAAGCTTAAAGC
TCCCCAGAGCATCTCATAAAGCTGTGGTCAATGAAACATTATGTGGGTTGTTGGAGGATATATGTTCAACCACTCAGATTATAACATGGTT
CTAGCGTATGACCTTGCTTCTAGGGAGTGGCTTCCACTAAACCGTTCTGTGAACAATGTGGTGTGTTAGATATGGTCATTCTTTGGCATTATA
CAAGGATAAAATTTACATGTATGGAGGAAAAATGATTCAACTGGGAATGTGACCAATGAGTTGAGAGTTTTTCACATTCTAATGAGTCAT
GGGTGTTGTTGACCCCTAAGGCAAAGGAGCAGTATGCAGTGTTGGGCACTCTGCACACATTGTTACACTGAAGAATGGCCGAGTGGTCATG
CTGGTCATCTTTGGTCACTGCCCTCTCTATGGATATATAAGCAATGTGCAGGAATATGATTGGATAAGAACACATGGAGTATATTACACAC
CCAGGGTGCCCTTGTCAGGGGGTTACGGCCATAGCAGTGTTTACGACCATAGGACCAGGGGCTATACGTTTATGGTGGCTACAAGGCTT
TCAGTGCCAATAAGTACCGGCTTGACAGATGATCTTACCAGATATGATGTGGATAACACAGATGTGGACCATTTCTTAAGGACAGCCGATTTTTTC
CGTTACTTGACACAGCTGTGATAGTGAGTGAACCATGCTGGTGTGTTGGGGGAAACACACACAATGACACATCTATGAGCCATGGCGCCAA
ATGCTTCTCTTCAGATTTTATGGECTATGACATTGCCTGTGACCGCTGGTCACTGCTTCCAGACCTGATCTCCACCATGATGTCAACAGAT
TTGGCCATTTCAGCAGTCTTACACAACAGCACCATGTATGTGTTCCGTTGGTTTCAATAGTCTCCTCCTCAGCGACATCCTGGTATTACCTCG
GAACAGTGTGATGCGCATCGGAGTGAAGCCGCTTGTGTTAGCAGCAGGACCTGGTATTEGGTGTGTGTGGAACACAGGGTTCGTCTCAGTGTAT
CTCGTGGGCGCTGGCAACTGATGAACAAGAAGAAAAGTTAAATCAGAAATGTTTTCCAAAAGAACTCTTGACCATGACAGATGTGACCAGC
ACACAGATTGTTACAGCTGCACAGCCAAACCAATGACTGCCACTGGTGCAATGACCATTGTGTCECCAGGAACCACAGCTGCTCAGAAGGC
CAGATCTCCATTTTATAGGTATGAGAATTGCCCCAAGGATAACCCCTATGTACTACTGTAACAAGAAGAACAGCTGCAGGAGCTGTGCECTGGA
CCAGAACTGCCAGTGGGAGCCCCGGAATCAGGAGTGCAATGGGCTGCCCGAAAATATCTGTGGCATTGGCTGGCATTGTTGGTTGAAACTCAT
GTTTGAAAATTACTACTGCCAAGGAGAATTATGACAAATGCTAAATGTTCTGTAGGAACCACAATGCCCTTTGGCTTCTCTTACAAGCCAG
AAGAAGGTAGAAATTTGTCCTTAAGCAGCTGGGAATAATGCAGTCATCTCAGAGCATGTCCAAGCTCAGCTTAACCECATGGGTGCGGCTTCG
GAAGATCAATGTGTCTACTGGTGCTGGGAAGATATGTCCCATTTACAAATAGTTTACTACAGTGGATGCCGTCTGAGCCAGTGATGCTG
GATTCTGTGGAATTTTATCAGAAACCACTACTCGGGGACTGAAGGCTGCAACCTGCATCAACCACTCAATGGTAGTGTCTGTGAAAGGECT
GCAAACCAAGTGTGTAAGCAGTGCCGGACACCATGTGCCCTTGAGGACAGCATGTGGAGATTGCACCAGGGGCAGCTCTGAGTGCATGTGGTG
CAGCAACATGAAGCAGTGTGTGGACTCCAATGCCATATGTGGCTTCCTTCCTTTTGGGECAGTGTATGGAATGGTATACGATGAGCACCTGCC
CCCCTGAAAATTGTTTACGGCTACTGTACCTGTAGTCATTGCTTGGAGCAACAGGCTGTGGCTGGTGTACTGATCCCAGCAATACTGGCAAA
GGGAAATGCATAGAGGGTTCTTATAAAGGACCAGTGAAGATGCCCTTCGCAAGGCCCTACAGGAAATTTCTATCCACAGGCCCTGCTCAATTC
CAGCATGTGTCTAGAGGACAGCAGATACAACCTGGTCTTTTCACTGCTCAGCTTGCCAATGCAACGGCCACAGTAAATGCATCAATCAGA
GCATCTGTGAGAAGTGTGAGAACCTGACCACAGGCAAGCACTGCGAGACCTGCATATCTGGCTTCTACGGTGATCCCAACCAATGGAGGGAAA
TGTGAGCCATGCAAGTGCAATGGGCACGGCTCTCTGTGCAACACCAACAGGGGCAAGTGCTTCTGCACCACCAAGGGCGTCAAGGGGGACGA
GTGCCAGCTATGTGAGGTAGAAAATCGATACCAAGGAAACCTCTCAGAGGAACATGTTATTATACTCTTCTTATTGACTATCAGTTCAGCT
TTAGTCTATCCCAGGAAGATGATCGCTATTACACAGCTATCAATTTTGTGGCTACTCTGAEGAACAAAACAGGGATTTGGACATGTTTCATC
AATGCCCTCAAGAATTTCAACCTCAACATCACCTGGGCTGCCAGTTTCTCAGCTGGAAGCCAGGCTGGAGAAGAGATGCCGTGTGTTTCAA
AACCAACATTAAGGAGTACAAAGATAGTTTCTCTAATGAGAAGTTTGATTTTCGCAACCAGCCAAATATCACTTCTTTGTTTATGTGAGTA
ATTTACCTGGCCCATCAAAATTCAGATTGECTTCTCTCAGCACAGCAATTTATGGACCTGGTACAGTCTTCTCGTGACTTTCTTCAGTTGT
TTCTCTCTTTGCTCCTGGTGGCTGCTGTGGTTTGAAGATCAAAACAAAGTTGTTGGGCTCAGAGGTAGAGAGCAACTTCTTCGAGAGAT

FIG. 18A(1)

GCAACAGATGGCCAGCCGTCCTTTGCTCTGTAAATGTCGCCTTGGAAACAGATGAGGAGCCTCCTGATCTTATTGGGGGGAGTATAAAGA
CTGTTCCCAAACCCATTGCACTGGAGCCGTGTTTTGGCAACAAAGCCGCTGCTCTCTGTGTTTGTGAGGCTCCCTCGAGGCCTGGGTGGC
ATCCCTCCTCCTGGGCAGTCAGGTCTTGCTGTGGCCAGCGCCCTGGTGGACATTTCTCAGCAGATGCCGATAGTGACAAGGAGAAGTCAGG
AGCCGTGAGAAACCGGAAGCAGCAGCCCCCTGCACAGCCTGGGACCTGCATCTGATGCTGGGGCCAGGGACTCTCCACGCACGAGCTAGTG
AGTGGCACACCAGAGCCATCTGCAGGGAAGGGCGTGGCGGGGAAATGGCTGTGCGGTGCGGGACGGAAGACTGGAAACCCCTCAAAGCATCTG
ACTCACCTGCATGATCACAAGCTTTCTTTGACGGTTTCTCCATCCGTGTTCCAGCATCTAACCTTTTACTTTTGCATAGGAAATACTTGAT
TTAATTACAGGTCCAGGGATGAGCTGATGGTTGCTGGAGGAGGCCAGTGTAGAGCCAGTGAGAGAAGTACACTCAGGTTCACTGT
GGAAAACCTGTTCTTGGGACTGTCTCAACTGTGCAAAAAACAAAAGATGGAGTGTTTACAAGTAGACATTCGTCATCAGTTGTTCTTGAACAT
GGTCTTTTAAAACTAGTCAGATGAATTAACCTGTTTTCATCTGAAGCCTGCTATCTTTTTTAAAAAGATGTGCTATTATTCTTGCACGATT
TAGGCAATTATCTCTCTTCCAGGGAGTACCTTTTTTCTAGTTGAGAATTAATAATGGTCCATCTCTTTTGATCATATCAAGCTAGGATAGA
AGGGGGGCTATTTTAAATGTCAAGGTCAGCAGTGTACTTTGAATGTAACTGGTATAATAGGTAGTTTTCTATAGTAACTTGATTAATTTA
GTCTTAATCCATTTGAAACTCTCTCTTCTCTCTGCTGCTCCTCTCCTTCTCCATCTCACCTCCCTCTCTCACACATACACACACA
AACACATACACACAACACTAAGTGCCTAGACTTTAAATAGATCTAGCAATTGGAAAGTTAGTAAGCCTAAGTTTTTACATAATTGCATTCTCT
ACATTCTTGTAATAATTTAAATAGCTACCATTGGCAATCTGCTTTTTTCTAAATCTGATTGTCAGCCAGGAAAGAATTTTCTCACCCAAGG
AACATTGATCTAGCAGCAGGGATGAGAGGAAAGCAGAAATGAATGAACTGTGAAAGCTCCTGTTTTTATTATCAAAAAGGACACTGTCAAG
AAGGCGCCCCCTGCCCCACCCCCGTGCACCCTAGGCCCTGATAAGCGATCAGAGGAAAGGACTCATTATGTCACGCTTCTTGAGCAGAA
AAGAGCACTGAGAGCACTTGGGACCCCTGGATCAGAGAGCATCTGTGTGCTCTGCAGCCTCCTCTGAACTTGTGGTTTCTTCTCAGGCTGGG
GTGGACTCAGATGCCAGGAAAGGGACAGCCTCCCATTTGTGAGGAGGAGCTGCCCCAAGCCTGGAGAAGGACTTGTGTTGCCCTCTTTCCCCC
AGGAGGGGCTCGACCCACCCACCCCTCCCTCTCAGACCAAGGTGGTGGCTGTGAGGAGGGCAGCAAATGCTGACAAGGATGAAAAGCACATGG
AAAAAATGGACGAGGAGGGAATACTGTCCAAATGGAAAATGACCAAATTTAAGAGGGTGGGACAGTCCCTGCTCCTCTCCAGAGGGCA
CTGCTTGGAATTTGTTTCTCCCATTTATGGTGTCTGTATTCTGGCATTATGCAGCAGCCTCCAGAAAGCTCTCTTCTGCTTCAAAACCT
GGGATCTCTGGCATTACCCTATTGGGATGGACCGCTGGACAGCAATGCTCGAGTTTGTGAATTTGGAGAGATACTCAAAAGAGCTAAAACTG
CAGCATTTTACCTTTAAATGCACTGCTAGAGAGAGAGTATTGTCTCTTCCCCAACACTAACCCCACTCCCATGAAGAATTGCCTGGAAAGA
TGTTTTCAAGGAATTTGAACCATAAACACTATCTGATGCACAGAACACCTCTACTTTGAGACTCACCTCTCATAAAGCTTCTTTTTCACAT
TACTGTTAAAGACCAGACGTTCTAGAAAAGACCCCTCCTCTCATGAGCTCCCCCATCCCTGCTACAGAACACAGCACCCATGGCGCCTGCAG
TGGACTGGCCCCCTTAATTCCACAGGCCCCCCCCAGCAAGGCCAAAGGGAGGCCCTGGGTATTGTCTCTACAAGGAAGATCCTCTTTGTT
TGTTCAAAGGACAGTTTTCTAGGCCAAAGAAGTCTCTTCCCATGTTAGTCTATGCCCTTGAAATATCATGCACCATGACCCACAGCCAT
CTGGTTATGTCTTATTTTTTCTTAAAGATAATGTTTATTTTTAAAAAGGAAGGAAGAAGCAAGTGAAGTTTCTTCTGCTCCAGCGGTGG
GGAAGCCGCTGAATCCACCTGCTTCTCTTTGCAACCGACAGCAAACAGCTTTCTCCGGCCTCAGGGCAGAAAAAGGGAATGGCAGGGAGTA
AGAGGCGCTGGGCTCGGAGCCTGTTTCCAAGAAGGAATTGGTTGTCATCTGGCAGTGTGCGCGTCACAAGAGAGCCTGTATATAAATTTAA
ATAGTCAAGACAACACTGACCTTGCACCTGTACATAACTATACAGTAGTGTCCAGAATGTTTCAAGACATTCCGAGTGTACATAAAACAGAAAA
AATCTTCATGTATTTTATTAATAATAACAATGTCTGAGTTTACCTAAGATGTTTTTGTGCCATATGCTGGATATCCAGGTTCTCGCCAGG
CCCCGATACATGAATAACAAACCCAAAGAAACGCATCCCCATTGTGTGATGTGTTTTCAGATGCATCTGGCACCAATTAGGTATTTCTTAAACA
GGACTCATCTGTGAGAGTGCACATGAAAAATCAGGCAGGGAATCGAAACGACAGCGCTGGAGGAGACTCAGGAAGCAGAGGCGTCCCTGCCG
CTGCCCTTGGCCCTGCAAGCACATCATGACCCTTTCTGGCAGCCTCTTGGTGCTCTGGGTAGTGAGGGATGACCAGTCTTGTCTGAGAAAT
GTTTCTCTTAGTCTTTAAGTTCAAAGACTAACCTGTAGCAATCAGACTTTCCAAAAGGGGGTTCTCCATTTTTTGTAGTTTTGTCTAAATTT
TTAATGACCAATTTCTGGAATCAGTTTATTATACTGAAAACCTGGGGGTGGGAGTAGGGAGCTAGTTTTGTGATAAATAGTTCCCATTTCCCC
GTGGAGAATTTGACATACCCTGGACTCCTGTGTGCCTCCTGCCATCCCTGCACACAGCCTGGGGAGAAGCCTGTGCTCTCCCGTGTGGAGAG
AAGGCAACCCAGATCCCTGAGCTAACCCGGAGGAAAGGCAGTCTGGACAGAAGACTGTGAGCAGAAGGAAAGTACTGGACTACCCGTGG
GTAAGTCTGCCATTCAAGACTGGAGACACCTGGGAAATAAAAGAGCAGGGCACTGCTGGTGGGAAGAGGCATTTTACCTTCCAGTGCAAA
TCCTGCTCCTTTGATTTAATGGGGGTGACTGGGGCCAGGGGCTGATTCACTTCTTGGGAGATGGTGGTGTGTTTTCATGAACATCTTTGATCC
TTCCATTTTCAATTTATTCATCCATCCATTCAACAAGTATTTGCTAAACACTAACTAAGCTAATGCTAGGGTAGTGACTGAGATGTAAAAATA
GATTTTAGAATTAACAAATCCAAGTCTCACACCCTGTCTATCCAGGAGATCTTCTTGTGGTGGTTTTCTGTGAGAATTGGCCATCC

F16. 18 A (2)

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TGAGGACACAGCCAGGACGGCAGAGGCCTCCTGGCCTCAGGGCATGCCCTGCCTACCTTCTGAAATGTTTACCCCATTTGACCAAACCTGGCT
CCAGCCATTGCGGTGGTTTCTAGATAGCCAGGCCACCAAGAGATATTGCCCTTGATGAGAGTCAAACACCTGCCTACAAGGAGATGTTT
TGAAATGGAGAGGAAAATTGGCACCTCATCTTTTAAAGGCAGTAATGGAATTGATTTTCAGTAACTGAATTTGTGCACAAAACATTCTAAAC
ACTAGTGAAGCCTGTTTCGTTGAACTAATTCTGGCTCTGGAAATGTTTTGTTTTATAGTTATTTACGATTTGCTTTGTTTGGATTCAAGCT
TAGTTTGTTAATATGTATAATTTAGCATCTATTACACTCATGTAAATATGGAGTAAGTATTGTAACTATTTTCATTGCGGGGATTGTGGGTG
TTATACATACATTTAGGACTGCAATTTTTTGGTATTTTTTGTATTGTAAAATAACAGCTAATTTAAGCAGGAACAAGAGAATAAGGGAGGT
CTGTGCATTTTAAACACAAATGTGAAGAACTTGATATAAAACAAAAGTAAATACTATAATACAACTTCCTTCTGAAATAAAAGTAGATCTG
GTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIG. 18A(3)

MVAVAAAAATEARLRRRTAAALAGRSGGPHRPCTATGAWRPGPRARLCLPRVLSRALPPPLLPLLFSLLLLPLPREAEEAAVAAVSGS
 AAAEAKCEDRPCVNGGRCNEETGOCVC PAGWVGEQCQHCGRFRLTGSSGFVTDGPGNYKYKTKCTWLI EGQPNRIMRLRFNFATECSWDH
 LYVYDGD SIYAPLVAASFGLPERDGNETVPEVVATSGYALLHFFSDAAYNL TGFNITYS FDMCPNNCSGRGECKI SNSSDTVECECSENW
 KGEACDIPHCTDNCGFPHRGENTSSDVRGCSCFSDWQGP GCSVPVPANQSFWTREEYSNLKLPRASHKAVVNGNIMWVVGGMFNHSDYNMV
 LAYDLASREWLPNRSVNNVRYGHSLALYKDKIYMYGGKIDSTGNVTNELRVFHIHNESWVLLTPKAKEQYAVVGHSAHIVTLKNGRVVM
 LVIFGHCPLYGYISNVOEYELDKNTWSILHTOGALVQGGYGHSSVYDHRTRALYVHGGYKAFSANKYRLADDLYRYD VDTQMWTILKDSRFF
 RYLHTAVIVSGTMLVFGGNTNDTSM SHGAKCFSSDFMAYDIACDRWSVLP RPD LHHDVNRFGHSAVLHNSTMYVFGGFSNLLS DILVFTS
 EQCDAHRSEAACLAAGPGIFWNTGSSQCISWALATDEQEEKLKSECF SKRTL DHDRCQHTDCY SCTANTNDCHWCNDHCVP RNHSCSEG
 QISIFRYENCPKDNPMYYCHYTSCRS CALDONCOWEPRNQECIALPENICGIGWHLVGNSCLKITTAKENYD NAKLFCRNHNALLASLTTO
 KKVEFVLKQLRIMQSSQSMSYLTLPWVGLRKINVS YCWEDMSPFTNSLQWMPSEPSDAGFCILSEPSTRGLKAATCINPLNGSV CERP
 ANHSAKQCRTPCALRTACGETSGSSECMWCSNMKQCVDSNAYVASFPFGQCMEWYTMSTCPPENC SGYCTCSHCLEQPGCGWCTDPSNTGK
 GKCIEGSYKGPVKMPSQAPT NFYPOPLLNSSMCLEDSRYNWSFIHCPACQCNHSHK CINQSICEK CENLTGKHCETCISGFYGDPTNGGK
 CQPCCKNGHASLCNTNTGKCFCTTKGVKGDECQLCEVENRYQGNPLRGTCY YTLIDYQFTFSLSQEDDRYTTAINFVATPDEQNRDLDMFI
 NASKNFNLNITWAASFAGTQAGEEMPVVS KTNIEKYKDSFSNEKFDFRNHPNITFFVYVSNFTWPIKIQIAFSQHSNFM DLVQFVTF FSC
 FLSLLLVA AVVWKIKQSCWASRRREQLLREMOMASRPFASVNV ALETDEEPPDLIGGSIKTVPKPIALEPCFGNKA AVLSVFVRLPRGLGG
 IPPPGQSGLAVASALVDISQMPPIVYKEKSGAVNRKQOPPAQPGTCICWGOGLSHARASEWHTRAICREGRGGEMAVRCGTEDWKPSKHLT
 HLHDHKL SLTVSPIRVPASHLLLHRKYLILQVQADGCWRRPVSOENEHSGSLWKTVLGT VSTVQKTKDGVFTSRHSSSVVLEHGLL KTSQ
 MNLVFI SLLSFLKDVLFILAPFROLSLFQGV PFFLVENWSISFDHIKLGKGGYFKCQGOQCYFECKLVVVFYSNLINLVLIHLKLSLPFSLP
 VPLLHLTLPLSHIHTQTHNTKCLDFKIQLES AVFTLHSYILVKFKLFLAICFFSKI FAARKEFSHPRNISSSRDERKAEMNELKLLFLL
 SKRTL SRRRPLPPPCHPRPDKRSEERTHSCHASLSRKEHEHLGPLDQASVC PAASSELV VHSQAGVDS DARKGTASHCQAEAAQSLEKDL
 FALFPPGGARPTHPPSQT KVVAVVRAANADKDEKHMEKNRGGKTL PNGKPNLRGWDSP LLSQRALLGNCVFPPIYGALYSGIMQOPPRSSL
 LLQNLGSLALPYWDG PLDSHARVCEFG EILKRAKTA AFYLMQCLEREYCLFPNTNPTPMKNCLERCFOGITIKHYLMHRTPLLDSP LIKLLF
 HITVKDQTFKRPLLSAPPSLLQNTAPMAPAVDWPLNSHRPPQOQOREAPGYCPTRKILFVCSKDQFSAKEVSSPCS YALKYHAPPTAIWLC
 LIFFLKDNVYFKGRKKQVKFHSAPAVGKPLNPPASPLQPTANSFLRPQGRKREWGQVRGAGLGACFQEGIGCHLAVLRVTREP VYKLKSROH
 PCTCTLYSSVQNVQTFGVYIKOKKSSCIFIKYNNVVS PKMFLCHMLDIQVLARPRYMNNKPKKRIPIVCVQMH LAPIRYFLKQDSSVRVHMK
 NQAGNRNDSAGGDSGRGVPAALGPASTSPFLAASWCSGGMTSLVLRNVSLSLVQRLTCSNQT FQKGV LHFLFCLNFPFPGISLLYKLGVG
 VGSFVDKFPFPRGEFDIPWTPVCLLP SLHTAWGEACASPCGEKATPDPLSPGGKAVLDRRLSAEGKYWTTRGVLPFKTGDTWEIKRAGHCWW
 EEA FYLPVQI LLLFNGVYWGGLIHFLGRWWCFHEHLSFHFIYSSIHSTSICTLTANARVVTEMKILELKQNPSPHTPVIPGDL SLWWFLEL
 AILRTQGRQRPPLRACPAYLLKCLPHPNLAPAI AVSRPGPPRDIAPESNTLPTRRCFEMERKIGTSSFKGSGNIDFQLNLCTKHSKHS
 FRTNSGSGNVFVLLFTISFVW IQAFVNMYNLASITLMIWSKYCKLFHCGDCGCYTYIDCNFLVFFVLNNSFKQEQENGRSVHFKHKCEELVY
 KOKILYKLPSEIKVDLVKKKKKKKKK

FIG. 18B

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ATGGTGGCGGTGGCCGAGCGCGGCAACTGAGGCAAGGCTGAGGAGGAGGACGGTGGCGACGGCAGCGCTGGCGGGCAGGAGGGCGGGCCGACCGACCTGCACC
GCGACAGGGGCGCTGGAGGCGGGGACCGCGCGCCCGGCTGTGTCTCCCGCGGGTGTGTGTGCGGGGCGCTGCCCCGCGCGCGCTGTGCCGCTGTCTTTTCGCTGTGTG
CTGCTGCCGCTGCCCCGGGAGGCGGAGGCGGCTGCGGTGGCGGGCGGGTGTCCGCTCGGGCGCAGCGAGGCAAGGAATGTGACCGGCGGTGTGTCAACGGCGGT
CGCTGCAACCTGGCACCGGCCAGTGGCTGTGCCCGCGGGCTGGGTGGGCGAGCAATGCCAGCACTGCGGGGGCGGCTTACAGCTAACTGGATCTTCTGGGTTTGTG
ACAGATGGACCTGGAAATTATAAATACAAAACGAAGTGCACGTGGCTCATTGAAGGACAGCCAAATAGAATAATGAGACTTCGTTTCAATCATTITGTACAGAGTGT
AGTTGGGACCAATTATATGTTTATGATGGGACTCAATTTATGCACCGCTAGTTGTGCAITTTAGTGGCCTCATTGTTCTGAGAGAGATGGCAATGAGACTGTCCCT
GAGGTTGTTGCCACATCAGGTTATGCCITGCTGCAITTTTTTATGATGCTGCTTATAATTTGACTGGATTTAATATTACTTACAGTTTGTATGTGTCCAAATAAC
TGCTCAGGCGGAGGAGAGTGAAGATCAGTAATAGCAGCGATACTGTTGAATGTGAATGTTCTGAAAACCTGGAAAGGTGAAGCATGTGACATTCTCCTCCTGTACAGAC
AACTGTGGTTTTCTCATCGAGGCATCTGCAATTCAAGTGATGTGACAGGATGCTCTGCTTCTCAGACTGGCAGGGTCTGGATGTTCAAGTTCTGTACCAGCTAAC
CAGTCATTTTGGACTCGAGAGGAATATTCTAACTTAAAGCTCCCCAGAGCATCTCATAAAGCTGTGGTCAATGGAAACATTATGTGGGTTGTTGGAGGATATATGTTT
AACCCTCAGATTATAACATGGTTCTAGCGTATGACCTTGCTTCTAGGAGTGGCTTCCACTAAACCGTTCTGTGAACAATGTGGTTGTAGATATGGTCATTCTTTG
GCATTATACAAGGATAAAATTTACATGTATGGAGGAAAAATTGATTCAACTGGGAAATGTGACCAATGAGTTGAGAGTTTTTACATTATAATGAGTCATGGGTGTGTG
TTGACCCCTAAGGCAAGGAGCAGTATGCAGTGGTTGGGCACTCTGCACACATTGTTACACTGAAGAATGGCCGAGTGGTCATGCTGGTCATCTTTGGTCAGTGCCT
CTCTATGGATATATAAGCAATGTGACGGAATATGATTTGGATAAGAACACATGGAGTATATTACACACCCAGGGTGGCCTTGTGAAGGGGGTTACGGGCATAGCAGT
GTTTACGACCATAGGACCGGGCCCTATACGTTTATGGTGGCTACAGGCTTTTCAAGTCCAAATAAGTACCGGCTTGCAGATGATCTCTACCGATATGATGTGGATACC
CAGATGTGGACCACTTCTAAGGACAGCCGATTTTTCCGTTACTTGACACAGCTGTGATAGTGAGTGGAAACCATGCTGGTGTGTTGGGGGAAACACACAAATGACACA
TCTATGAGCCATGGCGCAATGCTTCTCTTCAAGTTTATGGCTATGACATTGCTGTGACCGCTGGTCAGTGTCTCCAGACCTGATCTCCACCATGATGTCAAC
AGATTTGGCCATTGAGCAGTCTTACACAACAGCACCATGTATGTGTTGGTGGTTTCAATAGTCTCTCTCAGCGACATCTGGTATTACCTCGGAACAGTGTGAT
GCGCATCGGAGTGAAGCGCTTGTTTAGCAGCAGGACCTGGTATTGGTGTGTGTGGAACACAGGGTCTGCTCAGTGTATCTGTTGGGCGCTGGCAACTGATGAACAA
GAAGAAAAGTTAAATCAGAAATGTTTTTCCAAAGAATCTTGACCATGACAGATGTGACGAGCACAAGATTGTTACAGCTGCACAGCCAAACCAATGACTGCCAC
TGGTGCAATGACCATTGTGTCCCCAGGAACACAGCTGCTCAGAAGGCCAGATCTCCATTTTTAGGTATGAGAATTGCCCAAGGATAACCCCTATGTACTACTGTAAAC
AAGAAGACCAGCTGCAGGAGCTGTGCCCTGGACAGAACTGCCAGTGGGAGCCCCGGAATCAGGAGTGCATTGCCCTGCCCGAAATATCTGTGGCATTGGCTGGCAT
TTGGTTGGAACCTCATGTTTGAATTTACTACTGCCAAGGAGAATTATGACAATGCTAAATTTGTTCTGTAGGAACCAATGCCCTTTTGGCTTCTCTTACAACCCAG
AAGAAGGTAGAATTTGCTCTTAAGCAGCTGCGAATAATGCAGTCATCTCAGAGCATGTCCAGCTCACCTTAACCCCATGGGTGGGCTTTCGGAAGATCAATGTGTCC
TACTGGTGTGGGAAGATATGTCCCATTTACAAATAGTTTACTACAGTGGATGCCGCTGAGCCAGTGTGCTGGATTCTGTGGAATTTTATCAGAACCAGTACT
CGGGGACTGAAGGCTGCAACCTGCATCAACCCACTCAATGGTAGTGTCTGTGAAAGGCTGCAAAACACAGTGTAAAGCAGTGGCGGACACCATGTGCCCTTGAGGACA
GCATGTGGAGATTGCACAGCGGCAGCTCTGAGTGCATGTGGTGCAGCAACGAAGCAGTGTGTGGACTCCAATGCCATGTGGCTTCTTCCCTTTTGGCCAGTGT
ATGGAATGGTATACGATGAGCACCTGCCCCCTGAAAATTTGTTAGGCTACTGTACCTGTAGTCAATTGCTTGGAGCAACAGGCTGTGGCTGGTGTACTGATCCAGC
AATACTGGCAAAGGGAATGCATAGAGGTTTCTATAAAGGACAGTGAAGATGCTTTCGCAAGCCCCACAGGAAATTTCTATCCACAGGCCCCGTCAATTCCAGC
ATGTGTCTAGAGGACAGCAGATACAACCTGGTCTTTTATTCTGCTCCAGCTTGCCAAATGCAAGGCCACAGTAAATGCATCAATCAGAGCATCTGTGAGAAGTGTGAG
AACCTGACCACAGGCAAGCACTGCGAGACCTGCATATCTGGCTTCTACGGTGTATCCACCAATGGAGGAAATGTGAGCCATGCAAGTGAATGGGCACGGCTCTCTG
TGCAACACCAACACGGGCAAGTGTCTTGCACCACCAAGGGCGTCAAGGGGACGAGTGGCAGCTATGTGAGGTAGAAAATCGATACCAAGGAAACCTCTCAGAGGA
ACATGTTATTATACTCTTCTATTGACTATCAGTTTACCTTTAGTCTATCCCAGGAAGATGATCGCTATTACACAGCTATCAATTTTGTGGCTACTCTGACGAACAA
AACAGGGATTTGGACATGTTTCAATGCCCTCAAGAATTTCAACCTCAACATCACCTGGGCTGCCAGTTTCTCAGCTGGAACCCAGGCTGGAGAAGAGATGCCCTGT
GTTTCAAAAACCAATTAAGGAGTACAAAGATAGTTTCTCTAATGAGAAGTTTATTTTTCGCAACCCCAATATCACTTTCTTTGTTTATGTGAGTAATTTTACC
TGGCCCATCAAAATTCAGGTGCAAACTGAACAATGAGGACGATGGACACAGGAAGGGGAACATCACACACAGGGGCTGTGTGGGGTGGGGGAAGGGGAAGGGAT
AGCATTAGGGGATATACCTAATGTTAAATGACGAGTTAATGGGTGCAGCACACCAACATGGCATATGTATACATATGTAACAAACCTGCATGTTGTGCATGTATACC
TAAACTTAAAGTATAATTAATAAA

FIG. 19A

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MVAVAAAAATEARLRRRTAATAALAGRSGGPHRPCTATGAWRPGPRARLCLPRVLSRALPPPPLLPLLSL LLLPLPREAEAAAAVAVSGSAAAEKECDRPCVNGG
RCNPGTGQCVCPCAGWVGEQCQHCGRFRLTGSSGFVTDGPGNYKYTKCTWLI EGQPNRIMRLRFNH FATECSWDHLYVYDGDSIYAPLVAAFSGLIVPERDGNETVP
EVVATSGYALLHFFSDAAYNL TGFNITYSFDMPNCSGRGECKISNSSDTVECECSENWKGACDI PHCTDNCGFPHRGICNSSDVRGCSCFSDWOGPGCSVPVPAN
QSFWTREEYSNLKLPRASHKAVVNGNIMWVVGGMFNHSDYNNMVLAYDLASREWLPLNRSVNNVVRYGHSALYKDKIYMYGGKIDSTGNVTNELRVFHIHNESWVL
LTPKAKEQYAVVGHSAHIVTLKNGRVVMLVIFGHCPLYGYISNVQEYDLDKNTWSILHTQGALVQGGYGHSSVYDHRTRALYVHGGYKAFSANKYRLADDLYRYDVT
QMWITLKDSRFFRYLHTAVIVSGTMLVFGGNTHNDTSMSHGAKCFSSDFMAYDIACDRWSVLPRPDLHHDVNRFGHSAVLHNSTMYVFGGFNSLLSDILVFTSEQCD
AHRSEAACLAAGPGIRCWNVTGSSQCI SWALATDEQEEKLKSECFSKRTL DHDRCQHTDCYSCTANTNDCHWCNDHCVPRNHSCSEGOISI FRYENC PKDNPMYYCN
KKTSCRS CALDQNCQWEPRNQECIALPENICGIGWHLVGN SCLKIT TAKENYDNAKLF CRNHNALLASLT TOKKVEFVLKQLRIMOSSQSMSKLTLPWVGLRKINVS
YWCWEDMSPFTNSLLQWMPSEPSDAGFCGILSEPSTRGLKAATCINPLNGSV CERPANHS AKQCRTPCALRTACGDCTSGSSECMWCSNMKQCVD SNAYVASFPFGQC
MEWYTMSTCPPENC SGYCTCSHCLEQPGCGWCTDPSNTGKGKCI EGSYKGPVKMPSQAPTGNFYPOPLLNSSMCLEDSRYNWSFIHCPACQCNHSGK CINO SICEKCE
NLTTGKHCETCISGFYGDPTNGGKCQPC KNGHASLCNTNTGKCFCTTKGVKGD ECOLCEVENRYOGNPLRGTCYTTLLIDYQFTFSLSQEDDRYYTAINFVATPDEO
NRDLDMFINASKNFNLNITWAASFSAGTQAGEEMPVVS KTN IKEYKDSFSNEKFDFRNHPNITFFVYVS NFWPIKIQVQTEQGRMDTGRGTSHTRACCGVGGRGRDS
IRGYTCMTSWVQHTNMAYVYICNKPACCAHVPNLKYNNKKKKKKKKKKKKKKKKKK

FIG. 19B

ATGGTGGCGGTGGCCGACGCGCGGCACTGAGGCAAGGCTGAGGAGGAGGACGGCGGACGCGCAGCGCTCGCGGGCAGGAGCGGCGGCGGCGCACGACCGCTGCACC
GCGACAGGGGCGCTGGAGGCGGGGACCGCGCGCCCGGCTGTGTCTCCCGCGGGTGTGTCTCGCGGGCGCTGCCCGCGCGCGCTGTGCGCGCTGCTCTTTTCGCTGCTG
CTGCTGCCGCTGCCCGGGAGGCGGAGGCGGCTGCGGTGGCGGGCGGGTGTCCGGCTCGGCGCGCAGCGGAGGCCAAGGAATGTGACGCGCGGTGTGTCAACGGGGT
CGCTGCAACCTGGCACCAGGCGAGTGGCTGTGCCCGCGGCTGGGTGGGCGAGCAATGCCAGCACTGCGGGGGCGCTTCAGACTAACTGGATCTTCTGGGTTTGTG
ACAGATGGACCTGGAAATTATAAATACAAAACGAAGTGCACGTGGCTCATTGAAGGACAGCCAAATAGAATAATGAGACTTCGTTTCAATCATTCTGCTACAGAGTGT
AGTTGGGACCATTTATATGTTTATGATGGGACTCAATTTATGCACCGCTAGTTGCTGCATTTAGTGGCCTCATTGTTCTGAGAGAGATGGCAATGAGACTGTCCCT
GAGGTTGTTGCCACATCAGGTTATGCCTTGTGCTGCTTTTATGATGCTGCTTATAATTTGACTGGATTTAATATTACTTACAGTTTGTATGTGTCCAAATAAC
TGCTCAGGCGGAGGAGTGTAAATCAGTAATAGCAGCGATACTGTTGAATGTGAATGTTCTGAAAACCTGGAAAGGTGAAGCATGTGACATTCTCACTGTACAGAC
AATCTGGTTTTCTCATCGAGGCATCTGCAATTCAGTGATGTGAGAGGATGCTCCTGCTTCTCAGACTGGCAGGGTCTGGATGTTGAGTTCTGTACCAGCTAAC
CAGTCATTTTGGACTCGAGAGGAATATTCTAACTTAAAGCTCCCCAGAGCATCTCATAAAGCTGTGGTCAATGGAACATTATGTGGGTTGTTGGAGGATATATGTTT
AACCCTCAGATTATAACATGGTTCTAGCGTATGACCTTGCTTCTAGGGAGTGGCTTCCACTAAACCGTTCTGTGAACAATGTGGTTGTTAGATATGGTCATTCTTTG
GCATTATACAAGGATAAAATTTACATGTATGGAGGAAAAATTGATTCAACTGGGAATGTGACCAATGAGTTGAGAGTTTTTCACATTCTAATGAGTCATGGGTGTTG
TTGACCCCTAAGGCAAAGGAGCAGTATGCAGTGGTTGGGCACTCTGCACACATTGTTACACTGAAGAATGGCCGAGTGGTCATGCTGGTCATCTTTGGTCACTGCCCT
CTCTATGGATATATAAGCAATGTGCAGGAATATGATTGGATAAAGACACATGGAGTATATTACACACCCAGGGTGGCTTGTGCAAGGGGGTTACGGCCATAGCAGT
GTTTACGACCATAGGACCGGGCCCTATACGTTTATGGTGGCTACAAGGCTTTCAGTGCCAATAAGTACCGGCTTGACAGATGATCTCTACCGATATGATGTGGATACC
CAGATGTGGACCATTTCTTAAGGACAGCCGATTTTTCCGTTACTTGACACAGCTGTGATAGTGAGTGGAAACCATGCTGGTGTGTTGGGGGAAACACACACAATGACACA
TCTATGAGCCATGGCGCCAAATGCTTCTCTTCAGATTTTATGGCCTATGACATTGCTGTGACCGCTGGTCAGTGCTTCCAGAGCTGATCTCCACCATGATGTCAAC
AGATTTGGCCATTGAGCAGTCTTACACAACAGCACCATGTATGTGTTGGTGGTTTCAATAGTCTCCTCCTCAGCGACATCCTGGTATTGAGCTCGGAACAGTGTGAT
GCGCATCGGAGTGAAGCCGCTTGTGTTAGCAGCAGGACCTGGTATTGCGTGTGTGTTGGAACACAGGGTCGTCTCAGTGTATCTCGTGGGCGCTGGCAACTGATGAACAA
GAAGAAAAGTTAAATCAGAAATGTTTTCCAAAAGAACTCTTGACCATGACAGATGTGACAGCACACAGATTGTTACAGCTGCACAGCCAACACCAATGACTGCCAC
TGGTGCAATGACCATTTGTGTTCCCGAGGAACACAGCTGCTCAGAAGGCCAGATCTCCATTTTAGGTATGAGAATTGCCCAAGGATAACCTATGTACTACTGTAAAC
AAGAAGACCAGCTGCAGGAGCTGTGCCCTGGACCAGAAGTCCAGTGGGAGCCCGGAATCAGGAGTGCATTGCCCTGCCCGGTAGGCCTTGACGGGTCTCTTGGTG
TGTGTGGGTCCATTACTTCAGCTGCTTCCCCAACACTGTGCAGCCTAAGTTGAACCTAGCAGAGGGGAAGAGCTAATTCTGTCCATTCTATCCCCACACAGATTT
ATGGGCTTTTTGTTTTAACTAAAATACAGTTCTTAAGTATTGTTCTACTGTCCTTTGAAATAAAGTGAACATCCTTTGCTGCTCTGTAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIG. 20A

MVAVAAAAATEARLRRRTAATAALAGRSGGPHRPCTATGAWRPGPRARLCI.PRVLSRALPPPLLPPLFSLLLPLPREAEEAAVAAVSGSAAAEAKECDRPCVNGG
RCNPGTGQCVCPCAGWVGEQCHCGGRFRLTGSSGFVTDGPGNYKYKTKCTWLI.EGQPNRIMRLRFNFHATECSWDHLYVYDGDSIYAPLVAAFSGLIVPERDGNETVP
EUVATSGYALLHFFSDAAYNLTFGNITYS.FDMCPNNCSGRGECKISNSSDTVECECSENWKGEACDI.PHCTDNCGFPHRGICNSSDVRGCSCFSDWQGPSCSVPPAN
QSEWTRREEYSNLKLPRAASHKAVVNGNIMWVVGGMFNHSDYNMVLAYDLASREWLPLNRSVNNVVRYGHS.LALYKDKIYMYGGKIDSTGNVTNELRVFHIHNESWVL
LTPKAKEQYAVVGHS.AHIVTLKNGRVVMLVIFGHCP.LYGYISNVQ.EYDLDKNTWSILHTQ.GALVQGGYGHSSVYDHRTRALYVHGGYKAFSANKYRLADDLYRYD.VDT
QMW.TI.LKDSRFFRYLHTAVIVSGTMLVF.GGNT.HNDTSMH.GAKCFSSDFMAYDIACDRWSVLPRPDL.HHDV.NRFGHS.AVLHNSTMYVFGGFNS.LLLSDI.LVFTSE.QCD
AHRSEAACLAAGPGIRCVWNTGSSQCISWALATDEQE.EKLKSECF.SKRTL.DH.DRCDQHTDCYSCTANTNDCHWCNDHCVPRNHSCSE.GQISIFRYENC.PKDNPMYYCN
KKTSCRS.CALDONCQWEP.RNQECIALPGRPCRVILVCVG.PLLQ.PAS.PNTVQPKLNLAEGK.SFC.FI.PHTSIMG.FFVFNNTVLKYL.FLLSFEIKNILCCSVK.KKKKKKK
KKKKKKKK

FIG. 20B

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(54) Title: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY			
(57) Abstract <p>The present invention relates to mammalian mahogany genes, including the human mahogany gene, which are novel genes involved in the control of mammalian body weight. The invention encompasses nucleotide sequences of the mahogany gene, host cell expression systems of the mahogany gene, and hosts which have been transformed by these expression systems, including transgenic animals. The invention also encompasses novel mahogany gene products, including mahogany proteins, polypeptides and peptides containing amino acid sequences mahogany proteins, fusion proteins of mahogany proteins polypeptides and peptides, and antibodies directed against such mahogany gene products. The present invention also relates to methods and compositions for the diagnosis and treatment of mammalian body weight disorders, including obesity, cachexia, and anorexia, and for the identification of subjects susceptible to such disorders. Further, the invention relates to methods of using the mahogany gene and gene products of the invention for the identification of compounds which modulate the expression of the mahogany gene and/or the activity of the mahogany gene product. Such compounds can be useful as therapeutic agents in the treatment of mammalian body weight disorders, including obesity, cachexia, and anorexia.</p>			

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INTERNATIONAL SEARCH REPORT

International Application No.
PCT/US 99/16484

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C07K14/705 A61K38/17 G01N33/68 C07K16/28

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C07K C12N A61K G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	NAGASE ET AL.: "Prediction of the coding sequences of unidentified human genes IX: the complete sequences of 100 new clones from brain which can code for large proteins in vitro" DNA RESEARCH, vol. 5, 1998, pages 31-39, XP000884356 table 2	1,2,5,11
X	DATABASE GENBAN 'Online! Accession no. AB11120, 10 April 1998 (1998-04-10) NAGASE ET AL.: "Prediction of the coding sequences of unidentified human genes" XP002135391 abstract	1,2,5,11

☒ Further documents are listed in the continuation of box C.

☐ Patent family members are listed in annex.

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INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 99/16484

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P, X	<p>NAGLE ET AL.: "The mahogany protein is a receptor involved in suppression of obesity"</p> <p>NATURE, vol. 398, 11 March 1999 (1999-03-11), pages 148-152, XP002135389 the whole document</p>	1-28
P, X	<p>GUNN ET AL.: "The mouse mahogany locus encodes a transmembrane form of attractin"</p> <p>NATURE, vol. 398, 11 March 1999 (1999-03-11), pages 152-156, XP002135390 the whole document</p>	1-28
X	<p>DUKE-COHAN ET AL.: "A novel form of dipeptidylpeptidase IV found in human serum"</p> <p>J. BIOL. CHEM., vol. 270, no. 23, 9 June 1995 (1995-06-09), pages 14107-14114, XP000579864 page 14109 -page 14111</p>	16-18

Form PCT/SA/210 (continuation of second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 99/ 16484

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
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Remark: Although claims 26-28 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

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2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY

(57) Abstract: The present invention relates to mammalian mahogany genes, including the human mahogany gene, which are novel genes involved in the control of mammalian body weight. The invention encompasses nucleotide sequences of the mahogany gene, host cell expression systems of the mahogany gene, and hosts which have been transformed by these expression systems, including transgenic animals. The invention also encompasses novel mahogany gene products, including mahogany proteins, polypeptides and peptides containing amino acid sequences mahogany proteins, fusion proteins of mahogany proteins polypeptides and peptides, and antibodies directed against such mahogany gene products. The present invention also relates to methods and compositions for the diagnosis and treatment of mammalian body weight disorders, including obesity, cachexia, and anorexia, and for the identification of subjects susceptible to such disorders. Further, the invention relates to methods of using the mahogany gene and gene products of the invention for the identification of compounds which modulate the expression of the mahogany gene and/or the activity of the mahogany gene product. Such compounds can be useful as therapeutic agents in the treatment of mammalian body weight disorders, including obesity, cachexia, and anorexia.

WO 00/05373 A3

**METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY**

Priority of provisional application no. 60/093,630 filed
5 on July 21, 1998 and of provisional application no.
60/104,978 filed on October 20, 1998, each of which is
incorporated herein by reference in its entirety, is claimed
under 35 U.S.C. § 119(e)(1).

10 1.

INTRODUCTION

The present invention relates to mammalian mahogany
genes, including the human mahogany gene, which are novel
genes involved in the control of mammalian body weight. The
invention encompasses nucleotide sequences of the mahogany
15 gene, host cell expression systems of the mahogany gene, and
hosts which have been transformed by these expression
systems, including transgenic animals. The invention also
encompasses novel mahogany gene products, including mahogany
proteins, polypeptides and peptides containing amino acid
sequences mahogany proteins, fusion proteins of mahogany
20 proteins polypeptides and peptides, and antibodies directed
against such mahogany gene products.

The present invention also relates to methods and
compositions for the diagnosis and treatment of mammalian
body weight disorders, including obesity, cachexia, and
25 anorexia, and for the identification of subjects susceptible
to such disorders. Further, the invention relates to methods
of using the mahogany gene and gene products of the invention
for the identification of compounds which modulate the
expression of the mahogany gene and/or the activity of the
mahogany gene product. Such compounds can be useful as
30 therapeutic agents in the treatment of mammalian body weight
disorders, including obesity, cachexia, and anorexia.

BACKGROUND OF THE INVENTION

2.

Obesity represents the most prevalent of body weight disorders, and it is the most important nutritional disorder in the western world, with estimates of its prevalence ranging from 30% to 50% within the middle-aged population. Other body weight disorders, such as anorexia nervosa and bulimia nervosa, which together affect approximately 0.2% of the female population of the western world, also pose serious health threats. Further, such disorders as anorexia and cachexia (wasting) are also prominent features of other diseases such as cancer, cystic fibrosis, and AIDS.

Obesity, defined as an excess of body fat relative to lean body mass, also contributes to other diseases. For example, this disorder is responsible for increased incidence of diseases such as coronary artery disease, hypertension, stroke, diabetes, hyperlipidemia, and some cancers (See, e.g., Nishina, P.M. et al., 1994, Metab. 43: 554-558; Grundy, S.M. & Barnett, J.P., 1990, Dis. Mon. 36: 641-731). Obesity is not merely a behavioral problem, i.e., the result of voluntary hyperphagia. Rather, the differential body composition observed between obese and normal subjects results from differences in both metabolism and neurologic/metabolic interactions. These differences seem to be, to some extent, due to differences in gene expression, and/or level of gene products or activity (Friedman, J.M. et al., 1991, Mammalian Gene 1: 130-144).

The epidemiology of obesity strongly shows that the disorder exhibits inherited characteristics (Stunkard, 1990, N. Eng. J. Med. 322: 1438). Moll et al. have reported that, in many populations, obesity seems to be controlled by a few genetic loci (Moll et al., 1991, Am. J. Hum. Gen. 49: 1243). In addition, human twin studies strongly suggest a substantial genetic basis in the control of body weight, with estimates of heritability of 80-90% (Simopoulos, A.P. &

Childs, B., eds., 1989, in "Genetic Variation and Nutrition in Obesity", World Review of Nutrition and Diabetes 63, S. Karger, Basel, Switzerland; Borjeson, M., 1976, Acta. Paediatr. Scand. 65: 279-287).

5 In other studies, non-obese persons who deliberately attempted to gain weight by systematically over-eating were found to be more resistant to such weight gain and able to maintain an elevated weight only by very high caloric intake. In contrast, spontaneously obese individuals are able to maintain their status with normal or only moderately elevated
10 caloric intake. In addition, it is a commonplace experience in animal husbandry that different strains of swine, cattle, etc., have different predispositions to obesity. Studies of the genetics of human obesity, and of animal models of obesity demonstrate that obesity results from complex
15 defective regulation of both food intake, food induced energy expenditure, and of the balance between lipid and lean body anabolism.

There are a number of genetic diseases in man and other species which feature obesity among their more prominent
20 symptoms, along with, frequently, dysmorphic features and mental retardation. For example, Prader-Willi syndrome (PWS; reviewed in Knoll, J.H. et al., 1993, Am. J. Med. Genet. 46: 2-6) affects approximately 1 in 20,000 live births, and involves poor neonatal muscle tone, facial and genital deformities, and generally obesity.

25 In addition to PWS, many other pleiotropic syndromes have been characterized which include obesity as a symptom. These syndromes are genetically straightforward, and appear to involve autosomal recessive alleles. Such diseases include, among others, Ahlstroem, Carpenter, Bardet-Biedl,
30 Cohen, and Morgagni-Stewart-Monel Syndromes.

A number of models exists for the study of obesity (see, e.g., Bray, G. A., 1992, Prog. Brain Res. 93: 333-341; and

Bray, G.A., 1989, Amer. J. Clin. Nutr. 5: 891-902). For example, animals having mutations which lead to syndromes that include obesity symptoms have also been identified. Attempts have been made to utilize such animals as models for the study of obesity, and the best studied animal models to date for genetic obesity are mice. For reviews, see, e.g., Friedman, J.M. et al., 1991, Mamm. Gen. 1: 130-144; Friedman, J.M. and Liebel, R.L., 1992, Cell 69: 217-220.

Studies utilizing mice have confirmed that obesity is a very complex trait with a high degree of heritability. Mutations at a number of loci have been identified which lead to obese phenotypes. These include the autosomal recessive mutations obese (*ob*), diabetes (*db*), fat (*fat*), and tubby (*tub*).

The dominant Yellow mutation (*Ay*) at the agouti locus causes a pleiotropic syndrome which causes moderate adult onset obesity, a yellow coat color, and a high incidence of tumor formation (Herberg, L. and Coleman, D.L., 1977, Metabolism 26:59), and an abnormal anatomic distribution of body fat (Coleman, D.L., 1978, Diabetologia 14:141-148). The mutation causes the widespread expression of a protein which is normally seen only in neonatal skin (Michaud, E. J. et al., 1994, Genes Devel. 8:1463-1472). The agouti protein has been reported to be a competitive antagonist of α -MSH binding to the melanocortin receptors MC1-R and MC4-R in vitro (Lu et al., 1996, Nature 371:799-802), and the authors speculated that de-regulated ubiquitous expression of agouti may lead to obesity by antagonism of melanocortin receptors expressed outside the hair follicles.

Mahogany (*mg*) and mahoganoid (*md*) are mutations that suppress the phenotypic effects of agouti protein in vivo (Lane and Green, 1960, J. Hered. 51: 228-230). The mahogany and mahoganoid mutation have been mapped to mouse chromosomes 2 and 16, respectively (Green, 1989, "Catalog of mutant genes

and polymorphic loci", pp. 12-403 in Genetic Variants and Strains of the Laboratory Mouse, Lyon, M. F. and Searle, A.G., eds., Oxford University Press, Oxford). Mutations of both *mg* and *md* have been shown to suppress the effects of agouti on obesity as well as on coat color (Miller et al.,
5 1997, Genetics 146: 1407-1415).

In summary, therefore, obesity, which poses a major, worldwide health problem, represents a complex, highly heritable trait. Given the severity, prevalence, and potential heterogeneity of such disorders, there exists a
10 great need for the identification of those genes that participate in the control of body weight.

3.

SUMMARY OF THE INVENTION

The present invention relates to the identification of
15 novel nucleic acid molecules and proteins encoded by such nucleic acid molecules that are involved in the control of mammalian body weight, and which, further, are associated with mammalian body weight disorders such as obesity, cachexia, and anorexia. The nucleic acid molecules of the present invention represent the genes corresponding to the
20 mammalian mahogany gene, including the human mahogany gene.

In particular, the compositions of the present invention include nucleic acid molecules which comprise the following sequences: (a) nucleotide sequences of the mahogany gene, including, e.g., murine mahogany sequences as shown in FIGS.
25 2A, 3B-D, 6A-B, 8A-C, and 9A, as well as allelic variants and homologs thereof, and human mahogany sequences, as shown, e.g., in FIGS. 10A, 18A-C, 19A-C and 20A-B, as well as allelic variants and homologs thereof; (b) nucleotide sequences that encode the mahogany gene product amino acid
30 sequences, as shown, e.g., in in FIGS. 2B, 8D, 9B, 10B, 17A-D, 18B-D, 19D and 20C; (c) nucleotide sequences that encode portions of the mahogany gene product corresponding to its functional domains

and individual exons; (d) nucleotide sequences comprising the novel mahogany gene sequences disclosed herein that encode mutants of the mahogany gene product in which all or a part of one or more of the domains is deleted or altered, as shown, e.g., in FIG. 6; (e) nucleotide sequences that encode fusion proteins comprising the mahogany gene product, or one or more of its domains fused to a heterologous polypeptide; (f) nucleotide sequences within the mahogany gene, as well as chromosome sequences flanking the mahogany gene, see, e.g., FIG. 3, which can be utilized as part of the methods of the present invention for the diagnosis of mammalian body weight disorders, including obesity, cachexia, and anorexia, which are mediated by the mahogany gene, as well as for the identification of subjects susceptible to such disorders; (g) nucleic acid sequences that hybridize to the above described sequences under stringent or moderately stringent conditions, particularly human mg homologs. The nucleic acid molecules of the invention include, but are not limited to, cDNA and genomic DNA sequences of the mahogany gene.

The present invention also encompasses expression products of the nucleic acid molecules listed above; i.e., proteins and/or polypeptides that are encoded by the above mahogany nucleic acid molecules.

Agonists and antagonists of the mahogany gene and/or gene product are also included in the present invention. Such agonists and antagonists will include, for example, small molecules, large molecules, and antibodies directed against the mahogany gene product. Agonists and antagonists of the invention also include nucleotide sequences, such as antisense and ribozyme molecules, and gene or regulatory sequence replacement constructs, that can be used to inhibit or enhance expression of the mahogany gene.

The present invention further encompasses cloning vectors, including expression vectors, that contain the

nucleic acid molecules of the invention and can be used to express those nucleic acid molecules in host organisms. The present invention also relates to host cells engineered to contain and/or express the nucleic acid molecules of the invention. Further, host organisms which have been transformed with these nucleic acid molecules are also encompassed in the present invention. Host organisms of the invention include organisms transformed with the cloning vectors described above, e.g., transgenic animals, particularly non-human transgenic animals, and particularly transgenic non-human mammals.

The transgenic animals of the invention include animals that express a mutant variant or polymorphism of a mahogany gene, particularly a mutant variant or polymorphism of a mahogany gene that is associated with a weight disorder such as obesity, cachexia, or anorexia. The transgenic animals of the invention further include those that express a mahogany transgene at higher or lower levels than normal. The transgenic animals of the invention further include those which express the mahogany gene in all their cells, "mosaic" animals which express the mahogany gene in only some of their cells, and those in which the mahogany gene is selectively introduced into and expressed in a specific cell type(s). The transgenic animals of the invention also include "knock-out" animals. Knock-out animals comprise animals which have been engineered to no longer express the mahogany gene.

The present invention also relates to methods and compositions for the diagnosis of mammalian body weight disorders, including obesity, cachexia, and anorexia, as well as for the identification of subjects susceptible to such disorders. Such methods comprise, for example, measuring expression of the mahogany gene in a patient sample, or detecting a mutation in the mahogany gene in the genome of a mammal, including a human, suspected of exhibiting such a

weight disorder. The nucleic acid molecules of the invention can also be used as diagnostic hybridization probes, or as primers for diagnostic PCR analysis to identify of mahogany gene mutations, allelic variations, or regulatory defects, such as defects in the expression of the mahogany gene. Such diagnostic PCR analyses can be used to diagnose individuals with a body weight disorder associated with a particular mahogany gene mutation, allelic variation, or regulatory defect. Such diagnostic PCR analyses can also be used to identify individuals susceptible to such body weight disorders and hyperphagia.

Methods and compositions, including pharmaceutical compositions, for the treatment of body weight disorders such as obesity, cachexia, and anorexia are also included in the invention. Such methods and compositions are capable of modulating the level of mahogany gene expression and/or the level of activity of the mahogany gene product. Such methods include, for example, modulating the expression of the mahogany gene and/or the activity of the mahogany gene product for the treatment of a body weight disorder which is mediated by some other gene, for example by the agouti gene.

The invention still further relates to methods for identifying compounds which modulate the expression of the mammalian mahogany gene and/or the synthesis or activity of mammalian mahogany gene products. Such compounds include therapeutic compounds which can be used as pharmaceutical compositions to reduce or eliminate the symptoms of mammalian body weight disorders such as obesity, cachexia, and anorexia. Cellular and non-cellular assays are described that can be used to identify compounds that interact with the mahogany gene and/or gene product, e.g., modulate the activity of the mahogany gene and/or bind to the mahogany gene product. Such cell-based assays of the invention

utilize cells, cell lines, or engineered cells or cell lines that express the mahogany gene product.

In one embodiment, such methods comprise contacting a compound to a cell that expresses a mahogany gene, measuring
5 the level of mahogany gene expression, gene product expression, or gene product activity, and comparing this level to the level of mahogany gene expression, gene product expression, or gene product activity produced by the cell in the absence of the compound, such that if the level obtained
10 in the presence of the compound differs from that obtained in its absence, a compound that modulates the expression of the mammalian mahogany gene and/or the synthesis or activity of mammalian mahogany gene products has been identified.

In an alternative embodiment, such methods comprise administering a compound to a host, e.g., a transgenic animal
15 that expresses a mahogany transgene or a mutant mahogany transgene, and measuring the level of mahogany gene expression, gene product expression, or gene product activity. The measured level is compared to the level of mahogany gene expression, gene product expression, or gene
20 product activity in a host that is not exposed to the compound, such that if the level obtained when the host is exposed to the compound differs from that obtained when the host is not exposed to the compound, a compound that modulates the expression of the mammalian mahogany gene
25 and/or the synthesis or activity of mammalian mahogany gene products, and/or the symptoms of a mammalian body weight disorder, such as obesity, cachexia, or anorexia, has been identified.

The Example presented in Section 6, below, describes the genetic and physical mapping of the mahogany gene to a
30 specific 700 kb interval of mouse chromosome 2. The example presented in Section 7, below, describes the identification of a transcription unit within this chromosome interval,

referred to herein as the MG gene, which represents the mahogany gene. The expression and sequence analysis of this candidate mahogany gene is described in the example presented in Section 8, below. These experiments prove that the candidate gene MG is indeed the mahogany gene. The example
5 presented in Section 9, below, presents data demonstrating that the mechanism of mahogany action is specific for diet-induced obesity, therefore supporting the use of mahogany antagonists as a specific therapeutic for treatment of diet-induced body weight disorders. The example presented in
10 Section 10, below, presents the identification and characterization of the human mg gene, variants thereof and polypeptides encoded by the human mahogany sequences.

DEFINITIONS

15 As used herein, the following terms shall have the abbreviations indicated.

BAC, bacterial artificial chromosomes
bp, base pair(s)
EST, expressed sequence tag
mg, mahogany gene
20 RFLP, restriction fragment length polymorphism
RT-PCR, reverse transcriptase PCR
SSCP, single-stranded conformational polymorphism
SSLP, simple sequence length polymorphisms
STS, short tag sequence
25 YAC, yeast artificial chromosome

4. BRIEF DESCRIPTION OF THE FIGURES

FIG. 1. Physical map of the mahogany interval of mouse chromosome 2.

30 FIG. 2. Panels A(1)-A(9): cDNA nucleotide sequence of the wild-type (C57BL/6J) murine mahogany gene (SEQ ID NO: 1),

including the 5' and 3' untranslated regions, and Panel B: the derived amino acid sequence (SEQ ID NO: 2) of the mahogany gene product.

FIG. 3. Genomic structure and nucleotide sequences derived from the wild-type (C57BL/6J) mouse genomic regions containing the mg gene. Panel A, genomic structure; Panel B(1)-B(17), genomic sequence c56 (SEQ ID NO: 3); Panel C(1)-C(6), genomic sequence c96 (SEQ ID NO: 4); Panel D(1)-D(86), genomic sequence of c110/111 (SEQ ID NO: 5).

FIG. 4. Structural depiction of MG cDNA without introns. CUB=CUB domain, metal=metallothionin domain; T-transmembrane domain.

FIG. 5(1)-5(4). Nucleotide sequence of primers used to amplify each of the exons in the mg gene.

FIG. 6. Nucleotide sequence of the wild-type (SEQ ID NO: 6) and mahogany mutant (SEQ ID NO: 7) sequences in exon 15 of the MG gene. Bases shown in bold are deleted in Mg3J mutant mg.

FIG. 7. Differential 5' start sequences in the murine mahogany gene showing splice forms akml003 and akml004.

FIGS. 8A-E. Panels A-C, cDNA sequence (SEQ ID NO: 8) from one form of the differential 5' start site found in the murine (akml003), Panel D, amino acid sequence (SEQ ID NO: 9) encoded by the cDNA of Panels A-C; Panel E, hydropathy plot of the akml003 amino acid sequence.

FIGS. 9A-C. Panel A, cDNA sequence (SEQ ID NO: 10) from one form of the differential 5' start site found in the

murine (akml004); Panel B, amino acid sequence (SEQ ID NO: 11) encoded by the cDNA of Panel A; Panel C, hydropathy plot of the akml004 amino acid sequence.

FIGS. 10A-B. Nucleotide sequence (SEQ ID NO: 12) of a
5 contig containing a portion of the human MG cDNA, panel A(1)-A(7) and the translated amino acid sequence (SEQ ID NO: 13), panel B.

FIGS. 11A-B. Effect of *mg* on *MC4r* -/- induced weight
10 gain in females (FIG. 11A) and males (FIG. 11B); values depicted are the mean +/- SD within a designated time interval.

FIGS. 12A-D. Effect of *mg* on monogenic obese mutants
15 *Lepr^{db}* (FIG. 12A), *tub* (FIG. 12B), *Cpe^{fat}* (FIG. 12C), and on high fat diet induced obesity (FIG. 12D); the values indicated are the mean +/- SD of the weight length ratio for each animal.

FIG. 13. Genetic and physical map of the region
20 surrounding the *mg* locus; all MIT markers are presented with shortened names, e.g., D2MIT77 is indicated as D2M77; locations of loci which also mapped on the human cytogenetic map are indicated in parentheses after the gene symbol.

Panel A. The genetic map of the *mg* gene region on
25 the Millennium BSB mapping panel (Misumi, D.J. et al., 1997, *Science* 278:135-138);

Panel B. The genetic map obtained from crosses segregating *mg* mutant alleles;

Panel C. The -1 Mb BAC contig across the *mg* gene
30 region of mouse Chromosome 2;

Panel D. The transcriptional units identified in the *mg* region; the filled box indicates the *mg* gene,

whereas the hatched box is a member of the High Mobility Group (HMG) gene family which sits between coding exons 21 and 22 of the *mg* gene.

5 FIG. 14. Northern blot analysis with C3H/HeJ (lane 1), and three mutant alleles of *mg*: C3HeB/FeJ-*mg*^{3J} (Lane 2), LDJ/Le-*mg* (Lane 3), and C3H/HeJ-*mg*^J (Lane 4); the size marker is shown on the left, and hybridization with actin is shown below for loading comparisons.

10 FIGS. 15A-D. In situ hybridization data: FIG. 15A demonstrates widespread expression of *mg* throughout the mouse brain is seen in an antisense autoradiographic image of a C3H/HeJ brain at the level of the 3rd ventricle; decreased expression in *mg* mutants is documented in selected antisense
15 darkfield images of 10 μ m whole mount cross sections of the ventromedial hypothalamic nucleic (VMH) of C3H/HeJ (FIG. 15B), LDJ/Le-*mg* (FIG. 15C), and C3HeB/FeJ-*mg*^{3J} (FIG. 15D).

FIGS. 16A-B. Alignment of the MG protein sequence with
20 its family members showing the transmembrane region (indicated in brackets) and cytoplasmic tail (FIG. 16A); and a schematic of the molecular modular architecture of MG (FIG 16B).

FIGS. 17A-D. Sequence alignment of the predicted MG
25 protein sequence (top) with the Attractin protein sequence. Characteristic MG domains are as indicated. See Section 10.2 for details.

FIG. 18A-D. Panels A(1-8): cDNA nucleotide sequence
30 (SEQ ID NO: 14) of the long splice variant of the human ortholog of the mahogany gene, and Panels B-D: the derived amino acid sequence (SEQ ID NO: 15) of the mahogany gene product which it encodes.

FIG. 19A-D. Panels A-C: cDNA nucleotide sequence (SEQ ID NO: 16) of a shorter splice variant of the human ortholog of the mahogany gene, and Panel D: the derived amino acid sequence (SEQ ID NO: 17) of the mahogany gene product which it encodes.

5

FIG. 20A-C. Panels A-B: cDNA nucleotide sequence (SEQ ID NO: 18) of a second shorter splice variant of the human ortholog of the mahogany gene, and Panel C: the derived amino acid sequence (SEQ ID NO: 19) of the mahogany gene product which it encodes.

10

5.

DETAILED DESCRIPTION OF THE INVENTION

Described herein is the identification of the novel mammalian mahogany (*mg*) gene, including the human mahogany gene, which is involved in the control of mammalian body weight. Also described are recombinant mammalian, including human mahogany DNA molecules, cloned genes, and degenerate variants thereof. The compositions of the present invention further include *mg* gene products (e.g., proteins) that are encoded by the *mg* DNA molecules of the invention, and the modulation of *mg* gene expression and/or *mg* gene product activity in the treatment of mammalian body weight disorders, including obesity, cachexia, and anorexia. Also described herein are antibodies against *mg* gene products (e.g., proteins), or conserved variants or fragments thereof, and nucleic acid probes useful for the identification of *mg* gene mutations, and the use of such nucleic acid probes in diagnosing mammalian body weight disorders, including obesity, cachexia, and anorexia. Further described are methods for the use of the *mg* gene and/or *mg* gene products in the identification of compounds which modulate the activity of the *mg* gene product.

5.1.

THE MAHOGANY GENE

The mahogany genes are novel mammalian genes involved in the control of body weight. The nucleic acid sequences of the mahogany genes, including the murine mahogany gene sequences shown in FIGS. 2A, 3B-D, 6A-B, 8A-C, and 9A, as well as allelic variants and homologs thereof, and human mahogany sequences, as shown, e.g., in FIGS. 10A, 18A, 19A-C and 20A-B, as well as allelic variants and homologs thereof. The genomic sequence and structure, *i.e.*, the intron/exon structure, of the mahogany genes have also been elucidated, FIG. 3.

The mahogany gene nucleic acid molecules of the present invention comprise: (a) the DNA sequence shown in FIGS. 2A, 3, 6A-B, 8A-C, 9A, 10A, 18A, 19A-C or 20A-B, or any DNA sequence that encodes the amino acid sequence of the mahogany gene product shown in FIGS. 2B, 8D, 9B, 10B, 17A-D, 18B-D, 19D or 20C; (b) nucleotide sequences comprising the novel mahogany sequences disclosed herein that encode mutants of the mahogany gene product in which all or a part of one or more of the domains is deleted or altered, as shown, e.g., FIG. 6; (c) nucleotide sequences that encode fusion proteins comprising a mahogany gene product, or one of its domains fused to a heterologous polypeptide; and (d) nucleotide sequences within a mahogany gene, nucleotide sequences on the chromosome flanking the mahogany gene, see, e.g., FIG. 3 and human genomic sequences syntenic to the sequences depicted in FIG. 3, which can be utilized as part of the methods of the invention for identifying and diagnosing individuals who exhibit or are susceptible to weight disorders, including obesity, cachexia, and anorexia.

The mahogany nucleotide sequences of the invention further comprise: (a) any nucleotide sequence that hybridizes to the complement of a nucleic acid molecule that encodes a mahogany gene product under highly stringent conditions, e.g., hybridization to filter-bound DNA in 0.5 M

NaHPO₄, 7% sodium dodecyl sulfate (SDS), 1 mM EDTA at 65°C, and washing in 0.1xSSC/0.1% SDS at 68°C (Ausubel F.M. et al., eds., 1989, Current Protocols in Molecular Biology, Vol. I, Green Publishing Associates, Inc., and John Wiley & Sons, Inc., New York, at p. 2.10.3) particularly human *mg* sequences, FIG. 10; and (b) any nucleotide sequence that hybridizes to the complement of a nucleic acid molecule that encodes a mahogany gene product under less stringent conditions, such as moderately stringent conditions, e.g., washing in 0.2xSSC/0.1% SDS at 42 °C (Ausubel et al., 1989, *supra*), yet which still encodes a functionally equivalent mahogany gene product.

"Functionally equivalent", as utilized herein, refers to a gene product (e.g., a protein) capable of exhibiting a substantially similar *in vivo* activity as the endogenous *mg* gene products encoded by the *mg* gene sequences described above. The *in vivo* activity of the *mg* gene product, as used herein, refers to the ability of the *mg* gene product, when present in an appropriate cell type, to ameliorate, prevent, or delay the appearance of the mahogany phenotype relative to its appearance when that cell type lacks a functional mahogany gene product.

The invention also includes nucleic acid molecules, preferably DNA molecules, that are the complements of the nucleotide sequences described above. Among the nucleic acid molecules of the invention are deoxyoligonucleotides ("oligos") which hybridize under highly stringent or moderately stringent conditions to the mahogany nucleic acid molecules described above. Exemplary highly stringent conditions may refer, e.g., to washing in 6xSSC/0.05% sodium pyrophosphate at 37°C (for 14-base oligos), 48°C (for 17-base oligos), 55°C (for 20-base oligos), and 60°C (for 23-base oligos). These nucleic acid molecules may encode or act as antisense molecules, useful, for example, in mahogany gene

regulation, and/or as antisense primers in amplification reactions of mahogany gene nucleic acid sequences. With respect to mahogany gene regulation, such techniques can be used to regulate, for example, weight disorders such as obesity, cachexia, or anorexia. Such sequences may also be
5 used as part of ribozyme and/or triple helix sequences, which are also useful for mahogany gene regulation. Still further, such molecules may be used as components of diagnostic methods whereby, for example, the presence of a particular mahogany allele associated with a weight disorder, such as
10 obesity, cachexia, or anorexia, may be detected. Among the molecules which can be used for diagnostic methods, such as those which involve amplification of genomic mahogany sequences, are primers or probes that can routinely be obtained using the genomic and cDNA sequences disclosed herein.

15 In one embodiment, the nucleic acid molecules of the invention do not include nucleic acid molecules that consist solely of the nucleotide sequence that encodes the attractin protein sequence depicted in FIGS. 17A-D.

The mahogany nucleic acid sequences of the invention
20 further include fragments of the nucleic acid sequences described above. For example, mahogany nucleic acid fragments can include fragments of at least 10, 12, 15, 20, 30, 40, 50, 100, 150, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900,
25 2000 or more nucleotides.

The nucleotide sequences of the present invention also include (a) DNA vectors that contain any of the foregoing mahogany coding sequences and/or their complements; (b) DNA expression vectors that contain any of the foregoing mahogany coding sequences operatively associated with a regulatory
30 element that directs the expression of the coding sequences; and (c) genetically engineered host cells and organisms that

contain any of the foregoing mahogany coding sequences operatively associated with a regulatory element that directs the expression of the coding sequence in the host cell. As used herein, regulatory elements include, but are not limited to inducible and non-inducible promoters, enhancers, operators, and other elements known to those skilled in the art that drive and regulate gene expression. Such regulatory elements include, but are not limited to, the cytomegalovirus hCMV immediate early gene, the early or late promoters of SV40 adenovirus, the lac system, the trp system, the TAC system, the TRC system, the major operator and promoter regions of phage A, the control regions of fd coat protein, the promoter for 3'-phosphoglycerate kinase, the promoters of acid phosphatase, and the promoters of the yeast alpha-mating factors.

In addition to the mahogany gene sequences described above, homologs of such sequences, exhibiting extensive homology to one or more domains of the mahogany gene product can be present in other species. In a preferred embodiment, the mahogany gene homologue maps to a chromosomal region that is syntenic to the chromosomal region of the mahogany gene. In a particularly preferred embodiment, a human mahogany gene homologue sequence maps to a human chromosome region that is syntenic to the region of mouse chromosome 2 to which the murine mahogany gene maps, namely 20p15, and comprises the contiged human MG cDNA provided herein. Further, there can also exist homologue genes at other genetic loci within the genome of the same species which encode proteins having extensive homology to one or more domains of the mahogany gene product. Such mahogany homologs can include, for example, secreted forms of the mahogany sequences, see, e.g., Duke-Cohan, J.S. et al. (1998, *Proc. Natl. Acad. Sci. U.S.A.* 95:11336-11341). Such sequences, can be used, for example, in the screening assays, described in Section 5.4.2 below,

for compounds that interact with the mahogany gene and/or its gene product and that may therefore be useful in treating and ameliorating body weight disorders.

Other mahogany homologs can be identified and readily
5 isolated, without undue experimentation, by molecular
biological techniques well known in the art, and are
therefore within the scope of the present invention. As an
example, in order to clone a human mahogany gene homologue
using isolated murine mahogany gene sequences, such murine
mahogany gene sequences may be labeled and used to screen a
10 cDNA library constructed from mRNA obtained from appropriate
cells or tissues derived from the organism (in this case,
human) of interest. With respect to the cloning of such a
human mahogany homologue, a human cDNA library may, for
example be used for screening, such as a cDNA library
15 obtained from mRNA isolated from brain tissues, particularly
containing hypothalamic regions.

The hybridization washing conditions used should be of a
lower stringency when the cDNA library is derived from an
organism different from the type of organism from which the
20 labeled sequence was derived. With respect to the cloning of
a human mahogany homologue, for example, hybridization can be
performed for 4 hours at 65°C using Amersham Rapid Hyb™
buffer (Cat. #RPN1639) according to manufacturer's protocol,
followed by washing, with a final washing stringency of
1.0xSSC/0.1% SDS at 50°C for 20 minutes being preferred.
25

Low stringency conditions are well known to those of
skill in the art, and will vary predictably depending on the
specific organisms from which the library and the labeled
sequences are derived. For guidance regarding such
conditions see, for example, Sambrook et al., 1989, Molecular
30 Cloning, A Laboratory Manual, Cold Springs Harbor Press,
N.Y.; and Ausubel et al., 1989, Current Protocols in

Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y.

Alternatively, the labeled fragment may be used to screen a genomic library derived from the organism of interest, again, using appropriately stringent conditions.

Further, a mahogany gene homologue may be isolated from nucleic acid of the organism of interest by performing PCR using two degenerate oligonucleotide primer pools designed on the basis of amino acid sequences within the mahogany gene product disclosed herein. The template for the reaction may be cDNA obtained by reverse transcription of mRNA prepared from, for example, human or non-human cell lines or tissue known or suspected to express a mahogany gene allele.

The PCR product may be subcloned and sequenced to ensure that the amplified sequences represent the sequences of a mahogany gene nucleic acid sequence. The PCR fragment may then be used to isolate a full length cDNA clone by a variety of methods. For example, the amplified fragment may be labeled and used to screen a cDNA library, such as a bacteriophage cDNA library. Alternatively, the labeled fragment may be used to isolate genomic clones via the screening of a genomic library. This method has been used to isolate sequences encoding each of the murine MG gene exons as well as to isolate contigs containing the human MG sequences provided herein, FIG. 10.

PCR technology may also be utilized to isolate full length cDNA sequences. For example, RNA may be isolated, following standard procedures, from an appropriate cellular or tissue source (i.e., one known, or suspected, to express the mahogany gene). A reverse transcription reaction may be performed on the RNA using an oligonucleotide primer specific for the most 5' end of the amplified fragment for the priming of the first strand synthesis. The resulting RNA/DNA hybrid may then be "tailed" with guanines using a standard terminal

transferase reaction, they hybrid may be digested with RNAase H, and second strand synthesis may then be primed with a poly-C primer. Thus, cDNA sequences upstream of the amplified fragment may easily be isolated. For a review of
5 cloning strategies which may be used, see e.g., Sambrook et al., 1989 *supra*.

Mahogany gene sequences may additionally be used to isolate mutant mahogany alleles. Such mutant alleles may be isolated from individuals either known or proposed to have a
10 phenotype which contributes to the symptoms of body weight disorders such as obesity, cachexia, or anorexia or disorders associated with hyperphagia. Mutant alleles and mutant allele products may then be utilized in the therapeutic and diagnostic systems described below. Additionally, such mahogany gene sequences can be used to detect mahogany gene
15 regulatory (e.g. promoter) defects which can affect body weight.

A cDNA of a mutant mahogany gene may be isolated, for example, by using PCR, a technique which is well known to those of skill in the art. In this case, the first cDNA
20 strand may be synthesized by hybridizing an oligo-dT oligonucleotide to mRNA isolated from tissue known or suspected to be expressed in an individual putatively carrying the mutant mahogany allele, and by extending the new strand with reverse transcriptase. The second strand of the
25 cDNA is then synthesized using an oligonucleotide that hybridizes specifically to the 5' end of the normal gene. Using these two primers, the product is then amplified via PCR, cloned into a suitable vector, and subjected to DNA sequence analysis through methods well known to those of skill in the art. By comparing the DNA sequence of the
30 mutant mahogany allele to that of the normal mahogany allele, the mutation(s) responsible for the loss of alteration of

activity of the mutant mahogany gene product can be ascertained.

Alternatively, a genomic library can be constructed using DNA obtained from an individual suspected of or known
5 to carry the mutant mahogany allele, or a cDNA library can be constructed using RNA from a tissue known, or suspected to express the mutant mahogany allele. The normal mahogany gene or any suitable fragment thereof may then be labeled and used as a probe to identify the corresponding mutant mahogany
10 allele in such libraries. Clones containing the mutant mahogany gene sequences may then be purified and subjected to sequence analysis according to methods well known to those of skill in the art.

Additionally, an expression library can be constructed utilizing cDNA synthesized from, for example, RNA isolated
15 from a tissue known, or suspected to express a mutant mahogany allele in an individual suspected of or known to carry such a mutant allele. In this manner, gene products made by the putatively mutant tissue may be expressed and screened using standard antibody screening techniques in
20 conjunction with antibodies raised against the normal mahogany gene product as described, below, in Section 5.3. For screening techniques, see, for example, Harlow, E. and Lane, eds., 1988, "Antibodies: A Laboratory Manual", Cold Spring Harbor Press, Cold Spring Harbor. In cases where a
25 mahogany mutation results in an expressed gene product with altered function (e.g., as a result of a missense or a frameshift mutation) a polyclonal set of anti-mahogany gene product antibodies are likely to cross-react with the mutant mahogany gene product. Library clones detected via their reaction with such labeled antibodies can be purified and
30 subjected to sequence analysis according to methods well known to those of skill in the art.

5.2. PROTEIN PRODUCTS OF THE MAHOGANY GENE

Mahogany gene products (e.g., proteins), polypeptides and peptide fragments, mutant, truncated, or deleted forms of the mahogany gene product, and/or fusion proteins of the mahogany gene product can be prepared for a variety of uses.

5 For example, such gene products, or peptide fragments thereof, can be used for the generation of antibodies in diagnostic assays, or for the identification of other cellular or extracellular products involved in the regulation of mammalian body weight.

10 Mahogany gene products, also referred to herein as mahogany proteins, of the present invention include those gene products encoded by the mahogany gene sequences described in Section 5.1, above. For example, FIG. 2B, 8D and 9B depict murine mahogany amino acid sequences. Mahogany
15 gene products also include human mahogany gene products as shown, e.g., in FIGS. 10B, 17A-D, 18B-D, 19D, and 20C.

In addition, mahogany gene products may include proteins that represent functionally equivalent gene products. Such an equivalent mahogany gene product may contain deletions, including internal deletions, additions, including additions
20 yielding fusion proteins, or substitutions of amino acid residues within and/or adjacent to the amino acid sequence encoded by the mahogany gene sequences described, in Section 5.1, above, but that result in a "silent" change, in that the change produces a functionally equivalent mahogany gene
25 product. Such amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example, nonpolar (hydrophobic) amino acids include alanine, leucine,
30 isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and

glutamine; positively charged (basic) amino acids include arginine, lysine, and histidine; and negatively charged (acidic) amino acids include aspartic acid and glutamic acid.

"Functionally equivalent", as utilized herein, refers to
5 a gene product (e.g., a protein) capable of exhibiting a substantially similar *in vivo* activity as the endogenous *mg* gene products encoded by the *mg* gene sequences described in Section 5.1, above. The *in vivo* activity of the *mg* gene product, as used herein, refers to the ability of the *mg* gene
10 product, when present in an appropriate cell type, to ameliorate, prevent, or delay the appearance of the mahogany phenotype relative to its appearance when that cell type lacks a functional mahogany gene product.

Alternatively, where alteration of function is desired, deletion or non-conservative alterations can produce altered,
15 including reduced-activity, mahogany gene products. Such alterations can, for example, alter one or more of the biological functions of the mahogany gene product. Further, such alterations can be selected so as to generate mahogany gene products that are better suited for expression, scale
20 up, etc. in the host cells chosen. For example, cysteine residues can be deleted or substituted with another amino acid residue in order to eliminate disulfide bridges.

As another example, altered mahogany gene products can be engineered that correspond to mutants or variants of the mahogany gene product associated with mammalian weight
25 disorders, such as obesity, cachexia, or anorexia. Altered mahogany gene products can also be engineered that correspond to mutants or variants of the mahogany gene product known to neutralize or ameliorate the symptoms of body weight disorders, such as obesity, cachexia, or anorexia, which are
30 mediated by some other gene, including, but not limited to, body weight disorders mediated by the *agouti* gene.

Also within the scope of the present invention are peptides and/or proteins corresponding to one or more domains of the mahogany protein or any one of the individual exon encoded regions of the MG protein, as well as fusion proteins in which the full length mahogany protein, a mahogany
5 peptide, or a truncated mahogany protein or peptide is fused to an unrelated heterologous protein. Such proteins and peptides can be designed on the basis of the mahogany nucleotide sequence disclosed in Section 5.1, above, and/or on the basis of the mahogany amino acid sequence disclosed in
10 the Section.

The mahogany gene products of the invention further include fragments of the gene products described herein. For example, mahogany gene product fragments can include fragments of at least 10, 12, 15, 20, 30, 40, 50, 100, 150,
15 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300 or more amino acids in length.

In one embodiment, it is understood that the gene products of the present invention do not include a gene product that consists solely of the amino acid sequence of the attractin polypeptide depicted in FIGS. 17A-D.

20 Fusion proteins of the invention include, but are not limited to, IgFc fusions which stabilize the mahogany protein or peptide and prolong half life *in vivo*; or fusions to any amino acid sequence that allows the fusion protein to be anchored to the cell membrane; or fusions to an enzyme,
25 fluorescent protein, or luminescent protein which provides a marker function.

The mahogany gene products, peptide fragments thereof and fusion proteins thereof, may be produced by recombinant DNA technology using techniques well known in the art. Thus,
30 methods for preparing the mahogany gene products, polypeptides, peptides, fusion peptide and fusion polypeptides of the invention by expressing nucleic acid

containing mahogany gene sequences are described herein. Methods that are well known to those skilled in the art can be used to construct expression vectors containing mahogany gene product coding sequences and appropriate transcriptional
5 and translational control signals. These methods include, for example, *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. See, for example, the techniques described in Sambrook, et al., 1989, *supra*, and Ausubel, et al., 1989, *supra*. Alternatively, RNA
10 capable of encoding mahogany gene product sequences may be chemically synthesized using, for example, synthesizers. See, for example, the techniques described in "Oligonucleotide Synthesis", 1984, Gait, ed., IRL Press, Oxford.

A variety of host-expression vector systems may be
15 utilized to express the mahogany gene product coding sequences of the invention. Such host-expression systems represent vehicles by which the coding sequences of interest may be produced and subsequently purified, but also represent cells that may, when transformed or transfected with the
20 appropriate nucleotide coding sequences, exhibit the mahogany gene product of the invention *in situ*. These include but are not limited to microorganisms such as bacteria (e.g., *E. coli*, *B. subtilis*) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing
25 mahogany gene product coding sequences; yeast (e.g., *Saccharomyces*, *Pichia*) transformed with recombinant yeast expression vectors containing the mahogany gene product coding sequences; insect cell systems infected with recombinant virus expression vectors (e.g., baculovirus)
30 containing the mahogany gene product coding sequences; plant cell systems infected with recombinant virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expres-

sion vectors (e.g., Ti plasmid) containing mahogany gene product coding sequences; or mammalian cell systems (e.g., COS, CHO, BHK, 293, 3T3) harboring recombinant expression constructs containing promoters derived from the genome of 5 mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter).

In bacterial systems, a number of expression vectors may be advantageously selected depending upon the use intended for the mahogany gene product being expressed. For example, 10 when a large quantity of such a protein is to be produced, for the generation of pharmaceutical compositions of mahogany gene product or for raising antibodies to mahogany gene product, for example, vectors that direct the expression of high levels of fusion protein products that are readily 15 purified may be desirable. Such vectors include, but are not limited, to the *E. coli* expression vector pUR278 (Ruther et al., 1983, EMBO J. 2, 1791), in which the mahogany gene product coding sequence may be ligated individually into the vector in frame with the *lac Z* coding region so that a fusion 20 protein is produced; pIN vectors (Inouye and Inouye, 1985, Nucleic Acids Res. 13, 3101-3109; Van Heeke and Schuster, 1989, J. Biol. Chem. 264, 5503-5509); and the like. pGEX vectors may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In 25 general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. The pGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned target gene product can be released from the GST 30 moiety.

In an insect system, *Autographa californica*, nuclear polyhidrosis virus (AcNPV) is used as a vector to express

foreign genes. The virus grows in *Spodoptera frugiperda* cells. The mahogany gene product coding sequence may be cloned individually into non-essential regions (for example the polyhedrin gene) of the virus and placed under control of
5 an AcNPV promoter (for example the polyhedrin promoter).

Successful insertion of mahogany gene product coding sequence will result in inactivation of the polyhedrin gene and production of non-occluded recombinant virus (i.e., virus lacking the proteinaceous coat coded for by the polyhedrin
10 gene). These recombinant viruses are then used to infect *Spodoptera frugiperda* cells in which the inserted gene is expressed. (e.g., see Smith, et al., 1983, J. Virol. 46, 584; Smith, U.S. Patent No. 4,215,051).

In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an
15 adenovirus is used as an expression vector, the mahogany gene product coding sequence of interest may be ligated to an adenovirus transcription/translation control complex, e.g., the late promoter and tripartite leader sequence. This chimeric gene may then be inserted in the adenovirus genome
20 by *in vitro* or *in vivo* recombination. Insertion in a non-essential region of the viral genome (e.g., region E1 or E3) will result in a recombinant virus that is viable and capable of expressing mahogany gene product in infected hosts.

(e.g., See Logan and Shenk, 1984, Proc. Natl. Acad. Sci. USA
25 81, 3655-3659). Specific initiation signals may also be required for efficient translation of inserted mahogany gene product coding sequences. These signals include the ATG initiation codon and adjacent sequences. In cases where an entire mahogany gene, including its own initiation codon and
30 adjacent sequences, is inserted into the appropriate expression vector, no additional translational control signals may be needed. However, in cases where only a portion of the mahogany gene coding sequence is inserted,

exogenous translational control signals, including, perhaps, the ATG initiation codon, must be provided. Furthermore, the initiation codon must be in phase with the reading frame of the desired coding sequence to ensure translation of the entire insert. These exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements, transcription terminators, etc. (see Bittner, et al., 1987, Methods in Enzymol. 153, 516-544).

In addition, a host cell strain may be chosen that modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Such modifications (e.g., glycosylation) and processing (e.g., cleavage) of protein products may be important for the function of the protein. Different host cells have characteristic and specific mechanisms for the post-translational processing and modification of proteins and gene products. Appropriate cell lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed. To this end, eukaryotic host cells that possess the cellular machinery for proper processing of the primary transcript, glycosylation, and phosphorylation of the gene product may be used. Such mammalian host cells include but are not limited to CHO, VERO, BHK, HeLa, COS, MDCK, 293, 3T3, and WI38.

For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines that stably express the mahogany gene product may be engineered. Rather than using expression vectors that contain viral origins of replication, host cells can be transformed with DNA controlled by appropriate expression control elements (e.g., promoter, enhancer, sequences, transcription terminators, polyadenylation sites, etc.), and

a selectable marker. Following the introduction of the foreign DNA, engineered cells may be allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant
5 plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci that in turn can be cloned and expanded into cell lines. This method may advantageously be used to engineer cell lines that express the mahogany gene product. Such engineered cell lines may be particularly useful in
10 screening and evaluation of compounds that affect the endogenous activity of the mahogany gene product.

A number of selection systems may be used, including but not limited to the herpes simplex virus thymidine kinase (Wigler, et al., 1977, Cell 11, 223), hypoxanthine-guanine
15 phosphoribosyltransferase (Szybalska and Szybalski, 1962, Proc. Natl. Acad. Sci. USA 48, 2026), and adenine phosphoribosyltransferase (Lowy, et al., 1980, Cell 22, 817) genes can be employed in tk⁻, hgp⁺ or ap⁺ cells, respectively. Also, antimetabolite resistance can be used as
20 the basis of selection for the following genes: dhfr, which confers resistance to methotrexate (Wigler, et al., 1980, Natl. Acad. Sci. USA 77, 3567; O'Hare, et al., 1981, Proc. Natl. Acad. Sci. USA 78, 1527); gpt, which confers resistance to mycophenolic acid (Mulligan and Berg, 1981, Proc. Natl.
25 Acad. Sci. USA 78, 2072); neo, which confers resistance to the aminoglycoside G-418 (Colberre-Garapin, et al., 1981, J. Mol. Biol. 150, 1); and hyg⁺, which confers resistance to hygromycin (Santerre, et al., 1984, Gene 30, 147).

Alternatively, the expression characteristic of an endogenous mahogany gene within a cell line or microorganism
30 may be modified by inserting a heterologous DNA regulatory element into the genome of a stable cell line or cloned microorganism such that the inserted regulatory element is

operatively linked with the endogenous mahogany gene. For example, an endogenous mahogany gene which is normally "transcriptionally silent", i.e., a mahogany gene which is normally not expressed, or is expressed only a very low levels in a cell line or microorganism, may be activated by inserting a regulatory element which is capable of promoting the expression of a normally expressed gene product in that cell line or microorganism. Alternatively, a transcriptionally silent, endogenous mahogany gene may be activated by insertion of a promiscuous regulatory element that works across cell types.

A heterologous regulatory element may be inserted into a stable cell line or cloned microorganism, such it is operatively linked with an endogenous mahogany gene, using techniques, such as targeted homologous recombination, which are well known to those of skill in the art, and described e.g., in Chappel, U.S. Patent No. 4,215,051; U.S. Patent No. 5,578,461 to Sherwin et al.; International Application No. PCT/US92/09627 (WO93/09222) by Selden et al.; and International Application No. PCT/US90/06436 (WO91/06667) by Skoultchi et al., each of which is incorporated by reference herein in its entirety.

Alternatively, any fusion protein may be readily purified by utilizing an antibody specific for the fusion protein being expressed. For example, a system described by Janknecht, et al. allows for the ready purification of non-denatured fusion proteins expressed in human cell lines (Janknecht, et al., 1991, Proc. Natl. Acad. Sci. USA 88, 8972-8976). In this system, the gene of interest is subcloned into a vaccinia recombination plasmid such that the gene's open reading frame is translationally fused to an amino-terminal tag consisting of six histidine residues. Extracts from cells infected with recombinant vaccinia virus are loaded onto Ni^{2+} -nitriloacetic acid-agarose columns and

histidine-tagged proteins are selectively eluted with imidazole-containing buffers.

The mahogany gene products can also be expressed in transgenic animals. Animals of any species, including, but not limited to, mice, rats, rabbits, guinea pigs, pigs, micro-pigs, goats, sheep, and non-human primates, e.g., baboons, monkeys, and chimpanzees may be used to generate mahogany transgenic animals. The term "transgenic," as used herein, refers to animals expressing mahogany gene sequences from a different species (e.g., mice expressing human mahogany gene sequences), as well as animals that have been genetically engineered to over express endogenous (i.e., same species) mahogany sequences or animals that have been genetically engineered to no longer express endogenous mahogany gene sequences (i.e., "knock-out" animals), and their progeny.

Any technique known in the art may be used to introduce a mahogany gene transgene into animals to produce the founder lines of transgenic animals. Such techniques include, but are not limited to pronuclear microinjection (Hoppe and Wagner, 1989, U.S. Pat. No. 4,873,191); retrovirus mediated gene transfer into germ lines (Van der Putten, et al., 1985, Proc. Natl. Acad. Sci., USA 82, 6148-6152); gene targeting in embryonic stem cells (Thompson, et al., 1989, Cell 56, 313-321); electroporation of embryos (Lo, 1983, Mol. Cell. Biol. 3, 1803-1814); and sperm-mediated gene transfer (Lavitrano et al., 1989, Cell 57, 717-723) (For a review of such techniques, see Gordon, 1989, Transgenic Animals, Intl. Rev. Cytol. 115, 171-229)

Any technique known in the art may be used to produce transgenic animal clones containing a mahogany transgene, for example, nuclear transfer into enucleated oocytes of nuclei from cultured embryonic, fetal or adult cells induced to

quiescence (Campbell, et al., 1996, Nature 380, 64-66; Wilmut, et al., Nature 385, 810-813).

The present invention provides for transgenic animals that carry a mahogany transgene in all their cells, as well
5 as animals that carry the transgene in some, but not all their cells, i.e., mosaic animals. The transgene may be integrated as a single transgene or in concatamers, e.g., head-to-head tandems or head-to-tail tandems. The transgene may also be selectively introduced into and activated in a
10 particular cell type by following, for example, the teaching of Lasko et al. (Lasko, et al., 1992, Proc. Natl. Acad. Sci. USA 89, 6232-6236). The regulatory sequences required for such a cell-type specific activation will depend upon the particular cell type of interest, and will be apparent to
15 those of skill in the art. When it is desired that the mahogany transgene be integrated into the chromosomal site of the endogenous mahogany gene, gene targeting is preferred. Briefly, when such a technique is to be utilized, vectors containing some nucleotide sequences homologous to the endogenous mahogany gene are designed for the purpose of
20 integrating, via homologous recombination with chromosomal sequences, into and disrupting the function of the nucleotide sequence of the endogenous mahogany gene. The transgene may also be selectively introduced into a particular cell type, thus inactivating the endogenous mahogany gene in only that
25 cell type, by following, for example, the teaching of Gu, et al. (Gu, et al., 1994, Science 265, 103-106). The regulatory sequences required for such a cell-type specific inactivation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art.

30 Once transgenic animals have been generated, the expression of the recombinant mahogany gene may be assayed utilizing standard techniques. Initial screening may be accomplished by Southern blot analysis or PCR techniques to

analyze animal tissues to assay whether integration of the transgene has taken place. The level of mRNA expression of the transgene in the tissues of the transgenic animals may also be assessed using techniques that include but are not
5 limited to Northern blot analysis of tissue samples obtained from the animal, in situ hybridization analysis, and RT-PCR (reverse transcriptase PCR). Samples of mahogany gene-expressing tissue, may also be evaluated immunocytochemically using antibodies specific for the mahogany transgene product.

10

5.3. ANTIBODIES TO MAHOGANY GENE PRODUCTS

Described herein are methods for the production of antibodies capable of specifically recognizing one or more *mg* gene product epitopes, or epitopes of conserved variants, or peptide fragments of the *mg* gene products. Further,
15 antibodies that specifically recognize mutant forms of *mg* gene products, are encompassed by the invention.

Such antibodies may include, but are not limited to, polyclonal antibodies, monoclonal antibodies (mAbs), humanized or chimeric antibodies, single chain antibodies,
20 Fab fragments, F(ab'), fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies, and epitope-binding fragments of any of the above. Such antibodies may be used, for example, in the detection of a *mg* gene product in an biological sample and may, therefore, be
25 utilized as part of a diagnostic or prognostic technique whereby patients may be tested for abnormal levels of *mg* gene products, and/or for the presence of abnormal forms of such gene products. Such antibodies may also be utilized in conjunction with, for example, compound screening schemes, as
30 described, below, in Section 5.4.2, for the evaluation of the effect of test compounds on *mg* gene product levels and/or activity. Additionally, such antibodies can be used in conjunction with the gene therapy techniques described,

below, in Section 5.4.3.2, to, for example, evaluate the normal and/or engineered mahogany-expressing cells prior to their introduction into the patient.

Anti-*mg* gene product antibodies may additionally be used in methods for inhibiting abnormal *mg* gene product activity. Thus, such antibodies may, therefore, be utilized as part of weight disorder treatment methods.

For the production of antibodies against a *mg* gene product, various host animals may be immunized by injection with a *mg* gene product, or a portion thereof. Such host animals may include, but are not limited to rabbits, mice, and rats, to name but a few. Various adjuvants may be used to increase the immunological response, depending on the host species, including but not limited to Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and *Corynebacterium parvum*.

Polyclonal antibodies are heterogeneous populations of antibody molecules derived from the sera of animals immunized with an antigen, such as a *mg* gene product, or an antigenic functional derivative thereof. For the production of polyclonal antibodies, host animals such as those described above, may be immunized by injection with *mg* gene product supplemented with adjuvants as also described above.

Monoclonal antibodies, which are homogeneous populations of antibodies to a particular antigen, may be obtained by any technique that provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique of Kohler and Milstein, (1975, Nature 256, 495-497; and U.S. Patent No. 4,376,110), the human B-cell hybridoma technique

(Kosbor et al., 1983, Immunology Today 4, 72; Cole et al., 1983, Proc. Natl. Acad. Sci. USA 80, 2026-2030), and the EBV-hybridoma technique (Cole et al., 1985, Monoclonal Antibodies And Cancer Therapy, Alan R. Liss, Inc., pp. 77-96). Such
5 antibodies may be of any immunoglobulin class including IgG, IgM, IgE, IgA, IgD and any subclass thereof. The hybridoma producing the mAb of this invention may be cultivated in vitro or in vivo. Production of high titers of mAbs in vivo makes this the presently preferred method of production.

10 In addition, techniques developed for the production of "chimeric antibodies" (Morrison, et al., 1984, Proc. Natl. Acad. Sci., 81, 6851-6855; Neuberger, et al., 1984, Nature 312, 604-608; Takeda, et al., 1985, Nature, 314, 452-454) by splicing the genes from a mouse antibody molecule of
15 appropriate antigen specificity together with genes from a human antibody molecule of appropriate biological activity can be used. A chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region. (See, e.g.,
20 Cabilly et al., U.S. Patent No. 4,816,567; and Boss et al., U.S. Patent No. 4,816397, which are incorporated herein by reference in their entirety.)

In addition, techniques have been developed for the production of humanized antibodies. (See, e.g., Queen, U.S.
25 Patent No. 5,585,089, which is incorporated herein by reference in its entirety.) An immunoglobulin light or heavy chain variable region consists of a "framework" region interrupted by three hypervariable regions, referred to as complementarily determining regions (CDRs). The extent of
30 the framework region and CDRs have been precisely defined (see, "Sequences of Proteins of Immunological Interest", Kabat, E. et al., U.S. Department of Health and Human Services (1983). Briefly, humanized antibodies are antibody

molecules from non-human species having one or more CDRs from the non-human species and a framework region from a human immunoglobulin molecule.

Alternatively, techniques described for the production
5 of single chain antibodies (U.S. Patent 4,946,778; Bird, 1988, Science 242, 423-426; Huston, et al., 1988, Proc. Natl. Acad. Sci. USA 85, 5879-5883; and Ward, et al., 1989, Nature 334, 544-546) can be adapted to produce single chain
antibodies against mahogany gene products. Single chain
antibodies are formed by linking the heavy and light chain
10 fragments of the Fv region via an amino acid bridge, resulting in a single chain polypeptide.

Antibody fragments that recognize specific epitopes may be generated by known techniques. For example, such fragments include but are not limited to: the F(ab')₂,
15 fragments, which can be produced by pepsin digestion of the antibody molecule and the Fab fragments, which can be generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed (Huse, et al., 1989, Science, 246, 1275-1281) to
20 allow rapid and easy identification of monoclonal Fab fragments with the desired specificity.

5.4.

USES OF THE MAHOGANY GENES, GENE PRODUCTS, AND ANTIBODIES

Described herein are various applications of the
25 mahogany genes, of the mahogany gene products, including peptide fragments thereof, and of antibodies directed against mahogany gene products and peptide fragments thereof. Such applications include, for example, prognostic and diagnostic evaluation of body weight disorders and the identification of
30 subjects with a predisposition to such disorders, as described below, in Section 5.4.1. Additionally, such applications include methods for the treatment of body weight

and body weight disorders, as described, below, in Section 5.4.2, and for the identification of compounds which modulate the expression of the mahogany gene and/or the activity of the mahogany gene product, as described in Section 5.4.3, below. Such compounds can include, for example, other cellular products which are involved in body weight regulation. These compounds can be used, for example, in the amelioration of body weight disorders, including obesity, cachexia, and anorexia.

While, for clarity, the uses described in this section are primarily uses related to body weight disorder abnormalities, it is to be noted that each of the diagnostic and therapeutic treatments described herein can additionally be utilized in connection with other defects associated with the mahogany gene, such as hyperpigmentation, hyperphagia and other disorders resulting in increased metabolic rates.

5.4.1. DIAGNOSIS OF BODY WEIGHT DISORDER ABNORMALITIES

A variety of methods can be employed for the diagnostic and prognostic evaluation of body weight disorders, including obesity, cachexia, and anorexia, and for the identification of subjects having a predisposition to such disorders.

Such methods may, for example, utilize reagents such as the mahogany gene nucleotide sequences described in Section 5.1, and antibodies directed against mahogany gene products, including peptide fragments thereof, as described, above, in Section 5.3. Specifically, such reagents may be used, for example, for:

(1) the detection of the presence of mahogany gene mutations, or the detection of either over- or under-expression of mahogany gene relative to levels of mahogany expression in a wild-type, non-body weight disorder state.

which correlates with certain body weight disorders or susceptibility toward such body weight disorders;

(2) the detection of over- or under-abundance of mahogany gene product relative to the abundance of mahogany gene product in a wild-type non-body weight disorder state which correlates with certain body weight disorders or susceptibility toward such body weight disorders; and

(3) the detection of an aberrant level of mahogany gene product activity relative to mahogany gene product activity levels in a wild-type, non-body weight disorder state which correlates with certain body weight disorders or susceptibility toward such body weight disorders.

Mahogany gene nucleotide sequences can, for example, be used to diagnose a body weight disorder using, for example, the techniques for detecting mutations in the mahogany gene described above in Section 5.1, above.

The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one specific mahogany gene nucleic acid or anti-mahogany gene product antibody reagent described herein, which may be conveniently used, e.g., in clinical settings, to screen and diagnose patients exhibiting body weight disorder abnormalities, and to screen those individuals exhibiting a predisposition to developing a body weight disorder abnormality.

For the detection of mahogany gene mutations, any nucleated cell can be used as a starting source for genomic nucleic acid. For the detection of mahogany gene expression or mahogany gene products, any cell type or tissue in which the mahogany gene is expressed may be utilized, such as, for example, tissues or cells shown herein to express the MG gene.

Nucleic acid-based detection techniques are described, below, in Section 5.4.1.1. Peptide detection techniques are described, below, in Section 5.4.1.2.

5 5.4.1.1. DETECTION OF MAHOGANY GENE NUCLEIC ACID MOLECULES

10 Mutations or polymorphisms within the mahogany gene can be detected by utilizing a number of techniques. Nucleic acid from any nucleated cell can be used as the starting point for such assay techniques, and may be isolated according to standard nucleic acid preparation procedures which are well known to those of skill in the art.

15 Genomic DNA may be used in hybridization or amplification assays of biological samples to detect abnormalities involving mahogany gene structure, including point mutations, insertions, deletions and chromosomal rearrangements. Such assays may include, but are not limited to, Southern analyses, single stranded conformation polymorphism analyses (SSCP), and PCR analyses.

20 Diagnostic methods for the detection of mahogany gene-specific mutations can involve for example, contacting and incubating nucleic acids obtained from a sample, e.g., derived from a patient sample or other appropriate cellular source with one or more labeled nucleic acid reagents including recombinant DNA molecules, cloned genes or
25 degenerate variants thereof, such as described in Section 5.1, above, under conditions favorable for the specific annealing of these reagents to their complementary sequences within or flanking the mahogany gene. Preferably, the lengths of these nucleic acid reagents are at least 15 to 30
30 nucleotides.

 After incubation, all non-annealed nucleic acids are removed from the nucleic acid:mahogany molecule hybrid. The presence of nucleic acids that have hybridized, if any such

molecules exist, is then detected. Using such a detection scheme, the nucleic acid from the cell type or tissue of interest can be immobilized, for example, to a solid support such as a membrane, or a plastic surface such as that on a microtiter plate or polystyrene beads. In this case, after incubation, non-annealed, labeled nucleic acid reagents of the type described in Section 5.1 are easily removed. Detection of the remaining, annealed, labeled mahogany nucleic acid reagents is accomplished using standard techniques well-known to those in the art. The mahogany gene sequences to which the nucleic acid reagents have annealed can be compared to the annealing pattern expected from a normal mahogany gene sequence in order to determine whether a mahogany gene mutation is present.

In a preferred embodiment, mahogany gene mutations or polymorphisms can be detected by using a microassay of mahogany nucleic acid sequences immobilized to a substrate or "gene chip" (see, e.g. Cronin, et al., 1996, Human Mutation 7:244-255).

Alternative diagnostic methods for the detection of mahogany gene specific nucleic acid molecules, in patient samples or other appropriate cell sources, may involve their amplification, e.g., by PCR (the experimental embodiment set forth in Mullis, 1987, U.S. Patent No. 4,683,202), followed by the analysis of the amplified molecules using techniques well known to those of skill in the art, such as, for example, those listed above. The resulting amplified sequences can be compared to those that would be expected if the nucleic acid being amplified contained only normal copies of the mahogany gene in order to determine whether a mahogany gene mutation exists.

Among those mahogany nucleic acid sequences which are preferred for such amplification-related diagnostic screening analyses are oligonucleotide primers which amplify mahogany

exon sequences. The sequences of such oligonucleotide primers are, therefore, preferably derived from mahogany intron sequences so that the entire exon, or coding region, can be analyzed as discussed below. Primer pairs useful for
5 amplification of mahogany exons are preferably derived from adjacent introns. Appropriate primer pairs can be chosen such that each of the 25 mahogany exons are amplified. Primers for the amplification of mahogany exons can be routinely designed by one of ordinary skill in the art by utilizing the exon and intron sequences of mahogany shown in
10 Figures, particularly FIGS. 3 and 5.

Additional mahogany nucleic acid sequences which are preferred for such amplification-related analyses are those which will detect the presence of a mahogany polymorphism which differs from the consensus mahogany sequence depicted
15 in Figures, particularly those that detect the polymorphism identified in exon 15 (Figure 7). Such polymorphisms include ones which represent mutations associated with body weight disorders such as obesity, cachexia, or anorexia.

Further, well-known genotyping techniques can be
20 performed to type polymorphisms that are in close proximity to mutations in the mahogany gene itself, including mutations associated with weight disorders such as obesity, cachexia, or anorexia. Such polymorphisms can be used to identify individuals in families likely to carry mutations in the mahogany gene. If a polymorphism exhibits linkage
25 disequilibrium with mutations in the mahogany gene, the polymorphism can also be used to identify individuals in the general population who are likely to carry such mutations. Polymorphisms that can be used in this way include restriction fragment length polymorphisms (RFLPs), which
30 involve sequence variations in restriction enzyme target sequences, single-base polymorphisms, and simple sequence length polymorphisms (SSLPs).

For example, Weber (U.S. Pat. No. 5,075,217) describes a DNA marker based on length polymorphisms in blocks of (dC-dA)_n-(dG-dT)_n short tandem repeats. The average separation of (dC-dA)_n-(dG-dT)_n blocks is estimated to be 30,000-60,000 bp. Markers that are so closely spaced exhibit a high frequency co-inheritance, and are extremely useful in the identification of genetic mutations, such as, for example, mutations within the mahogany gene, and the diagnosis of diseases and disorders related to mutations in the mahogany gene.

Also, Caskey et al. (U.S. Pat.No. 5,364,759) describe a DNA profiling assay for detecting short tri and tetra nucleotide repeat sequences. The process includes extracting the DNA of interest, such as the mahogany gene, amplifying the extracted DNA, and labelling the repeat sequences to form a genotypic map of the individual's DNA.

A mahogany probe could additionally be used to directly identify RFLPs. Further, a mahogany probe or primers derived from the mahogany sequence could be used to isolate genomic clones such as YACs, BACs, PACs, cosmids, phage, or plasmids. The DNA contained in these clones can be screened for single-base polymorphisms or SSLPs using standard hybridization or sequencing procedures.

The level of mahogany gene expression can also be assayed. For example, RNA from a cell type or tissue known, or suspected, to express the mahogany gene, such as muscle, brain, kidney, testes, heart, liver, lung, skin, hypothalamus, spleen, and adipose tissue may be isolated and tested utilizing hybridization or PCR techniques such as are described, above. The isolated cells can be derived from cell culture or from a patient. The analysis of cells taken from culture may be a necessary step in the assessment of cells to be used as part of a cell-based gene therapy technique or, alternatively, to test the effect of compounds

on the expression of the mahogany gene. Such analyses may reveal both quantitative and qualitative aspects of the expression pattern of the mahogany gene, including activation or inactivation of mahogany gene expression.

5 In one embodiment of such a detection scheme, a cDNA molecule is synthesized from an RNA molecule of interest (e.g., by reverse transcription of the RNA molecule into cDNA). All or part of the resulting cDNA is then used as the template for a nucleic acid amplification reaction, such as a
10 PCR amplification reaction, or the like. The nucleic acid reagents used as synthesis initiation reagents (e.g., primers) in the reverse transcription and nucleic acid amplification steps of this method are chosen from among the mahogany gene nucleic acid reagents described in Section 5.1. The preferred lengths of such nucleic acid reagents are at
15 least 9-30 nucleotides.

For detection of the amplified product, the nucleic acid amplification may be performed using radioactively or non-radioactively labeled nucleotides. Alternatively, enough amplified product may be made such that the product may be
20 visualized by standard ethidium bromide staining or by utilizing any other suitable nucleic acid staining method.

As an alternative to amplification techniques, standard Northern analyses can be performed to determine the level of mRNA expression of the mahogany gene, if a sufficient
25 quantity of the appropriate cells can be obtained.

Additionally, it is possible to perform such mahogany gene expression assays "in situ", i.e., directly upon tissue sections (fixed and/or frozen) of patient tissue obtained from biopsies or resections, such that no nucleic acid purification is necessary. Nucleic acid reagents such as
30 those described in Section 5.1 may be used as probes and/or primers for such in situ procedures (see, for example, Nuovo,

G.J., 1992, "PCR In Situ Hybridization: Protocols And Applications", Raven Press, NY).

5

5.4.1.2. DETECTION OF MAHOGANY GENE PRODUCTS

Mahogany gene products, including both wild-type and mutant mahogany gene products, conserved variants, and polypeptide fragments thereof, which are discussed, above, in Section 5.2, may be detected using antibodies which are
10 directed against such mahogany gene products. Such antibodies, which are discussed in Section 5.3, below, may thereby be used as diagnostics and prognostics for a body weight disorder. Such methods may be used to detect abnormalities in the level of mahogany gene expression or of
15 mahogany gene product synthesis, or abnormalities in the structure, temporal expression, and/or physical location of mahogany gene product. The antibodies and immunoassay methods described herein have, for example, important in vitro applications in assessing the efficacy of treatments
20 for body weight disorders such as obesity, cachexia, and anorexia. Antibodies, or fragments of antibodies, such as those described below, may be used to screen potentially therapeutic compounds in vitro to determine their effects on mahogany gene expression and mahogany gene product
25 production. The compounds that have beneficial effects on body weight disorders, such as obesity, cachexia, and anorexia, can thereby be identified, and a therapeutically effective dose determined.

In vitro immunoassays may also be used, for example, to assess the efficacy of cell-based gene therapy for a body
30 weight disorders, including obesity, cachexia, and anorexia. Antibodies directed against mahogany gene products may be used in vitro to determine, for example, the level of

mahogany gene expression achieved in cells genetically engineered to produce mahogany gene product. In the case of intracellular mahogany gene products, such an assessment is done, preferably, using cell lysates or extracts. Such analysis will allow for a determination of the number of transformed cells necessary to achieve therapeutic efficacy in vivo, as well as optimization of the gene replacement protocol.

The tissue or cell type to be analyzed will generally include those that are known, or suspected, to express the mahogany gene. The protein isolation methods employed herein may, for example, be such as those described in Harlow and Lane (1988, "Antibodies: A Laboratory Manual", Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York). The isolated cells can be derived from cell culture or from a patient. The analysis of cells taken from culture may be a necessary step in the assessment of cells to be used as part of a cell-based gene therapy technique or, alternatively, to test the effect of compounds on the expression of the mahogany gene.

Preferred diagnostic methods for the detection of mahogany gene products, conserved variants or peptide fragments thereof, may involve, for example, immunoassays wherein the mahogany gene products or conserved variants or peptide fragments are detected by their interaction with an anti-mahogany gene product-specific antibody.

For example, antibodies, or fragments of antibodies, such as those described, above, in Section 5.3, may be used to quantitatively or qualitatively detect the presence of mahogany gene products or conserved variants or peptide fragments thereof. This can be accomplished, for example, by immunofluorescence techniques employing a fluorescently labeled antibody (see below, this Section) coupled with light microscopic, flow cytometric, or fluorimetric detection.

Such techniques are especially preferred for mahogany gene products that are expressed on the cell surface.

The antibodies (or fragments thereof) useful in the present invention may, additionally, be employed
5 histologically, as in immunofluorescence or immunoelectron microscopy, for *in situ* detection of mahogany gene products, conserved variants or peptide fragments thereof. *In situ* detection may be accomplished by removing a histological specimen from a patient, and applying thereto a labeled
10 antibody that binds to a mahogany polypeptide. The antibody (or fragment) is preferably applied by overlaying the labeled antibody (or fragment) onto a biological sample. Through the use of such a procedure, it is possible to determine not only the presence of the mahogany gene product, conserved variants or peptide fragments, but also its distribution in the
15 examined tissue. Using the present invention, those of ordinary skill will readily recognize that any of a wide variety of histological methods (such as staining procedures) can be modified in order to achieve *in situ* detection of a mahogany gene product.

20 Immunoassays for mahogany gene products, conserved variants, or peptide fragments thereof will typically comprise: (1) incubating a sample, such as a biological fluid, a tissue extract, freshly harvested cells, or lysates of cells in the presence of a detectably labeled antibody
25 capable of identifying mahogany gene products, conserved variants or peptide fragments thereof; and (2) detecting the bound antibody by any of a number of techniques well-known in the art.

The biological sample may be brought in contact with and immobilized onto a solid phase support or carrier, such as
30 nitrocellulose, that is capable of immobilizing cells, cell particles or soluble proteins. The support may then be washed with suitable buffers followed by treatment with the

detectably labeled mahogany gene product specific antibody. The solid phase support may then be washed with the buffer a second time to remove unbound antibody. The amount of bound label on the solid support may then be detected by
5 conventional means.

By "solid phase support or carrier" is intended any support capable of binding an antigen or an antibody. Well-known supports or carriers include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases,
10 natural and modified celluloses, polyacrylamides, gabbros, and magnetite. The nature of the carrier can be either soluble to some extent or insoluble for the purposes of the present invention. The support material may have virtually any possible structural configuration so long as the coupled molecule is capable of binding to an antigen or antibody.

15 Thus, the support configuration may be spherical, as in a bead, or cylindrical, as in the inside surface of a test tube, or the external surface of a rod. Alternatively, the surface may be flat such as a sheet, test strip, etc.

Preferred supports include polystyrene beads. Those skilled
20 in the art will know many other suitable carriers for binding antibody or antigen, or will be able to ascertain the same by use of routine experimentation.

One of the ways in which the mahogany gene product-specific antibody can be detectably labeled is by linking the same to an enzyme, such as for use in an enzyme immunoassay
25 (EIA) (Voller, A., "The Enzyme Linked Immunosorbent Assay (ELISA)", 1978, Diagnostic Horizons 2, 1-7, Microbiological Associates Quarterly Publication, Walkersville, MD); Voller, A. et al., 1978, J. Clin. Pathol. 31, 507-520; Butler, J.E., 1981, Meth. Enzymol. 73, 482-523; Maggio, E. (ed.), 1980,
30 Enzyme Immunoassay, CRC Press, Boca Raton, FL.; Ishikawa, E. et al., (eds.), 1981, Enzyme Immunoassay, Kigaku Shoin, Tokyo). The enzyme which is bound to the antibody will react

with an appropriate substrate, preferably a chromogenic substrate, in such a manner as to produce a chemical moiety that can be detected, for example, by spectrophotometric, fluorimetric or by visual means. Enzymes that can be used to
5 detectably label the antibody include, but are not limited to, malate dehydrogenase, staphylococcal nuclease, delta-5-steroid isomerase, yeast alcohol dehydrogenase, α -glycerophosphate, dehydrogenase, triose phosphate isomerase, horseradish peroxidase, alkaline phosphatase, asparaginase,
10 glucose oxidase, β -galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase and acetylcholinesterase. The detection can be accomplished by colorimetric methods that employ a chromogenic substrate for the enzyme. Detection may also be accomplished by visual
15 comparison of the extent of enzymatic reaction of a substrate in comparison with similarly prepared standards.

Detection may also be accomplished using any of a variety of other immunoassays. For example, by radioactively labeling the antibodies or antibody fragments, it is possible to detect mahogany gene products through the use of a
20 radioimmunoassay (RIA) (see, for example, Weintraub, B., Principles of Radioimmunoassays, Seventh Training Course on Radioligand Assay Techniques, The Endocrine Society, March, 1986). The radioactive isotope can be detected by such means as the use of a gamma counter or a scintillation counter or
25 by autoradiography.

It is also possible to label the antibody with a fluorescent compound. When the fluorescently labeled antibody is exposed to light of the proper wave length, its presence can then be detected due to fluorescence. Among the most commonly used fluorescent labeling compounds are
30 fluorescein isothiocyanate, rhodamine, phycoerythrin, phycocyanin, allophycocyanin, o-phthaldehyde and fluorescamine.

The antibody can also be detectably labeled using fluorescence emitting metals such as ^{152}Eu , or others of the lanthanide series. These metals can be attached to the antibody using such metal chelating groups as
5 diethylenetriaminepentacetic acid (DTPA) or ethylenediaminetetraacetic acid (EDTA).

The antibody also can be detectably labeled by coupling it to a chemiluminescent compound. The presence of the chemiluminescent-tagged antibody is then determined by
10 detecting the presence of luminescence that arises during the course of a chemical reaction. Examples of particularly useful chemiluminescent labeling compounds are luminol, isoluminol, therrromatic acridinium ester, imidazole, acridinium salt and oxalate ester.

Likewise, a bioluminescent compound may be used to label
15 the antibody of the present invention. Bioluminescence is a type of chemiluminescence found in biological systems in which a catalytic protein increases the efficiency of the chemiluminescent reaction. The presence of a bioluminescent protein is determined by detecting the presence of
20 luminescence. Important bioluminescent compounds for purposes of labeling are luciferin, luciferase and aequorin.

5.4.2.SCREENING ASSAYS FOR COMPOUNDS THAT INTERACT WITH THE MAHOGANY GENE OR GENE PRODUCT

25 The following assays are designed to identify compounds that bind to a mahogany gene product, compounds that bind to proteins, or portions of proteins that interact with a mahogany gene product, compounds that interfere with the interaction of a mahogany gene product with proteins and
30 compounds that modulate the activity of the mahogany gene (i.e., modulate the level of mahogany gene expression and/or modulate the level of mahogany gene product activity). Assays may additionally be utilized that identify compounds

that bind to mahogany gene regulatory sequences (e.g., promoter sequences; see e.g., Platt, 1994, J. Biol. Chem. 269, 28558-28562), which is incorporated herein by reference in its entirety, and that can modulate the level of mahogany
5 gene expression. Such compounds may include, but are not limited to, small organic molecules, such as ones that are able to cross the blood-brain barrier, gain to and/or entry into an appropriate cell and affect expression of the mahogany gene or some other gene involved in the body weight
10 regulatory pathway, or intracellular proteins.

Methods for the identification of such proteins are described, below, in Section 5.4.2.2. Such proteins may be involved in the control and/or regulation of body weight. Further, among these compounds are compounds that affect the level of mahogany gene expression and/or mahogany gene
15 product activity and that can be used in the therapeutic treatment of body weight disorders, including obesity, cachexia, and anorexia, as described, below, in Section 5.9.

Compounds may include, but are not limited to, peptides such as, for example, soluble peptides, including but not
20 limited to, Ig-tailed fusion peptides, and members of random peptide libraries; (see, e.g., Lam, et al., 1991, Nature 354, 82-84; Houghten, et al., 1991, Nature 354, 84-86), and combinatorial chemistry-derived molecular library made of D- and/or L- configuration amino acids, phosphopeptides
25 (including, but not limited to members of random or partially degenerate, directed phosphopeptide libraries; see, e.g., Songyang, et al., 1993, Cell 72, 767-778), antibodies (including, but not limited to, polyclonal, monoclonal, humanized, anti-idiotypic, chimeric or single chain
30 antibodies, and FAb, F(ab'), and FAb expression library fragments, and epitope-binding fragments thereof), and small organic or inorganic molecules.

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and the test compound, which is not anchored, may be labeled, either directly or indirectly.

In practice, microtiter plates are conveniently utilized as the solid support. The anchored component may be
5 immobilized by non-covalent or covalent attachments. Non-covalent attachment may be accomplished by simply coating the solid surface with a solution of the protein and drying. Alternatively, an immobilized antibody, preferably a monoclonal antibody, specific for the protein to be
10 immobilized may be used to anchor the protein to the solid surface. The surfaces may be prepared in advance and stored.

In order to conduct the assay, the non-immobilized component is added to the coated surface containing the anchored component. After the reaction is complete, unreacted components are removed (e.g., by washing) under
15 conditions such that any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the previously non-immobilized component is pre-labeled, the detection of label immobilized on the
20 surface indicates that complexes were formed. Where the previously non-immobilized component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the previously non-immobilized component (the antibody, in turn, may be directly labeled or indirectly labeled with a labeled
25 anti-Ig antibody).

Alternatively, a reaction can be conducted in a liquid phase, the reaction products separated from unreacted components, and complexes detected; e.g., using an
30 immobilized antibody specific for mahogany gene product or the test compound to anchor any complexes formed in solution, and a labeled antibody specific for the other component of the possible complex to detect anchored complexes.

5.4.2.2. ASSAYS FOR PROTEINS THAT INTERACT WITH THE MAHOGANY GENE PRODUCT

Any method suitable for detecting protein-protein interactions may be employed for identifying mahogany gene product-protein interactions.

Among the traditional methods that may be employed are co-immunoprecipitation, cross-linking and co-purification through gradients or chromatographic columns. Utilizing procedures such as these allows for the identification of proteins that interact with mahogany gene products. Such proteins can include, but are not limited, the mahoganoid gene product.

Once isolated, such a protein can be identified and can be used in conjunction with standard techniques, to identify proteins it interacts with. For example, at least a portion of the amino acid sequence of a protein that interacts with the mahogany gene product can be ascertained using techniques well known to those of skill in the art, such as via the Edman degradation technique (see, e.g., Creighton, 1983, "Proteins: Structures and Molecular Principles," W.H. Freeman & Co., N.Y., pp.34-49). The amino acid sequence obtained may be used as a guide for the generation of oligonucleotide mixtures that can be used to screen for gene sequences encoding such proteins. Screening may be accomplished, for example, by standard hybridization or PCR techniques. Techniques for the generation of oligonucleotide mixtures and the screening are well-known. (See, e.g., Ausubel, supra, and 1990, "PCR Protocols: A Guide to Methods and Applications," Innis, et al., eds. Academic Press, Inc., New York).

Additionally, methods may be employed that result in the simultaneous identification of genes that encode a protein which interacts with a mahogany gene product. These methods include, for example, probing expression libraries with

labeled mahogany gene product, using mahogany gene product in a manner similar to the well known technique of antibody probing of λ gt11 libraries.

One method that detects protein interactions *in vivo*, the two-hybrid system, is described in detail for illustration only and not by way of limitation. One version of this system has been described (Chien, et al., 1991, Proc. Natl. Acad. Sci. USA, 88, 9578-9582) and is commercially available from Clontech (Palo Alto, CA).

Briefly, utilizing such a system, plasmids are constructed that encode two hybrid proteins: one consists of the DNA-binding domain of a transcription activator protein fused to the mahogany gene product and the other consists of the transcription activator protein's activation domain fused to an unknown protein that is encoded by a cDNA that has been recombined into this plasmid as part of a cDNA library. The DNA-binding domain fusion plasmid and the cDNA library are transformed into a strain of the yeast *Saccharomyces cerevisiae* that contains a reporter gene (e.g., HBS or *lacZ*) whose regulatory region contains the transcription activator's binding site. Either hybrid protein alone cannot activate transcription of the reporter gene: the DNA-binding domain hybrid cannot because it does not provide activation function and the activation domain hybrid cannot because it cannot localize to the activator's binding sites. Interaction of the two hybrid proteins reconstitutes the functional activator protein and results in expression of the reporter gene, which is detected by an assay for the reporter gene product.

The two-hybrid system or related methodologies may be used to screen activation domain libraries for proteins that interact with the "bait" gene product. By way of example, and not by way of limitation, mahogany gene products may be used as the bait gene product. Total genomic or cDNA

sequences are fused to the DNA encoding an activation domain. This library and a plasmid encoding a hybrid of a bait mahogany gene product fused to the DNA-binding domain are co-transformed into a yeast reporter strain, and the resulting
5 transformants are screened for those that express the reporter gene. For example, a bait mahogany gene sequence, such as the open reading frame of the mahogany gene, can be cloned into a vector such that it is translationally fused to the DNA encoding the DNA-binding domain of the GAL4 protein. These colonies are purified and the library plasmids
10 responsible for reporter gene expression are isolated. DNA sequencing is then used to identify the proteins encoded by the library plasmids.

A cDNA library of the cell line from which proteins that interact with bait mahogany gene product are to be detected
15 can be made using methods routinely practiced in the art. According to the particular system described herein, for example, the cDNA fragments can be inserted into a vector such that they are translationally fused to the transcriptional activation domain of GAL4. Such a library
20 can be co-transformed along with the bait mahogany gene-GAL4 fusion plasmid into a yeast strain that contains a lacZ gene driven by a promoter that contains GAL4 activation sequence. A cDNA encoded protein, fused to a GAL4 transcriptional activation domain that interacts with bait mahogany gene
25 product will reconstitute an active GAL4 protein and thereby drive expression of the HIS3 gene. Colonies that express HIS3 can be detected by their growth on petri dishes containing semi-solid agar based media lacking histidine. The cDNA can then be purified from these strains, and used to
30 produce and isolate the bait mahogany gene product-interacting protein using techniques routinely practiced in the art.

5.4.2.3. ASSAYS FOR COMPOUNDS THAT INTERFERE WITH MAHOGANY GENE PRODUCT MACROMOLECULE INTERACTION

The mahogany gene products may, *in vivo*, interact with
5 one or more macromolecules, such as proteins. For example,
the mahogany gene products may, *in vivo*, interact with the
mahoganoid gene products. Other macromolecules which
interact with the mahogany gene products may include, but are
not limited to, nucleic acid molecules and those proteins
10 identified via methods such as those described, above, in
Sections 5.4.2.1 - 5.4.2.2. For purposes of this discussion,
the macromolecules are referred to herein as "binding
partners". Compounds that disrupt mahogany gene product
binding to a binding partner may be useful in regulating the
activity of the mahogany gene product, especially mutant
15 mahogany gene products. Such compounds may include, but are
not limited to molecules such as peptides, and the like, as
described, for example, in Section 5.4.2.1 above.

The basic principle of an assay system used to identify
compounds that interfere with the interaction between the
20 mahogany gene product and a binding partner or partners
involves preparing a reaction mixture containing the mahogany
gene product and the binding partner under conditions and for
a time sufficient to allow the two to interact and bind, thus
forming a complex. In order to test a compound for
25 inhibitory activity, the reaction mixture is prepared in the
presence and absence of the test compound. The test compound
may be initially included in the reaction mixture, or may be
added at a time subsequent to the addition of mahogany gene
product and its binding partner. Control reaction mixtures
are incubated without the test compound or with a compound
30 which is known not to block complex formation. The formation
of any complexes between the mahogany gene product and the
binding partner is then detected. The formation of a complex

in the control reaction, but not in the reaction mixture containing the test compound, indicates that the compound interferes with the interaction of the mahogany gene product and the binding partner. Additionally, complex formation
5 within reaction mixtures containing the test compound and normal mahogany gene product may also be compared to complex formation within reaction mixtures containing the test compound and a mutant mahogany gene product. This comparison may be important in those cases wherein it is desirable to identify compounds that disrupt interactions of mutant but
10 not normal mahogany gene product.

The assay for compounds that interfere with the interaction of the mahogany gene products and binding partners can be conducted in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring either the
15 mahogany gene product or the binding partner onto a solid support and detecting complexes formed on the solid support at the end of the reaction. In homogeneous assays, the entire reaction is carried out in a liquid phase. In either approach, the order of addition of reactants can be varied to
20 obtain different information about the compounds being tested. For example, test compounds that interfere with the interaction between the mahogany gene products and the binding partners, e.g., by competition, can be identified by conducting the reaction in the presence of the test
25 substance; i.e., by adding the test substance to the reaction mixture prior to or simultaneously with the mahogany gene product and interactive intracellular binding partner. Alternatively, test compounds that disrupt preformed complexes, e.g., compounds with higher binding constants that displace one of the components from the complex, can be
30 tested by adding the test compound to the reaction mixture after complexes have been formed. The various formats are described briefly below.

In a heterogeneous assay system, either the mahogany gene product or the interactive binding partner, is anchored onto a solid surface, while the non-anchored species is labeled, either directly or indirectly. In practice, microtiter plates are conveniently utilized. The anchored species may be immobilized by non-covalent or covalent attachments. Non-covalent attachment may be accomplished simply by coating the solid surface with a solution of the mahogany gene product or binding partner and drying. Alternatively, an immobilized antibody specific for the species to be anchored may be used to anchor the species to the solid surface. The surfaces may be prepared in advance and stored.

In order to conduct the assay, the partner of the immobilized species is exposed to the coated surface with or without the test compound. After the reaction is complete, unreacted components are removed (e.g., by washing) and any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the non-immobilized species is pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the non-immobilized species is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the initially non-immobilized species (the antibody, in turn, may be directly labeled or indirectly labeled with a labeled anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds that inhibit complex formation or that disrupt preformed complexes can be detected.

Alternatively, the reaction can be conducted in a liquid phase in the presence or absence of the test compound, the reaction products separated from unreacted components, and

complexes detected; e.g., using an immobilized antibody specific for one of the binding components to anchor any complexes formed in solution, and a labeled antibody specific for the other partner to detect anchored complexes. Again, depending upon the order of addition of reactants to the liquid phase, test compounds that inhibit complex formation or that disrupt preformed complexes can be identified.

In an alternate embodiment of the invention, a homogeneous assay can be used. In this approach, a preformed complex of the mahogany gene product and the interactive binding partner is prepared in which either the mahogany gene product or its binding partners is labeled, but the signal generated by the label is quenched due to complex formation (see, e.g., U.S. Patent No. 4,109,496 by Rubenstein which utilizes this approach for immunoassays). The addition of a test substance that competes with and displaces one of the species from the preformed complex will result in the generation of a signal above background. In this way, test substances that disrupt mahogany gene product/binding partner interaction can be identified.

In another embodiment of the invention, these same techniques can be employed using peptide fragments that correspond to the binding domains of the mahogany gene product and/or the binding partner (in cases where the binding partner is a protein), in place of one or both of the full length proteins. Any number of methods routinely practiced in the art can be used to identify and isolate the binding sites. These methods include, but are not limited to, mutagenesis of the gene encoding one of the proteins and screening for disruption of binding in a co-immunoprecipitation assay. Compensating mutations in the gene encoding the second species in the complex can then be selected. Sequence analysis of the genes encoding the respective proteins will reveal the mutations that correspond

to the region of the protein involved in interactive binding. Alternatively, one protein can be anchored to a solid surface using methods described in this Section above, and allowed to interact with and bind to its labeled binding partner, which
5 has been treated with a proteolytic enzyme, such as trypsin. After washing, a short, labeled peptide comprising the binding domain may remain associated with the solid material, which can be isolated and identified by amino acid sequencing. Also, once the gene coding for the segments is
10 engineered to express peptide fragments of the protein, it can then be tested for binding activity and purified or synthesized.

For example, and not by way of limitation, a mahogany gene product can be anchored to a solid material as described, above, in this Section by making a GST-1 fusion
15 protein and allowing it to bind to glutathione agarose beads. The binding partner can be labeled with a radioactive isotope, such as ^{35}S , and cleaved with a proteolytic enzyme such as trypsin. Cleavage products can then be added to the anchored GST-1 fusion protein and allowed to bind. After
20 washing away unbound peptides, labeled bound material, representing the binding partner binding domain, can be eluted, purified, and analyzed for amino acid sequence by well-known methods. Peptides so identified can be produced synthetically or produced using recombinant DNA technology.

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5.4.2.4. ASSAYS FOR THE IDENTIFICATION OF COMPOUNDS THAT AMELIORATE BODY WEIGHT DISORDERS

Compounds, including but not limited to binding
30 compounds identified via assay techniques such as those described, above, in Sections 5.4.2.1 - 5.4.2.3, can be tested for the ability to ameliorate body weight disorder symptoms, including obesity, cachexia, and anorexia. It

should be noted that the assays described herein can identify compounds that affect mahogany activity by either affecting mahogany gene expression or by affecting the level of mahogany gene product activity. For example, compounds may be identified that are involved in another step in the pathway in which the mahogany gene and/or mahogany gene product is involved, such as, for example, a step which is either "upfield" or "downfield" of the step in the pathway mediated by the mahogany gene. Such compounds may, by affecting this same pathway, modulate the effect of mahogany on the development of body weight disorders. Such compounds can be used as part of a therapeutic method for the treatment of the disorder.

Described below are cell-based and animal model-based assays for the identification of compounds exhibiting such an ability to ameliorate body weight disorder symptoms.

First, cell-based systems can be used to identify compounds that may act to ameliorate body weight disorder symptoms. Such cell systems can include, for example, recombinant or non-recombinant cell, such as cell lines, that express the mahogany gene.

In utilizing such cell systems, cells that express mahogany may be exposed to a compound suspected of exhibiting an ability to ameliorate body weight disorder symptoms, at a sufficient concentration and for a sufficient time to elicit such an amelioration of such symptoms in the exposed cells. After exposure, the cells can be assayed to measure alterations in the expression of the mahogany gene, e.g., by assaying cell lysates for mahogany mRNA transcripts (e.g., by Northern analysis) or for mahogany gene products expressed by the cell; compounds that modulate expression of the mahogany gene are good candidates as therapeutics.

In addition, animal-based systems or models for a mammalian body weight disorder, for example, transgenic mice

containing a human or altered form of mahogany gene, may be used to identify compounds capable of ameliorating symptoms of the disorder. Such animal models may be used as test substrates for the identification of drugs, pharmaceuticals, therapies and interventions. For example, animal models may be exposed to a compound suspected of exhibiting an ability to ameliorate symptoms, at a sufficient concentration and for a sufficient time to elicit such an amelioration of body weight disorder symptoms. The response of the animals to the exposure may be monitored by assessing the reversal of the symptoms of the disorder.

With regard to intervention, any treatments that reverse any aspect of body weight disorder-like symptoms should be considered as candidates for human therapeutic intervention in such a disorder. Dosages of test agents may be determined by deriving dose-response curves, as discussed in Section 5.5.1, below.

5.4.3.COMPOUNDS AND METHODS FOR THE TREATMENT OF BODY WEIGHT DISORDERS

Described below are methods and compositions whereby body weight disorders, including obesity, cachexia, and anorexia, may be treated. Such methods can comprise, for example administering compounds which modulate the expression of a mammalian mahogany gene and/or the synthesis or activity of a mammalian mahogany gene product, so that symptoms of the body weight disorder are ameliorated. Alternatively, in those instances whereby the mammalian body weight disorder results from mahogany gene mutations, such methods can comprise supplying the mammal with a nucleic acid molecule encoding an unimpaired mahogany gene product such that an unimpaired mahogany gene product is expressed and symptoms of the disorder are ameliorated.

In another embodiment of methods for the treatment of mammalian body weight disorders resulting from mahogany gene mutations, such methods can comprise supplying the mammal with a cell comprising a nucleic acid molecule that encodes an unimpaired mahogany gene product such that the cell expresses the unimpaired mahogany gene product, and symptoms of the disorder are ameliorated.

Because a loss of normal mahogany gene function results in the restoration of a non-obese phenotype in individuals exhibiting an agouti mutation (e.g. individuals that ectopically express the agouti gene in all tissues) a decrease or elimination of normal mahogany gene product would facilitate progress towards a normal body weight state in such individuals. Methods for inhibiting or reducing the level of mahogany gene product synthesis or expression can include, for example, methods such as those described in Section 5.4.3.1.

Alternatively, symptoms of certain body weight disorders such as, for example, cachexia and anorexia, which involve a lower than normal body weight phenotype, may be ameliorated by increasing the level of mahogany gene expression and/or mahogany gene product activity. Methods for enhancing the expression or synthesis of mahogany can include, for example, methods such as those described below, in Section 5.4.3.2

5.4.3.1. INHIBITORY ANTISENSE, RIBOZYME AND TRIPLE HELIX APPROACHES

In another embodiment, symptoms of body weight disorders may be ameliorated by decreasing the level of mahogany gene expression and/or mahogany gene product activity by using mahogany gene sequences in conjunction with well-known antisense, gene "knock-out," ribozyme and/or triple helix methods to decrease the level of mahogany gene expression. Among the compounds that may exhibit the ability to modulate

the activity, expression or synthesis of the mahogany gene, including the ability to ameliorate the symptoms of a mammalian body weight disorder, are antisense, ribozyme, and triple helix molecules. Such molecules may be designed to
5 reduce or inhibit either unimpaired, or if appropriate, mutant target gene activity. Techniques for the production and use of such molecules are well known to those of skill in the art.

Antisense RNA and DNA molecules act to directly block the translation of mRNA by hybridizing to targeted mRNA and
10 preventing protein translation. Antisense approaches involve the design of oligonucleotides that are complementary to a target gene mRNA. The antisense oligonucleotides will bind to the complementary target gene mRNA transcripts and prevent translation. Absolute complementarity, although preferred,
15 is not required.

A sequence "complementary" to a portion of an RNA, as referred to herein, means a sequence having sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense
20 nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA it may contain and still form a stable duplex (or
25 triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

In one embodiment, oligonucleotides complementary to
30 non-coding regions of the mahogany gene could be used in an antisense approach to inhibit translation of endogenous mahogany mRNA. Antisense nucleic acids should be at least

six nucleotides in length, and are preferably oligonucleotides ranging from 6 to about 50 nucleotides in length. In specific aspects the oligonucleotide is at least 10 nucleotides, at least 17 nucleotides, at least 25 nucleotides or at least 50 nucleotides.

Regardless of the choice of target sequence, it is preferred that *in vitro* studies are first performed to quantitate the ability of the antisense oligonucleotide to inhibit gene expression. It is preferred that these studies utilize controls that distinguish between antisense gene inhibition and nonspecific biological effects of oligonucleotides. It is also preferred that these studies compare levels of the target RNA or protein with that of an internal control RNA or protein. Additionally, it is envisioned that results obtained using the antisense oligonucleotide are compared with those obtained using a control oligonucleotide. It is preferred that the control oligonucleotide is of approximately the same length as the test oligonucleotide and that the nucleotide sequence of the oligonucleotide differs from the antisense sequence no more than is necessary to prevent specific hybridization to the target sequence.

The oligonucleotides can be DNA or RNA or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, e.g., Letsinger, et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86, 6553-6556; Lemaitre, et al., 1987, Proc. Natl. Acad. Sci. U.S.A. 84, 648-652; PCT Publication No. WO88/09810, published December 15, 1988) or

the blood-brain barrier (see, e.g., PCT Publication No. WO89/10134, published April 25, 1988), hybridization-triggered cleavage agents (see, e.g., Krol et al., 1988, BioTechniques 6, 958-976) or intercalating agents (see, e.g., Zon, 1988, Pharm. Res. 5, 539-549). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

The antisense oligonucleotide may comprise at least one modified base moiety which is selected from the group including but not limited to 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

The antisense oligonucleotide may also comprise at least one modified sugar moiety selected from the group including but not limited to arabinose, 2-fluoroarabinose, xylulose, and hexose.

In yet another embodiment, the antisense oligonucleotide comprises at least one modified phosphate backbone selected

from the group consisting of a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, and a formacetal or analog thereof.

5 In yet another embodiment, the antisense oligonucleotide is an α -anomeric oligonucleotide. An α -anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gautier, et al., 1987, Nucl. Acids Res. 15, 6625-6641). The oligonucleotide
10 is a 2'-O-methylribonucleotide (Inoue, et al., 1987, Nucl. Acids Res. 15, 6131-6148), or a chimeric RNA-DNA analogue (Inoue, et al., 1987, FEBS Lett. 215, 327-330).

Oligonucleotides of the invention may be synthesized by standard methods known in the art, e.g., by use of an
15 automated DNA synthesizer (such as are commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein, et al. (1988, Nucl. Acids Res. 16, 3209), methylphosphonate oligonucleotides can be prepared by use of
20 controlled pore glass polymer supports (Sarin, et al., 1988, Proc. Natl. Acad. Sci. U.S.A. 85, 7448-7451), etc.

While antisense nucleotides complementary to the target gene coding region sequence could be used, those complementary to the transcribed, untranslated region are
25 most preferred.

Antisense molecules should be delivered to cells that express the target gene in vivo. A number of methods have been developed for delivering antisense DNA or RNA to cells; e.g., antisense molecules can be injected directly into the tissue site, or modified antisense molecules, designed to
30 target the desired cells (e.g., antisense linked to peptides or antibodies that specifically bind receptors or antigens

expressed on the target cell surface) can be administered systemically.

However, it is often difficult to achieve intracellular concentrations of the antisense sufficient to suppress translation of endogenous mRNAs. Therefore a preferred approach utilizes a recombinant DNA construct in which the antisense oligonucleotide is placed under the control of a strong pol III or pol II promoter. The use of such a construct to transfect target cells in the patient will result in the transcription of sufficient amounts of single stranded RNAs that will form complementary base pairs with the endogenous target gene transcripts and thereby prevent translation of the target gene mRNA. For example, a vector can be introduced e.g., such that it is taken up by a cell and directs the transcription of an antisense RNA. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art. Vectors can be plasmid, viral, or others known in the art, used for replication and expression in mammalian cells. Expression of the sequence encoding the antisense RNA can be by any promoter known in the art to act in mammalian, preferably human cells. Such promoters can be inducible or constitutive. Such promoters include but are not limited to: the SV40 early promoter region (Beruoist and Chambon, 1981, Nature 290, 304-310), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto, et al., 1980, Cell 22, 787-797), the herpes thymidine kinase promoter (Wagner, et al., 1981, Proc. Natl. Acad. Sci. U.S.A. 78, 1441-1445), the regulatory sequences of the metallothionein gene (Brinster, et al., 1982, Nature 296, 39-42), etc. Any type of plasmid, cosmid, YAC or viral vector can be used to prepare the recombinant DNA construct which can be introduced

directly into the tissue site. Alternatively, viral vectors can be used that selectively infect the desired tissue, in which case administration may be accomplished by another route (e.g., systemically).

5 Ribozyme molecules designed to catalytically cleave target gene mRNA transcripts can also be used to prevent translation of target gene mRNA and, therefore, expression of target gene product. (See, e.g., PCT International Publication WO90/11364, published October 4, 1990; Sarver, et
10 al., 1990, Science 247, 1222-1225).

10 Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. (For a review, see Rossi, 1994, Current Biology 4, 469-471). The mechanism of ribozyme action involves sequence specific hybridization of the ribozyme molecule to complementary target RNA, followed
15 by an endonucleolytic cleavage event. The composition of ribozyme molecules must include one or more sequences complementary to the target gene mRNA, and must include the well known catalytic sequence responsible for mRNA cleavage. For this sequence, see, e.g., U.S. Patent No. 5,093,246,
20 which is incorporated herein by reference in its entirety.

While ribozymes that cleave mRNA at site specific recognition sequences can be used to destroy target gene mRNAs, the use of hammerhead ribozymes is preferred. Hammerhead ribozymes cleave mRNAs at locations dictated by
25 flanking regions that form complementary base pairs with the target mRNA. The sole requirement is that the target mRNA have the following sequence of two bases: 5'-UG-3'. The construction and production of hammerhead ribozymes is well known in the art and is described more fully in Myers, 1995, *Molecular Biology and Biotechnology: A Comprehensive Desk*
30 Reference, VCH Publishers, New York, (see especially Figure 4, page 833) and in Haseloff and Gerlach, 1988, Nature, 334,

585-591, which is incorporated herein by reference in its entirety.

Preferably the ribozyme is engineered so that the cleavage recognition site is located near the 5' end of the target gene mRNA, i.e., to increase efficiency and minimize the intracellular accumulation of non-functional mRNA transcripts.

The ribozymes of the present invention also include RNA endoribonucleases (hereinafter "Cech-type ribozymes") such as the one that occurs naturally in *Tetrahymena thermophila* (known as the IVS, or L-19 IVS RNA) and that has been extensively described by Thomas Cech and collaborators (Zaug, et al., 1984, Science, 224, 574-578; Zaug and Cech, 1986, Science, 231, 470-475; Zaug, et al., 1986, Nature, 324, 429-433; published International patent application No. WO 88/04300 by University Patents Inc.; Been and Cech, 1986, Cell, 47, 207-216). The Cech-type ribozymes have an eight base pair active site which hybridizes to a target RNA sequence whereafter cleavage of the target RNA takes place. The invention encompasses those Cech-type ribozymes which target eight base-pair active site sequences that are present in the target gene.

As in the antisense approach, the ribozymes can be composed of modified oligonucleotides (e.g., for improved stability, targeting, etc.) and should be delivered to cells that express the target gene in vivo. A preferred method of delivery involves using a DNA construct "encoding" the ribozyme under the control of a strong constitutive pol III or pol II promoter, so that transfected cells will produce sufficient quantities of the ribozyme to destroy endogenous target gene messages and inhibit translation. Because ribozymes unlike antisense molecules, are catalytic, a lower intracellular concentration is required for efficiency.

Endogenous target gene expression can also be reduced by inactivating or "knocking out" the target gene or its promoter using targeted homologous recombination (e.g., see Smithies, et al., 1985, Nature 317, 230-234; Thomas and
5 Capecchi, 1987, Cell 51, 503-512; Thompson, et al., 1989, Cell 5, 313-321; each of which is incorporated by reference herein in its entirety). For example, a mutant, non-functional target gene (or a completely unrelated DNA
10 sequence) flanked by DNA homologous to the endogenous target gene (either the coding regions or regulatory regions of the target gene) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express the target gene *in vivo*. Insertion of the DNA
15 construct, via targeted homologous recombination, results in inactivation of the target gene. Such approaches are particularly suited in the agricultural field where modifications to ES (embryonic stem) cells can be used to generate animal offspring with an inactive target gene (e.g., see Thomas and Capecchi, 1987 and Thompson, 1989, *supra*). However this approach can be adapted for use in humans
20 provided the recombinant DNA constructs are directly administered or targeted to the required site *in vivo* using appropriate viral vectors.

Alternatively, endogenous target gene expression can be reduced by targeting deoxyribonucleotide sequences
25 complementary to the regulatory region of the target gene (i.e., the target gene promoter and/or enhancers) to form triple helical structures that prevent transcription of the target gene in target cells in the body. (See generally, Helene, 1991, Anticancer Drug Des., 6(6), 569-584; Helene, et al., 1992, Ann. N.Y. Acad. Sci., 660, 27-36; and Maher, 1992,
30 Bioassays 14(12), 807-815).

Nucleic acid molecules to be used in triplex helix formation for the inhibition of transcription should be

single stranded and composed of deoxynucleotides. The base composition of these oligonucleotides must be designed to promote triple helix formation via Hoogsteen base pairing rules, which generally require sizeable stretches of either
5 purines or pyrimidines to be present on one strand of a duplex. Nucleotide sequences may be pyrimidine-based, which will result in TAT and CGC triplets across the three associated strands of the resulting triple helix. The pyrimidine-rich molecules provide base complementarity to a
10 purine-rich region of a single strand of the duplex in a parallel orientation to that strand. In addition, nucleic acid molecules may be chosen that are purine-rich, for example, contain a stretch of G residues. These molecules will form a triple helix with a DNA duplex that is rich in GC pairs, in which the majority of the purine residues are
15 located on a single strand of the targeted duplex, resulting in GGC triplets across the three strands in the triplex.

Alternatively, the potential sequences that can be targeted for triple helix formation may be increased by creating a so called "switchback" nucleic acid molecule.
20 Switchback molecules are synthesized in an alternating 5'-3', 3'-5' manner, such that they base pair with first one strand of a duplex and then the other, eliminating the necessity for a sizeable stretch of either purines or pyrimidines to be present on one strand of a duplex.

In instances wherein the antisense, ribozyme, and/or
25 triple helix molecules described herein are utilized to inhibit mutant gene expression, it is possible that the technique may so efficiently reduce or inhibit the transcription (triple helix) and/or translation (antisense, ribozyme) of mRNA produced by normal target gene alleles that
30 the possibility may arise wherein the concentration of normal target gene product present may be lower than is necessary for a normal phenotype. In such cases, to ensure that

substantially normal levels of target gene activity are maintained, therefore, nucleic acid molecules that encode and express target gene polypeptides exhibiting normal target gene activity may, be introduced into cells via gene therapy methods such as those described, below, in Section 5.9.2 that do not contain sequences susceptible to whatever antisense, ribozyme, or triple helix treatments are being utilized. Alternatively, in instances whereby the target gene encodes an extracellular protein, it may be preferable to co-administer normal target gene protein in order to maintain the requisite level of target gene activity.

Anti-sense RNA and DNA, ribozyme, and triple helix molecules of the invention may be prepared by any method known in the art for the synthesis of DNA and RNA molecules, as discussed above. These include techniques for chemically synthesizing oligodeoxyribonucleotides and oligoribonucleotides well known in the art such as for example solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences encoding the antisense RNA molecule. Such DNA sequences may be incorporated into a wide variety of vectors that incorporate suitable RNA polymerase promoters such as the T7 or SP6 polymerase promoters. Alternatively, antisense cDNA constructs that synthesize antisense RNA constitutively or inducibly, depending on the promoter used, can be introduced stably into cell lines.

5.4.3.2. GENE REPLACEMENT THERAPY

Mahogany gene nucleic acid sequences, described above in Section 5.1, can be utilized for the treatment of a mammalian body weight disorders, including obesity, cachexia, and anorexia. Such treatment can be in the form of gene replacement therapy. Specifically, one or more copies of a

normal mahogany gene or a portion of the mahogany gene that directs the production of a mahogany gene product exhibiting normal mahogany gene function, may be inserted into the appropriate cells within a patient, using vectors that
5 include, but are not limited to adenovirus, adeno-associated virus, and retrovirus vectors, in addition to other particles that introduce DNA into cells, such as liposomes.

Because the mahogany gene is expressed in the brain, such gene replacement therapy techniques should be capable
10 delivering mahogany gene sequences to these cell types within patients. Thus, in one embodiment, techniques that are well known to those of skill in the art (see, e.g., PCT Publication No. WO89/10134, published April 25, 1988) can be used to enable mahogany gene sequences to cross the blood-brain barrier readily and to deliver the sequences to cells
15 in the brain. With respect to delivery that is capable of crossing the blood-brain barrier, viral vectors such as, for example, those described above, are preferable.

In another embodiment, techniques for delivery involve direct administration of such mahogany gene sequences to the
20 site of the cells in which the mahogany gene sequences are to be expressed.

Additional methods that may be utilized to increase the overall level of mahogany gene expression and/or mahogany gene product activity include using target homologous
25 recombination methods, discussed in Section 5.2, above, to modify the expression characteristic of an endogenous mahogany gene in a cell or microorganism by inserting a heterologous DNA regulatory element such that the inserted regulatory element is operatively linked with the endogenous mahogany gene in question. Targeted homologous recombination
30 can be thus used to activated transcription of an endogenous mahogany gene that is "transcriptionally silent", i.e., is

not normally expressed, or to enhance the expression of an endogenous mahogany gene that is normally expressed.

Further, the overall level of mahogany gene expression and/or mahogany gene product activity may be increased by the
5 introduction of appropriate mahogany-expressing cells, preferably autologous cells, into a patient at positions and in numbers that are sufficient to ameliorate body weight disorder symptoms. Such cells may be either recombinant or non-recombinant.

10 Among the cells that can be administered to increase the overall level of mahogany gene expression in a patient are normal cells, preferably brain cells, that express the mahogany gene. Alternatively, cells, preferably autologous cells, can be engineered to express mahogany gene sequences, and may then be introduced into a patient in positions
15 appropriate for the amelioration of the body weight disorder symptoms. Alternately, cells that express an unimpaired mahogany gene and that are from a MHC matched individual can be utilized, and may include, for example, brain cells. The expression of the mahogany gene sequences is controlled by
20 the appropriate gene regulatory sequences to allow such expression in the necessary cell types. Such gene regulatory sequences are well known to the skilled artisan. Such cell-based gene therapy techniques are well known to those skilled in the art, see, e.g., Anderson, U.S. Patent No. 5,399,349.

25 When the cells to be administered are non-autologous cells, they can be administered using well known techniques that prevent a host immune response against the introduced cells from developing. For example, the cells may be introduced in an encapsulated form which, while allowing for an exchange of components with the immediate extracellular
30 environment, does not allow the introduced cells to be recognized by the host immune system.

Additionally, compounds, such as those identified via techniques such as those described, above, in Section 5.4.2, that are capable of modulating mahogany gene product activity can be administered using standard techniques that are well known to those of skill in the art. In instances in which the compounds to be administered are to involve an interaction with brain cells, the administration techniques should include well known ones that allow for a crossing of the blood-brain barrier.

10

5.5. PHARMACEUTICAL PREPARATIONS AND METHODS OF ADMINISTRATION

The compounds that are determined to affect mahogany gene expression or gene product activity can be administered to a patient at therapeutically effective doses to treat or ameliorate body weight disorders, such as obesity, anorexia, or cachexia. A therapeutically effective dose refers to that amount of the compound sufficient to result in amelioration of symptoms of such a disorder.

20

5.5.1. EFFECTIVE DOSE

Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD_{50}/ED_{50} . Compounds that exhibit large therapeutic indices are preferred. While compounds that exhibit toxic side effects may be used, care should be taken to design a delivery system that targets such compounds to the site of affected tissue in order to minimize potential damage to uninfected cells and, thereby, reduce side effects.

The data obtained from the cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the IC_{50} (i.e., the concentration of the test compound that achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography.

5.5.2. FORMULATIONS AND USE

Pharmaceutical compositions for use in accordance with the present invention may be formulated in conventional manner using one or more physiologically acceptable carriers or excipients.

Thus, the compounds and their physiologically acceptable salts and solvates may be formulated for administration by inhalation or insufflation (either through the mouth or the nose) or oral, buccal, parenteral or rectal administration.

For oral administration, the pharmaceutical compositions may take the form of, for example, tablets or capsules prepared by conventional means with pharmaceutically acceptable excipients such as binding agents (e.g., pregelatinised maize starch, polyvinylpyrrolidone or hydroxypropyl methylcellulose); fillers (e.g., lactose, microcrystalline cellulose or calcium hydrogen phosphate);

lubricants (e.g., magnesium stearate, talc or silica);
disintegrants (e.g., potato starch or sodium starch
glycolate); or wetting agents (e.g., sodium lauryl sulphate).
The tablets may be coated by methods well known in the art.
5 Liquid preparations for oral administration may take the form
of, for example, solutions, syrups or suspensions, or they
may be presented as a dry product for constitution with water
or other suitable vehicle before use. Such liquid
preparations may be prepared by conventional means with
10 pharmaceutically acceptable additives such as suspending
agents (e.g., sorbitol syrup, cellulose derivatives or
hydrogenated edible fats); emulsifying agents (e.g., lecithin
or acacia); non-aqueous vehicles (e.g., almond oil, oily
esters, ethyl alcohol or fractionated vegetable oils); and
preservatives (e.g., methyl or propyl-p-hydroxybenzoates or
15 sorbic acid). The preparations may also contain buffer
salts, flavoring, coloring and sweetening agents as
appropriate.

Preparations for oral administration may be suitably
formulated to give controlled release of the active compound.

20 For buccal administration the compositions may take the
form of tablets or lozenges formulated in conventional
manner.

For administration by inhalation, the compounds for use
according to the present invention are conveniently delivered
25 in the form of an aerosol spray presentation from pressurized
packs or a nebulizer, with the use of a suitable propellant,
e.g., dichlorodifluoromethane, trichlorofluoromethane,
dichlorotetrafluoroethane, carbon dioxide or other suitable
gas. In the case of a pressurized aerosol the dosage unit
may be determined by providing a valve to deliver a metered
30 amount. Capsules and cartridges of e.g., gelatin for use in
an inhaler or insufflator may be formulated containing a

powder mix of the compound and a suitable powder base such as lactose or starch.

The compounds may be formulated for parenteral administration by injection, e.g., by bolus injection or
5 continuous infusion. Formulations for injection may be presented in unit dosage form, e.g., in ampoules or in multi-dose containers, with an added preservative. The compositions may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain
10 formulatory agents such as suspending, stabilizing and/or dispersing agents. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, e.g., sterile pyrogen-free water, before use.

The compounds may also be formulated in rectal compositions such as suppositories or retention enemas, e.g.,
15 containing conventional suppository bases such as cocoa butter or other glycerides.

In addition to the formulations described previously, the compounds may also be formulated as a depot preparation. Such long acting formulations may be administered by
20 implantation (for example subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds may be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble
25 salt.

The compositions may, if desired, be presented in a pack or dispenser device that may contain one or more unit dosage forms containing the active ingredient. The pack may for example comprise metal or plastic foil, such as a blister
30 pack. The pack or dispenser device may be accompanied by instructions for administration.

6. **EXAMPLE: GENETIC AND PHYSICAL MAPPING
OF THE MAHOGANY LOCUS**

In the Example presented herein, studies are described which, first, define the genetic interval on mouse chromosome 2 within which the mahogany gene lies, and second, successfully narrow the interval to approximately 0.29 cM. Further, the physical mapping of this interval is described.

Mouse crosses were performed to obtain homozygous mg/mg mice. First, LDJ-Le-mg mice were crossed with CAST/Ei mice. The F1s were back-crossed with LDJ-Le-mg mice and the resulting litters scored for coat color. Mice showing coat color of mg/mg homozygotes were genotyped to using D2/NDS3 and D2/MIT19 markers to identify meiotic events. Mice showing recombinant events were fine structure mapped using various markers shown in FIG. 1. All genotyping was performed using PCR-SSLP and then analyzed using PAGE.

After 2300 meioses, the mahogany gene was mapped to a 0.99 cM interval FIG. 1. This corresponded to an interval width of 700 kb.

Physical Mapping of the Genetic Interval: The 700 kb mahogany region on mouse chromosome 2 is shown in FIG. 1. Genetic markers, clones spanning the region and open reading frames in the interval are shown in the figure.

7. **EXAMPLE: IDENTIFICATION OF A CANDIDATE
MAHOGANY GENE**

In the Example presented herein, a gene is identified within the cloned DNA described in the Example in Section 6, above, which corresponds to a candidate mahogany gene.

Clones spanning the 700kb region were sequenced and open reading frames were identified and analyzed through this interval. Nucleic acid sequencing was performed using ABI sequencers and the manufactures recommended procedures. Many

novel sequences encoding proteins are located in this integral, see the bottom of FIG. 1. With each open reading frame identified, mutational analysis, primarily via SSCP analysis, was used with the three alleles of the mahogany phenotype mice to identify which of the open reading frames
5 within this interval contain a mutation in an mg mouse.

A mutation was found in one of the genomic/cDNA sequences found in the integral in mg3J mice. Figures 3 and 2 provide the genomic and cDNA sequences surrounding the mutation, FIG. 6 shows the mutation in mg3J, and FIGS. 8 and
10 9 show splice variants in the 5' end of the murine mg gene. The mutation in mg3J mice is a deletion of a GCTGC sequence which results in the creation of a frameshift. Based on the chromosomal location and mutation identification, the cDNA provided in Figure 2 and the corresponding genomic DNA which contains the contigs provided in Figure 3 represent the mg
15 gene/locus.

Further analysis of cDNA clones identified two distinct splice variants in the 5' end of the mg gene. Figure 7 provides an analysis of the structure of the two splice variants, denoted akml003 and akml004. Figures 8 and 9
20 provide the nucleic acid and amino acid sequence of the 5' ends of these splice variants and structural analysis of the protein encoded by the 5' regions.

Analysis of libraries of human cDNA sequences led to the identification of three forms of the human ortholog of the mg
25 gene: a long form (FIGS. 18A-D) and two shorter splice forms, each of which is shown in FIGS. 19A-D and 20A-C.

8. **EXAMPLE: CHARACTERIZATION OF
THE MAHOGANY GENE**

In the example presented herein, the nucleic acid
30 sequence of the mahogany gene transcript identified in the example presented in Section 7, above, is used to generate

Northern analysis data which characterize the expression of the mahogany transcript in a number of tissues both of wild type mice, and of mice exhibiting the mahogany phenotype. The results presented in this example are consistent with the 5 mg gene being the mahogany gene.

For Northern analysis, polyA RNA was isolated from wild-type and the original mg mutant, mg3J and mg-Lester mice and utilized from the Northern analysis following standard protocols. Northern blots prepared from this mRNA was hybridized with a probe obtained from sequences common to the 10 akml003 and akml004 sequences. Specifically PCR primers TTCCTCACTGG and GGACACACAG were used to amplify cDNA from the akml003 sequence which had been radiolabelled by random priming using a Gibco-BRL kit according to the manufacturer's recommended protocol.

15 An mg transcript was found in all mice examined in mRNA isolated from brain (minus the hypothalamus), kidney, heart, testes, liver, skin, and hypothalamus. No expression was seen in muscle.

In a Northern blot run on RNA samples from mahogany 20 mice, the mg transcript was found to be expressed at a reduced level in all tissues in mRNA isolated from mg3J mice, as a varied size fragment in mg-Lester derived mRNA, and at different levels and sizes in original mg mutant mice derived mRNA.

25 These results are consistent with the mg gene disclosed herein as being the mahogany gene.

9. **EXAMPLE: EFFECTS OF THE MAHOGANY GENE
ON GENETIC AND DIETARY OBESITY**

This section describes experiments which examine whether 30 the mg gene acts specifically within the agouti pathway. Specifically, these experiments test whether mg can suppress the obesity of other monogenic obese mutants as well as

whether it can suppress diet-induced obesity. The results show that *mg* does not suppress obesity in any of the monogenic obese mutants. However, *mg* can suppress diet-induced obesity. Thus, the *mg* gene and its corresponding gene product and compounds that modulate *mg* expression and/or activity have implications in the treatment of diet-induced obesity disorders, as well as in the treatment of disorders related directly to the *mg* or *agouti* gene.

9.1.

MATERIALS AND METHODS

Genetic crosses: The crosses, and the number of animals for each (n) were (LDJ/Le-*mg*/*mg* X CAST/Ei) X LDJ/Le-*mg*/*mg* (n=1588), (C3HeB/FeJ-*mg*^{3J}/*mg*^{3J} X CAST/Ei) X C3HeB/FeJ-*mg*^{3J}/*mg*^{3J} (n=324), (C3HeB/FeJ-*mg*^{3J}/*mg*^{3J} X MOLF/Ei) X C3HeB/FeJ-*mg*^{3J}/*mg*^{3J} (n=216) and (C3HeB/FeJ-*mg*^{3J}/*mg*^{3J} X C57BL6/J) X C3HeB/FeJ-*mg*^{3J}/*mg*^{3J} (n=309). The 2437 N₂ mice were analysed by coat colour to determine their genotype at the *mg* locus. As mice change color slightly at each hair molt and because the phenotype of *mg*/*mg* vs. *mg*/+ can be subtle, all mice were phenotyped at the same age by a single person. Genomic DNA was made from a tail biopsy of each mouse and analysed for multiple simple sequence length repeat polymorphism (SSLP) markers. The first ~100 mice were typed for a series of polymorphic Mit genetic markers (Deitrich, W.F. et al., 1996, Nature 380:149-152) from distal mouse chromosome 2 in order to accurately delimit the position of *mg*. With the first ~100 mice it was determined that *mg* mapped approximately 15cM proximal of Agouti between markers *D2Mit19* and *D2Nds3* (FIG. 13). All remaining animals were genotyped for *D2Mit19* and *D2Nds3*. Animals recombinant in that interval were typed with all available Mit markers between and for the ever growing number of markers developed during the project which, finally totaled 265 markers.

9.2.

RESULTS

The murine mahogany (*mg*) gene is known to act in a dosage dependent manner within the agouti pathway, to compensate for the agouti overexpression and for lack of signaling from the *nul* allele *McIr* (Miller, K.A. et al., 1997, *Genetics* 146:1407-1415; Dinulescu, D.M. et al., *Proc. Natl. Acad. Sci.*, in press; Robbins, L.S. et al., 1993, *Cell* 72:827-834). The phenotype of mice homozygous for both *mg* and a null allele of *McIr* (recessive yellow, *McIr^e*) is yellow, the same as the phenotype of *McIr^e/McIr^e* mice, indicating that *mg* is not acting downstream of *McIr*. A similar experiment was performed with obese *Mcr4* knock out mice (FIG. 11). For both sexes, all the animals homozygous for *Mcr4*^{-/-} were approximately equally obese and were heavier than the mice wild-type at *Mcr4* independent of the genotype for *mg*. This data strengthens and confirms the *McIr* data previously published, strongly suggesting that *mg* acts at or upstream of both melanocortin receptors.

To test whether *mg* acts specifically within the agouti pathway, experiments were performed to determine whether *mg* can suppress the obesity of other monogenic obese mutants of the mouse and whether it could suppress diet-induced obesity. Appropriate genetic crosses were set up to product mice segregating *mg* and one of the mouse obesity mutations *Cpe^{fat}*, *tub*, or *Lepr^{db}* such that all combinations of homozygous and heterozygous animals were on the same mix of genetic background. No suppression of obesity was seen for any of the monogenic obese mutants (FIG. 12) lending credence to the assumed specificity of action within the agouti pathway. To ask whether *mg* can suppress diet induced obesity C3HeB/FeJ-*mg^{3J}* and C3H/HeJ mice were placed, at weaning, either on normal chow having a physiological fuel value (PFV) of 3.63 kcal/gm with 9% fat, or onto a high fat diet having a PFV of 4.53 kcal/gm with 42.2% fat. Food consumption and body

weight were measured weekly. Converting the grams of food consumed to calories indicated that C3H/HeJ mice on normal chow and high fat diet consumed ~97 kCal/week and ~96 kCal/week, respectively. C3HeB/FeJ-*mg*^{3J} mice on normal chow and high fat diet consumed ~83 kCal/week and ~81 kCal/week, respectively. Despite the equal calorie intake, the C3H/HeJ mice on the high fat diet readily gained more weight than the C3H/HeJ mice on normal chow ($p=0.0004$). In stark contrast, the C3HeB/FeJ-*mg*^{3J} mice on either diet showed no statistically significant difference in weight (FIG. 12D). Female data showed the same trends, although there was no statistical significance between any of the mice on either diet.

10. EXPERIMENT: MAPPING AND SEQUENCING
OF THE MAHOGANY GENE

15 This section describes experiments wherein the murine mahogany gene was genetically and physically mapped to an approximately 0.6 cM interval, and then sequenced. The murine *mg* sequence obtained was then used to isolate and sequence the human *mg* gene. Northern and *in situ* analyses of *mg* expression in mouse tissue are also described, and sequence motifs of the predicted MG polypeptide are discussed.

10.1. MATERIALS AND METHODS

25 Physical Mapping: More than 36,000 individual sequences from the region were compared by BLAST (Altschul, S.F. et al., 1990, *J. Mol. Biol.* 215:403-410) to publicly available sequence databases and analyzed using GRail (Guan, X. et al., 1992, *Proc. Eighth IEEE Conference on AI Applications*:9-13) to identify potential coding sequence. In addition, sequences from overlapping BACs were assembled using phrap (Sing, C.F. et al., 1998, *Genome Res.* 8:175-185; Ewing B. and Green, P., 1998, *Genome Res.* 8:186-194; Gordon, D. et al.,

1998, *Genome Res.* 8:195-202), and the resulting contigs were also analyzed using BLAST and GRAIL to aid in gene prediction. This data was displayed in ACEDb (Durbin, Richard and Mieg, Jean Thierry, 1991, *A C. elegans Database*, Documentation, code, and data available from anonymous FTP servers at lirmm.lirmm.fr, cele, mrc-lmb.cam.ac.uk, and ncbi.nlm.nih.gov) to further visualize predicted exons and their relationships to each other.

10 Northern Blot Analysis: PolyA⁺ RNA was extracted from the tissues indicated from wild-type, C3H/HeJ and the three mutant alleles of *mg*, C3HeB/FeJ-*mg*^{3J}, LDJ/Le-*mg*, and C3H/HeJ-*mg*⁺, according to the manufacturer's instructions. RNA STAT-60 (Tel-Test, Inc., 1511 Sounty Rd. 129, Friendswood, TX 77546) was used to isolate total RNA. PolyA⁺ was isolated 15 using Poly(A)Pure™ mRNA purification kit (Ambion, Inc., 2130 Woodward St. #200, Austin, TX 78744). 2 µg of each mRNA was separated on a 1% agarose-formaldehyde gel, transferred to nylon, and hybridized with a probe for *mg* corresponding to nt 990-1406 of the murine cDNA sequence with Rapid-hyb Buffer 20 (Amersham LIFE SCIENCE, Gaithersberg, MD). Filters were washed with 0.11x SSC, 0.1% SDS and exposed to KODAK X-omat film overnight.

10.2. RESULTS

25 A positional cloning strategy was undertaken to identify the *mg* gene. Multiple genetic crosses were set up to produce second generation mice (n=2437) segregating *mg* which were used to genetically localise the *mg* locus (FIG 13B). When the genetic map critical interval for *mg* was resolved to 30 -0.6 cM physical mapping was initiated. Approximately 1 Mb was contiged with 30 BACs (FIG. 13C), most of which were made into random sheared libraries for shot gun sequencing. At completion of the project it was estimated that 85% sequence

coverage across the interval had been achieved and that all genes within the region had been found. Twenty-nine genes were identified, 15 of which are novel genes. Within the final minimal interval for *mg*, indicated by the arrows in
5 FIG. 13, there were eleven genes of which nine were unknown. All of these genes were tested as candidates for *mg* by examining the three mutant alleles of the mahogany locus, the original allele, *mg*, that arose in a stock of Swiss x C3H mice, and two alleles that have independently arisen on the C3H background, C3HeB/FeJ-*mg*^{3J}/*mg*^{3J} and C3H/He-*mg*^L/*mg*^L. Each
10 gene was examined by Northern blot analysis and RT-PCR analysis of RNA from tissues from wild-type and *mg* mutant mice, by Southern blot analysis of DNA from wild-type and *mg* mutant mice, and by SSCP analysis of genomic PCR products designed to cover the intron-exon boundaries of much of each
15 of the genes. In all, 20 genes were analyzed in this manner, one of which showed a northern blot difference between the wild type and mutant alleles (FIG. 14).

The wild type expression pattern of this gene gives three bands of size ~9 kb, 4.5 kb, and 3.8 kb, of which the
20 largest message is the most prominent (FIG 14). The smaller two bands can be seen in all tissues but, depending upon tissue, may require extended exposure. Each of the different *mg* alleles gave a different expression pattern. C3HeB/FeJ-*mg*^{3J}/*mg*^{3J} has extremely low expression, the 9 kb message only
25 being very faint in brain, hypothalamus, and fat on northern. C3H/He-*mg*^L/*mg*^L expresses a single aberrant band of approximately 9.5-10 kb in kidney, heart, muscle, fat, and, most prominently, brain and hypothalamus. The LDJ/Le-*mg*/*mg* shows an altered ratio of the three wild type messages: the
30 9 kb message is reduced, while the two smaller messages are more highly expressed, in particular being very abundant in fat and hypothalamus. *In situ* analysis was used to look more closely at *mg* expression in the brain and specifically the

hypothalamus. Overall hybridization in LDJ/Le-mg/mg looks equivalent to that of wild type, and the C3HeB/FeJ-mg^{3J}/mg^{3J} shows an overall reduction of expression. Close examination of the hypothalamic region in both wild type and mutant alleles revealed differences in the ventromedial hypothalamic nucleus (VMH). Both C3HeB/FeJ-mg^{3J}/mg^{3J} and the LDJ/Le-mg/mg have reduced VMH expression (FIG. 15) which is particularly interesting as many neuropeptides and receptors known to be involved in body weight regulation are expressed in the VMH, including Mc4r.

Initially, two overlapping mouse cDNAs of 1051 bps and 2419 bps were identified. Using these cDNAs as a starting point it was possible to build over 7990 bps of human sequences, using both the public EST database and an in house database, as well as identifying one cDNA clone from a human liver library. The 23 ESTs used in the contiging are listed in Table I below. Using the derived human sequence, it was then possible to estimate the intron-exon boundaries within the mouse genomic sequence. These were verified by PCR amplification and sequencing. In total, 4079 bps of mouse sequence was obtained, of which 4011 bp are coding sequence. The mouse genomic locus spans over 160 kb, and has 31 identified exons, at least one of which is differentially spliced.

TABLE I

<u>Gene Bank Accession #</u>	<u>Clone ID #</u>	<u>Clone Source</u>
NA	NA	Human Endothelial Cell (MPI)
AA062169	482948	Soares mouse P3NMF19.5
NA	NA	Human Liver (MPI)
AA350292	151062	Infant Brain
R87660	194640	Soares Fetal Liver Spleen 1 NFLS

	T69367	82898	Stratagene Liver
	T92696	118881	Stratagene Lung
	H11351	47626	Soares Infant Brain 1 NIB
5	AA350293	151062	Infant Brain
	AA297697	149184	Fetal Heart II
	AB011120	NA	Human Male Brain
	AA297214	129808	Embryo, 12 week I
	AA298732	184690	T-Lymphocyte
10	AI076479	1676623	Soares Total Fetus Nb2HF8 9W
	AA771958	1359202	Soares parathyroid tumor NbHPA
	R84298	194640	Soares Fetal Liver Spleen 1NFLS
	D81046	1178923	Human Fetal Brain (Tfujiwara)
15	AA378603	183010	Synovial Sarcoma
	D60710	962349	Clontech Human Fetal Brain (#6535)
	D20236	pm1235	Human Promyelocyte
	AA345684	147210	Gall Bladder I
20	H45413	182870	Soares Breast 3NbHBst
	AA044305	486349	Soares Pregnant Uterus NbHPu

The mutant mahogany alleles were also sequenced, checking all intron-exon boundaries. A 5 bp deletion at 2809 nt was found in the coding sequence of the *mg* gene from C3HeB/FeJ-*mg^{3J}*/*mg^{3J}* which introduces a stop codon a position 937, two codons 3' of the deletion. This mutation will result in a seriously truncated protein lacking many interesting domains, as discussed below. The *mg^{3J}* allele is the same allele that showed extremely low expression levels. The combined Northern blot analysis, in situ hybridization

analysis, and sequence analysis of the mutant *mg^{3j}* allele strongly suggest that this gene is the mouse mahogany gene.

The 4011 bp of open reading frame (ORF) of mouse MG predicts a 1336 amino acid polypeptide with molecular mass of 148,706 D (FIGS. 17A-D, top sequence). BLAST searches of the
5 NCBI and SwissProt protein databases identified two human paralogues with a similar modular architecture (KIAA0534, Genbank accession no. 3043592; and MEGF8, Genbank accession no. AB011541), as well as a *C. elegans* homologue (YC81_CAEEL, Genbank accession no. Q19981).

10 Another human protein, Attractin or DPPT-L (Duke-Cohen, J.S. et al., 1998, *Proc. Natl. Acad. Sci. U.S.A.* 95:11336-11341), appears to be a 1198 amino acid residue, approximately 134,000 D, secreted splice variant of the MG polypeptide. An alignment of the predicted MG (top) and
15 Attractin (bottom) amino acid sequences is shown in FIGS. 17A-D. Attractin has not identified as being involved in the regulation of body weight. Rather, the protein is reported to mediate an interaction between T lymphocytes and monocytes that leads to the adherence and spreading of monocytes that become foci for T lymphocyte clustering (see Duke-Cohen et
20 al., *supra*).

Searching the MG polypeptide with the SMART domain tool (Schultz, J. et al., 1998, *Proc. Natl. Acad. Sci. U.S.A.* 95:5857-5864) revealed sequence motifs that may provide further clues to its biological function (FIG. 16B, FIGS.
25 17A-D). The single transmembrane spanning MG protein has a large extracellular sequence of 1289 amino acids containing three EGF domains (Nakayama, M. et al., 1998, *Genomics* 51:27-34), two laminin-like EGF repeats, a CUB domain (Bork, P. and Beckmann, G., 1993, *Mol. Biol.* 231:539-545), a C-type lectin
30 domain (Drickamer, K., 1995, *Nat. Struct. Biol.* 6:437-439; Weis W. I., and Drickamer, K., 1996, *Ann. Rev. Biochem.* 65:441-473), two plexin-like repeats (Maestrini, E. et al.,

1996, *Proc. Natl. Acad. Sci. U.S.A.* 93:674-678), and six consecutive kelch repeats (Bork, P. and Doolittle, R.F., 1994, *J. Mol. Biol.* 236:1277-1282). Multiple EGF domains are commonly found in Type-1 membrane proteins involved in cell
5 adhesion and receptor-ligand interactions (Schultz, J. et al, 1998, *Proc. Natl. Acad. Sci. USA* 95:5857-5864). Laminin-EGF-like modules are found in a variety of proteoglycans such as perlecan and heparin sulphate proteoglycan. As CUB domains also frequently occur in glycosylated proteins and c-type
10 lectins are known to be carbohydrate binders, it is likely that MG is heavily glycosylated and that carbohydrate interactions are essential for its function. Many kelch motif containing proteins have been found that, like MG, have multiple consecutive domains. Such consecutive four-stranded β -sheet Kelch motifs form a bladed beta "propeller fold" that
15 is common in many sialidases and other enzymes (Maestrini, E. et al., *supra*). Unlike the other well recognized domains, the "plexin" repeat is less well defined. It was first recognized as a triple repeat in the *Xenopus* gene plexin that has similarity to MET (Bork, P. and Beckmann, G., 1993, *Mol.*
20 *Biol.* 231:539-545). Since then, this cysteine rich repeat has been found in 6 MET gene family members, three of which signal via tyrosine kinase and three of which are hypothesized to have putative signaling function via a novel conserved cytoplasmic domain. However, it is fascinating
25 that there is an eight amino acid stretch that is 100% conserved in the four proteins shown in FIG 16A from human, mouse, and *C. elegans*. The conservation of sequence across such widely evolutionary divergent species strongly indicates a functional domain, possible a putative signaling motif.

30 The multi-domain structure of MG is complex, but draws many similarities from receptor and receptor-like proteins. The full-length MG polypeptide is predicted to be a large membrane-spanning protein with multiple extracellular domains

that may have a binding or gathering function as well as a highly conserved putative signaling motif in the cytoplasmic tail.

5

The present invention is not to be limited in scope by the specific embodiments described herein, which are intended as single illustrations of individual aspects of the invention. Functionally equivalent methods and components are within the scope of the present invention. Indeed,
10 various modifications of the invention, in addition to those shown and described herein, will become apparent to those skilled in the art from the foregoing description and accompanying drawings.

All publications and patent applications mentioned in
15 the specification are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

20

25

30

WHAT IS CLAIMED IS:

1. An isolated nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO: 1 (FIG. 2A), SEQ ID NO: 8 (FIGS. 8A-C), SEQ ID NO: 10 (FIG. 9), SEQ ID NO: 12 (FIG. 10), SEQ ID NO: 14 (FIG. 18A), SEQ ID NO: 16 (FIGS. 19A-C),
5 or SEQ ID NO: 18 (FIG. 20A-B).

2. The isolated nucleic acid molecule of Claim 1, wherein the nucleic acid molecule comprises the nucleotide sequence of SEQ ID NO: 1 (FIG. 2A).

10

3. The isolated nucleic acid molecule of Claim 1, wherein the nucleic acid molecule comprises the nucleotide sequence of SEQ ID NO: 8 (FIGS. 8A-C).

15

4. The isolated nucleic acid molecule of Claim 1, wherein the nucleic acid molecule comprises the nucleotide sequence of SEQ ID NO: 10 (FIG. 9).

5. The isolated nucleic acid molecule of Claim 1, wherein the nucleic acid molecule comprises the nucleotide
20 sequence of SEQ ID NO: 12 (FIG. 10).

6. The isolated nucleic acid molecule of Claim 1, wherein the nucleic acid molecule comprises the nucleotide sequence of SEQ ID NO: 14 (FIG. 18A).

25

7. The isolated nucleic acid molecule of Claim 1, wherein the nucleic acid molecule comprises the nucleotide sequence of SEQ ID NO: 16 (FIGS. 19A-C).

30

8. The isolated nucleic acid molecule of Claim 1, wherein the nucleic acid molecule comprises the nucleotide sequence of SEQ ID NO: 18 (FIG. 20A-B).

9. A vector comprising the isolated nucleic acid molecule of any one of Claims 1-8.

5 10. An isolated host cell genetically engineered to express the nucleic acid of any one of Claims 1-8.

11. An isolated nucleic acid molecule comprising a nucleotide sequence that hybridizes to the complement of SEQ ID NO: 1 (FIG. 2A), SEQ ID NO: 8 (FIGS. 8A-C), SEQ ID NO: 10 (FIG. 9), SEQ ID NO: 12 (FIG. 10), SEQ ID NO: 14 (FIG. 18A), SEQ ID NO: 16 (FIGS. 19A-C), or SEQ ID NO: 18 (FIG. 20A-B) under stringent conditions comprising hybridization in 0.5 M NaHPO₄, 7% SDS, 1 mM EDTA at 68 °C.

15 12. A vector comprising the isolated nucleic acid molecule Claim 11.

13. An isolated host cell genetically engineered to express the nucleic acid of Claim 11.

20 14. A method of producing a mg gene product comprising culturing the genetically engineered host cell of Claim 10 so that the mg gene product is expressed in cell culture, and recovering the mg gene product from the cell culture.

25 15. A method of producing a mg gene product comprising culturing the genetically engineered host cell of Claim 14 so that the mg gene product is expressed in cell culture, and recovering the mg gene product from the cell culture.

30 16. An isolated gene product encoded by the nucleic acid molecule of any one of Claims 1-8.

17. The isolated gene product of Claim 16, wherein the gene product comprises the amino acid sequence shown in Figure 2B (SEQ. ID NO. 2), Figure 8D (SEQ. ID NO. 9), Figure 9 (SEQ. ID NO. 11), Figure 10B (SEQ. ID NO. 13), Figures 18B-
5 D (SEQ. ID NO. 15), Figure 19D (SEQ. ID NO. 17), or Figure 20C (SEQ. ID NO. 19).

18. An antibody that immunospecifically binds the gene product of Claim 16.

10

19. A method for diagnosing a body weight disorder in a mammal, comprising: measuring the level of *mg* gene expression in a patient sample and comparing the level to that of a control sample, so that if a difference between the levels is detected, a body weight disorder is diagnosed.

15

20. A method for diagnosing a body weight disorder in a mammal, comprising detecting a *mg* gene mutation contained in the genome of the mammal that correlates with presence of the disorder.

20

21. A method for diagnosing a body weight disorder in a mammal, comprising: measuring the level of *mg* activity in a patient sample and comparing the level to that of a control sample, so that if a difference between the levels is
25 detected, a body weight disorder is diagnosed.

22. A method for identifying a compound that modulates *mg* activity, comprising:

30

- a. contacting a compound to a cell that expresses a *mg* gene;
- b. measuring the level of *mg* gene expression in the cell; and

- c. comparing the level obtained in (b) to mg gene expression level obtained in the absence of the compound;

such that if the level obtained in (b) differs from that
5 obtained in the absence of the compound, a compound that modulates a mg activity is identified.

23. A method for identifying a compound that modulates a mg activity, comprising:

- 10 a. contacting a compound to a cell that contains a mg polypeptide;
b. measuring the level of mg polypeptide or activity in the cell; and
c. comparing the level obtained in (b) to the level of
15 mg polypeptide or activity obtained in the absence of the compound;

such that if the level obtained in (b) differs from that obtained in the absence of the compound, a compound that modulates a mg activity is identified.

20 24. The method of Claim 22 or 23 wherein the compound identified is capable of treating a body weight disorder.

25. A pharmaceutical composition comprising the compound identified by the method of claim 24.

25 26. The use of the pharmaceutical composition of Claim 25 for treating a body weight disorder in a mammal.

27. The use of the antibody of claim 18 for treating a body weight disorder in a mammal.

30 28. The use of a mg antisense, ribozyme or triple helix molecule for treating a body weight disorder in a mammal.

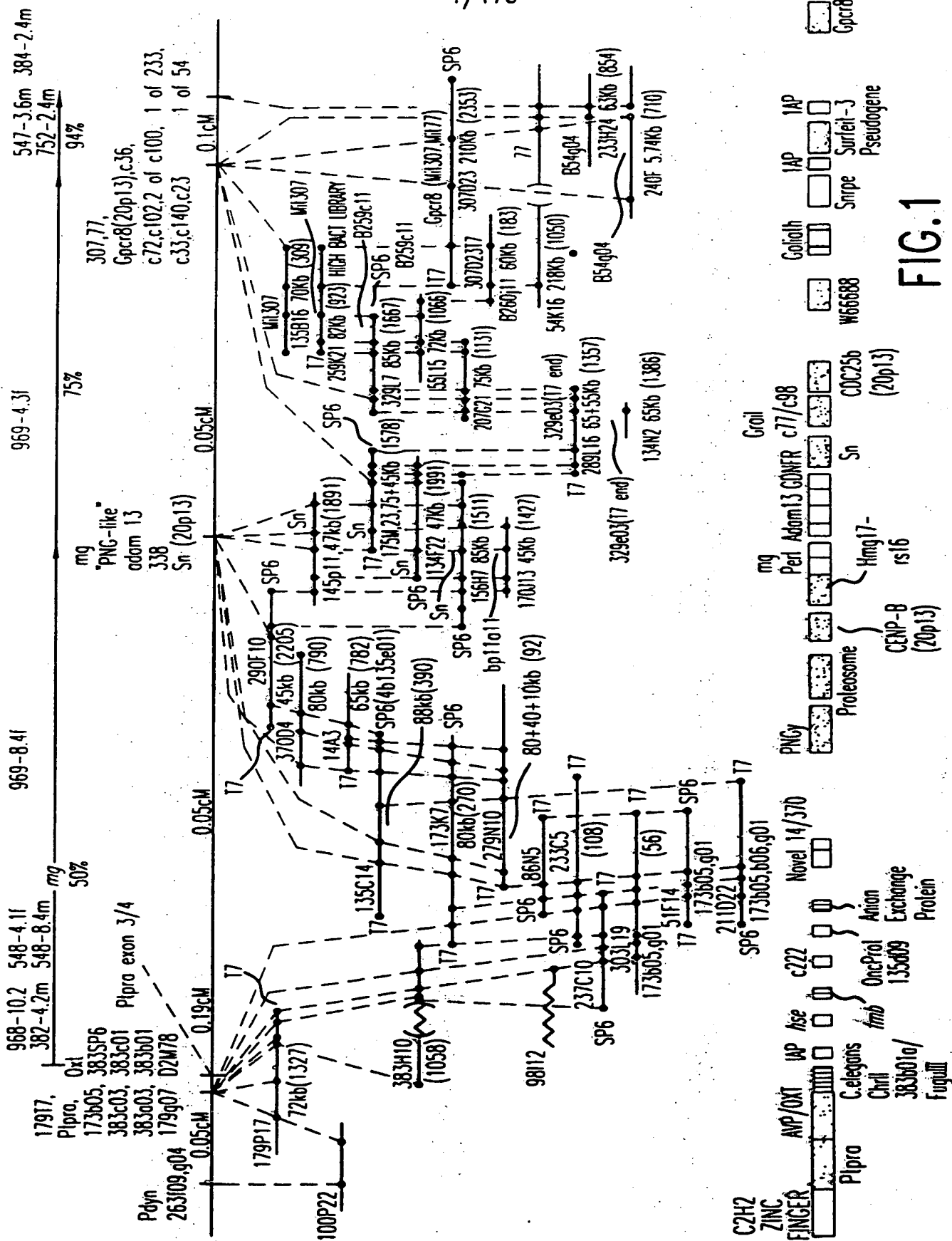


FIG. 1

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GAATTCGGGCGAAGGGAGCCGGGTGCGGGGTGTGTATGTTCGCTGGGCGCGGCTCAGCCCCAGGAAGATGGTG
GCGGTGGCGGGCGGGCGGACTGAGGCGCGGCTGAGGGGAGCACGAGGACGACAGCGCCTGCGGGCAGGAAGG
GCAGGCAGCACCGACCCCTGCACCGCGACAGGGGCTGGAGGCCGGGACCGCGCCGGCTGTGTCTCCCGGGGTGCT
GTCGCGGGCGCTGCCCGCGCGGCTGCTGCCGCTGCTCTTTTCGCTGCTGCTGCCGCTGCCCGGGAGGCCGAG
GCCGCTGCGGTGGCGGGCGGGGTGCCGCTCGGCCGAGCCGAGGCCAAGGAATGTACCGGCGGTGTCAACGGCG
GCCGCTGCAACCTGGCACCGGCCAGTGGCTGCCCCACGGGTGGGTGGGCGAGCAATGCCAGCACTCGCGGGGCGCG
CTTCAGGACATCTGTCTCAGCCTATAATCACAGCTGTTCGGAAGTGAGGCTGGAGGAACAGTTCGAGGCAAGCTTCG
GCTACAGAAATAGTTCAAGAGTAACCTGGGGCAACTTGGGCTTGCTCCAAAACCAAAATGAGCGAAAGGAGCAAGCT
AGAGCTTTTGGGAAAATTTTAGCTGACTAATTTTACCAGAGAACTAAGTGGCTCTCTGGATTTGTAACAGATGGAC
CTGGGAATTATAATAGACGAAGTGCACATGGCTCATTTGAAGGACAGCCAAATAGAATAATGAGACTTCGCTTCAA
CCATTTTGCTACAGAAATGAGTGGGACCATTATATGTTATGATGGGACTCAATCTACGCACCTCTGATTGCTGCC
TTTAGTGGCCTCATTTGTTCTGAAGAGATGGCAATGAGACGGCTCCTGAGGTCACTGTCACTTCAGGTTATGCACCTGC
TGCAATTTTTCAGTGCTGCTATAATCTGACTGGATTTAATATCACTTACAATTTTGACATGTGTCCGAATAATTG

FIG. 2A(1)

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CTCAGGCCGAGGAGGTGTAGAGCAGTAACAGCAGCAGCGCTGTTGAGTGTGAATGTTCTGAAAAC TGGAAGGGGAG
TCGTGTGACATTCCCTCACTGTACAGACAAC TGTGGCTTTCCCTACCGAGGCATCTGTATGCAAGCGATACCAGAGGGT
GCTCCTGCTTTCCCTCACTGGCAGGGTCTTGATGTTCAATTCCCTGTGCCAGCTAAC CAGICTTTTTTGGACTCGAGAAGA
ATATTCTGATTTAAAGCTTCCCAGAGCCTCTCATAAAGCTGTGGTCAATGGAAATAAATGTGGGTGTTGGCGGATAT
ATGTTCAACCATTCAGATTACAGCATGGTTTTAGCGTATGACCTGACTTCTAGGGAATGGCTTCCACTAAACCATTC TG
TGAACAGTGTGGTTGTAAAGATA TGGTCATTTCTGGCATTACATAAGGATAAAATCTACATGTATGGAGGAAAAATTGA
TTCAACAGGGAACGTGACCAATGAGCTGAGAGTATTTTCATATTTCAATAATGAATCATGGGTA TTGTTAACTCCGAAAGCT
AAGGATCAGTATGCAGTGGTTGGACACTCAGCACACATTTGTTACACTGGCATCTGGCCGTGGTTCATGTTGGTCACT
TCGGTCA TTGCCCACTCTATGGATATATAAGCGTTGTGCAGGAATATGACTTGGAAGAAGACACATGGAGTATATTACA
TACTCAGGGTGCTCTTTGTGCAAGGGGGTTATGGCCACAGTAGTGTTTATGATGACAGGACCAAGGCTCTGTACGTTTCAT
GGTGGCTACAAGGCTTTCAGCGGCCAACAAATACCGGCTTGCAGATGACCTCTACAGATACGATGTGGATACTCAGATGT
GGACCATTTCTTAAGGACAGCCGATTTTTCGGTTACTTTGCA TACAGCTGTGATAGTGAGTGGAAACCATGCTGGTGTGG
AGGGAACACACACAATGACACTTCCATGAGCCACGGTGCCAAATGCTTCTCCGACTTCATGGCTTATGACATTGCT

FIG. 2A(2)

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TGTGACCGATGGTCAGTGCTCCAGACCTGAGCTCCATCATGATGTCACAGATTTGGCCATTTCAGCAGTCTTGTACA
ACAGACCATGTATGTTCGGGGCTTCAACAGCCTCCTCCTCAGTGACGCTTGGTCTTTACCTCGGAGCAGTGCGGA
TGCACACCGCAGTGAAGCTGCTTGTGTGGCAGCAGGACCTGGTATCCGGTGTCTGTGGGACACACAGTCGTCGATGT
ACCTCCTGGGAGTTGGCAACTGAAGAACAGCAGAAAAAGTTAAAAATCAGAGTGTTTTCTAAAAGAACCCTTGACCATG
ACAGATGTGACCGACACAGATTGTTACAGCTGCACAGCCAATACCAATGACTGCCACTGGTGCAATGATCACTGTGT
CCCTGTGAACCCACAGCTGCACAGAAGGCCAGATCTCCATTGCCAAGTATGAGAGTTGCCCCCAAGGATAACCCCATGTAC
TACTGCAATAAGAAAAACCAGCTGCAGGAGCTGTGCCCTAGACCAGAACTGCCAGTGGGAGCCCCGGAAATCAAGAGTGCA
TCGCCCTGCCGGAAAAATATCTGTGGCAATGGCTGGCAATTTGGTTGGAAACTCGTGTCTGAAAAATCACTACTGCTAAGGA
GAATTATGACAAATGCTAAATTTGTCTGTAGGAACCAACAATGCCTTTTTGGCTTCCCTCACATCCAGAAAGGTGGAG
TTTGTCTTAAGCAGCTTCGATTAAATGCAATCATCTCAAAGTATGTCCAAGCTCACTCTGACTCCATGGGTTGGTCTTC
GGAAGATCAATGTGCTTACTGGTGTGGGAGGATATGCTCCATTACAAATAGTTTGTGCAGTGGATGCCATCTGA
GCCCAGTGATGCTGGCTTCTGTGGGATCTTGTACAGACCTAGTACTGGGGATTAAAGGCTGCAACCTGCAATCAACCCCT
CTCAATGGCAGCGTCTGTGAAAGGCCCTGCAAAACCACAGTGCCAAGCAGTGCCGGACACCATGTGCCCTGCGGACAGCGT

FIG. 2A(3)

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GTGGCGAGTGCACTAGCAGCAGCTCGGAGTGCATGTGGTGCACTAAGCAGTGTGTGGACTCCAATGCTACGT
GGCCTCCTTCCCCTTTTGGCCAGTGATGGAAATGGTATACGATGAGCAGCTGCCACCCTGAAAAATTGCTCTGGCTACTGT
ACCTGCAGCCATTGCTTTGGAGCAGCCAGGCTGTGGTTGGTGTACTGTATCCTAGCAATACTGGGAAAGGAAAAATGTATTG
AGGGCAGCTATAAAGGACCCTGTGAAGATGCCGTACAGGCCCTCTGCAGGAAATGTGTATCCACAGCCCCCTTCTGAATC
CAGCATGTGCTAGAGGACAGCAGATACAACCTGGTCTTTTCACTTCTCAGCTTGCCAGTTGCCAGTGCAACGGACACAGCAAA
TGCATCAACCAGAGTATCTGTGAGAAGTGTGAGGACCCTGACCACGGGCAAGCACTGCGAGACCTGCATATCTGGCTTCT
ATGGTGACCCGACTAATGGAGGCAATGTGAGCCATGCAAGTGCATGGGCACGCATCAGTGTGCAACCAACACCCGG
CAAGTGCTTCTGTACCACCAAGGTGTCAAGGGGACGAGTGCCAGCTATGTGAGGTAGAAAAATCGATACCAAGGAAAC
CCTCTCAAAGGAACATGCTACTATACCCCTTCTCATTTGACTATCAGTTCACCTTTAGCCTGTCCAGGAAGACGACCGCT
ACTACACAGCCATCAACTTTTGTGGCTACTCCTGATGAACAAAACAGGGATTTGGACATGTTTCATCAATGCCTCCAAAAA
CTTCAACCTCAACATCACCTGGGCCACCAGCTTCCCAGCCGGGAACCCAGACTGGAGAAGAGGTGCCCTGTGTTTCAAAA
ACCAACATCAAGGAATACAAAGATAGCTTCTCTAATGAGAAATTTGATTTTCGCAACGATCCAAACATCATCTTCTTTG
TTTATGTCAGTAATTTACCTTGGCCCCATCAAAATTCAGATTGCCCTTCTCCCAGCACAGCAACTTCATGGACCTGGTACA

FIG. 2A(4)

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GTTCTCGTGACTTCTTCAGTTGTTTCCCTCTCGCTGCTTCTGGTGGCTGCAGTGGTCTGGAAGATCAAGCAGAGCTGT
TGGGCATCCAGGCGGAGAGAGCAACTTCTTCGGGAGATGCAACAGATGGCCAGCGGCCCTTTGCTTCTGTAAACGTTG
CCTTGGAACAGATGAGGAGCCTCCTGATCTTATTGGGGGAGTATAAAGACTGTTCCCAACCCATTGCAC TGGAGCC
GTGTTTTGGCAACAAGCCGCTGTCCCTCTGTGTTGTGAGGCTCCCTCGAGGCCTGGGTGGCATCCCTCCTCTGGG
CAGTCAGGTCCTTGCTGTGGCCAGCGCCCTGGTGGACATTTCTCAGCAGATGCCGATAGTGTACAAGGAGAAGTCAGGAG
CCGTGAGAAACCGGAAGCAGCAGCCCCCTGCACAGCCTGGGACCTGCATCTGATGCTGGGGCCAGGGACTCTCCACGC
ACGAGCTAGTGAGTGGCACACAGAGCCATCTGCAGGAAGGCGTGGCGGGAAATGGCTGTGCGGTGCGGGACGGAA
GACTGGAACCCCTCAAAGCATCTGACTCACCTGCATGATCACAAGCTTCTTTGACGGTTTCTCCCATCCGTTGTTCCAG
CATCTAACCTTTTACTTTTGCTAGGAAATACTTGATTTTAAATTACAGGTCCAGGGATGAGCTGATGGTTGCTGGAGGAG
GCCAGGTAGAGCCAGTGAGAGAACTAGGAATGACACTCAGGTTCACTGTGGAAACTGTTCTTGGGACTGTCTCAACT
GTGCAAAAACAAAGATGGAGTGTTTACAAGTAGACATTCGTCATCAGTTGTTCTTGAACATGGTCTTTTAAAACTA
GTCAGATGAATTAACTTGTGTTTTCATCTGAAGCTGCTATCTTTTTTAAAGATGTGCTATTTATCTTGCACGATTTAG
GCAATTATCTCTCTCCAGGGAGTACCTTTTTTTCTAGTTGAGAATTAATAATGGTCCATCTCTTTTGATCATATCAAG

FIG. 2A(5)

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[illegible]

FIG. 2A(6)

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TAAACTGCAGCATTTTACCTTTAAATGCAGTGCCTAGAGAGAGAGTATTGTCTCTTCCCCAACACTAACCCCACTCCC
ATGAAGAATTGCCGTGGAAGATGTTTTCAAGGAATTTGAACCATAAAACACTATCTGATGCACAGAACACCTCTACTTT
GAGACTCACCTCTCATAAAGCTTCTTTTTTTCACATTACTGTTAAAGACCAGACGTTCTAGAAAAGACCCCTCCTCTCATG
AGCTCCCCCATCCCTGCTACAGAACACAGCACCCCATGGCGCCTGCAGTGGACTGGCCCCCTTAATCCACAGGCCCCCC
CAGCAAGGCCAAAGGAGGCCCTGGGTATTGTCTCTCTACAAGGAAGATCCTCTTTGTTGTTCAAAGGACCAGTTTTT
CCTAGGCCAAAGAAGTCTCTCCCCATGTTAGTCTCTATGCCTTGAAATATCATGCACCATGACCCACAGCCATCTGGTT
ATGCTTATTTTTTCTTAAAGATAATGTTTATTTTTTAAAGGAAGGAAGCAAGTGAAGTTTCATTCTGTCCA
GCGGTGGGAAGCGCTGAATCCACCTGCTTCTCTTTGCAACCGACAGCAACAGCTTTCTCGGGCTCAGGGCAGAA
AAAGGGAATGGCAGGGAGTAAGAGGCGCTGGGCTCGGAGCCTGTTTCCAAGGAAGGAATTGGTTGTCATCTGGCAGTGT
GCGGTCACAAGAGAGCCTGTATATAAATTAAATAGTCAAGACAACACTGACCTTGCACCTTGACATAACTATACAGT
AGTGTCAGAAATGTTCAGACATTCGGAGTGTACATAAAACAGAAAAAATCTTCATGATTTTTTATTAAATATAACAATG
TCTGAGTTTACCTAAGATGTTTTTGTGCCATATGCTGGATATCCAGGTTCTCGCCAGGCCCGGATACATGAATAACAA

FIG. 2A(7)

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ACCCAAGAAACGCATCCCCATTGTGTGATGTGTTAGATGCACTGGCACCAATTAGGATTTCTTAAACAGGACTCA
TCTGTAGAGTGCACATGAAAAATCAGGCAGGGAATCGAAACGACAGCGCTGGAGGAGACTCAGGAAGCAGAGGCGTCC
CTGCCGCTGCCCTTGGCCCTGCAAGCACATCATGACCCCTTCTGGCAGCCTCTTGGTGCTCTGGGTAGTGAGGGATGAC
CAGTCTTGTCCTGAGAAATGTTTCTTAGTCTTTAAGTTCAAGACTAACCTGTAGCAATCAGACTTTCCAAAAGGGG
GTTCTCCATTTTGTAGTTTGTCTAAATTTTAAATGACCATTTCTTGAATCAGTTTATTATCTGAAAAC TGGGGG
TGGGAGTAGGGAGCTAGTTTGTGATAAATAGTTCCCATTTCCCGTGGAGAAATTGACATACCCTGGACTCCTGTGTG
CCTCTGCCATCCCTGCACACAGCCTGGGGAGAAGCCTGTGCTCCCGTGTGGAGAGAAGCAACCCAGATCCCTCG
AGCTAACCCGGAGGAAGGCAGTCC TGGACAGAAAGACTGTACGAGAAAGTAAGTACTGGACTACCCGTGGGTAAGTCC
TGCCATTCAAGACTGGAGACACCCTGGGAAATAAAAAGAGCAGGGCAC TGTGTTGGGAAGAGGCATTTTACCTTCCAGT
GCAAAATCCTGCTCTTTGATTTAATGGGGTGTACTGGGGCCAGGGGCTGATTACACTTCC TTGGGAGATGGTGGTGT
CATGAACATCTTTGATCCTTCCATTTCATTTATTATCCATCCATTCAACAAGTATTTGCTAAACACTAACTTAAGCTA
ATGCTAGGGTAGTGACTGAGATGTAAAAATAGATTTTAGAATTAACAATAATCCAAAGTCTCACACCCCTGTCTATCCC
AGGAGATCTTTCTTGTGGTGGTTTCTGTGAGAAATTGGCCATCCTGAGGACACAGCCAGGACGGCAGAGGCCCTCCTGGC

FIG. 2A(8)

SUBSTITUTE SHEET (RULE 26)

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CTCAGGGCATGCCCTGCCCTACCTTCTGAAATGTTTACCCCATTTGACCAAACTTGGCTCCAGCCATTGGCGGTGGTTTCTA
GATAGCCAGGCCACCACAGAGATATTGCCCTTGATGAGAGTCAACACCCCTGCCTACAAGGAGATGTTTGAATGGA
GAGGAAAATTGGCACCTCATCTTTTAAAGGCAGTAATGGAATTGATTTTCAGTAACTGAATTTGTGCACAAAACATTCT
AAACACTAGTGAAGCCTGTTTCGTTGAACTAATTCGGCTCTGGAAATGTTTTTTTAGTTATTACGATTTTCGT
TTGTTTGGATTCAAGCTTAGTTTGTTAATATGTATAATTTAGCATCTATTACACTCATGTAAATATGGAGTAAGTATTG
TAAACTATTTTCATTGCGGGGATTGTGGGTGTTATACATACATTTAGGACTGCAATTTTGGTATTTTGTATTGTAA
AATAACAGCTAATTTAAGCAGGAACAAGAGAACTAAGGAGGTCTGTGCATTTTAAACACAAATGTGAAGAAGCTTGAT
ATAAACAAAAGTAAATACTATAATACAAACTTCCTTCTGAAATAAAAGTAGATCTGGT

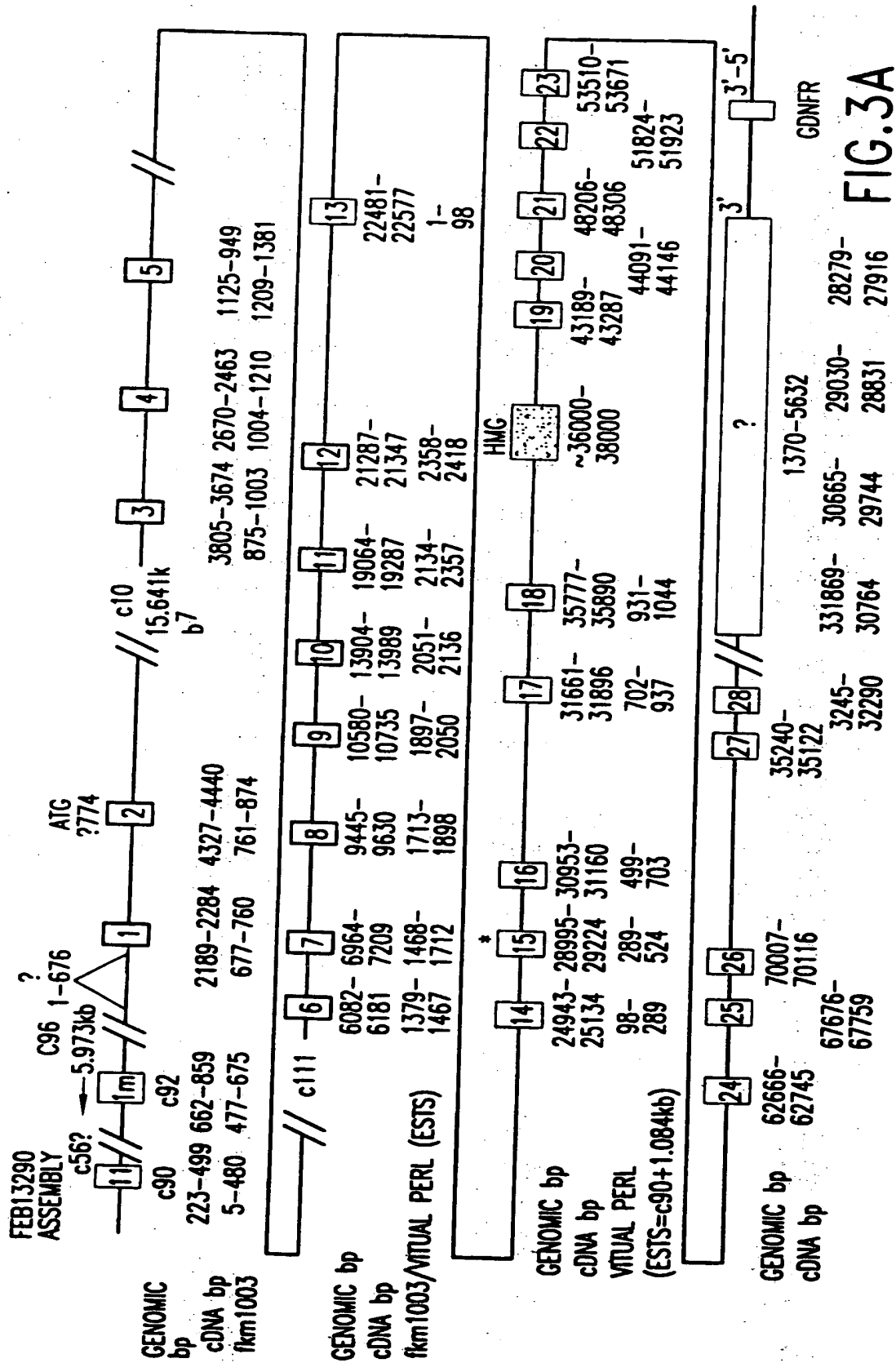
FIG. 2A(9)

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MRLRFNFHATECSWDHLVYVDGDSIYAPLIAAFSGLIVPERDGNETAPEVTVTSYALLHFFSDAAYNLTGFNITYNFD
 MCPNCSGRGECKSSNSSSAVECECSENWKGESCDIPHCTDNCGFPHRGICNASDTRGSCFPHWQGPCCIPVPANQS
 FWTREEYSDLKLPRASHKAVVNGNIMWVGGYMFNHSYDYSWLYADLTSREWLP LNHSVNSVWVRYGHSALHKKDKIYM
 YGKIDSTGNVTNELRVFIHNESWLLTPKAKDQYAVVGHSAHIVTLASGRVWMLVIFGHCPLYGYISVWQYDLEKN
 TWSILHTQALVQGGYGHSSVYDDRTKALYVHGGYKAFSANKYRLADDLYRYDVDOTQMTILKDSRFFRYLHTAVIVSG
 TMLVFGGNTHNDTSMHGAKECFSSDFMAYDIACDRWSVLPPELHHDVNRFHSAVLYNSTMYVFGGFNSLLSDVLVF
 TSEQCDAHRSEAACVAAGPGIRCLWDTSRRTSWELATEEQAELKSECFSKRTL DHRCDQHTDCYSCTANTNDCHW
 CNDHCVPVNHSCTEGQISIAKYESC PKDNPMYYCNKKTSCRSCALDQNCQWEPNQEIALPENICNGWHLVGN SCLK
 ITTAKENYDNAKLSRNHNAFLASLT SQKVEFVLKQLRLMQSSQMSKLTLPWVGLRKINVS YWCWEDMSPFTNSLL
 QWMPSEPSDAGFCGILSEPSTRGLKAATCINPLNGSVICERPANHS AKQCRTPCALRTACGECTSSSECMWCSNMKQCV
 DSNAYVASFPFGQCMEWYTMSSCPPENC SGYCTCHCLEQP GCGWCTDPSNTGKGKCIEGSYKGPVKMPSQASAGNVYP
 QPLLNSSMCLED SRYNWSFIHCPACQCNHSHKCIHQSI CEKCEDLT TGKHCECTISGFYGDPTNGGKCQPCCKCNHSHSL
 CNTNTGKCFCTTKGVKGDECQLCEVENRYQG NPLKGTCTYYTLLIDYQFTFSLSQEDDRYYTAINFVATPDEQNRDLDMF
 INASKNFNLNTWATSFPA GTQTGEEVPVWSKTN IKEYKDSFSNEKFD FRNHPNITFFVYVSNFTWPIKIQIAFSQHSN
 FMDLVQFFVTFFSCFLSLLVAAVWVKIKQSCWASRRREQLLREMQMASRPFASVNVVALETDEEPPDLIGGSIKTVPK
 PIALEPCFGNKA AVL SVFVRLPRGLGGIPPPGQSLAVASALVDISQQMP IVYKEKSGAVNRKQQPPAQP GTCI

FIG.2B

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AGATTTTATGCCTTCGTACACGCCTCCCATAAGATGGACAAGGTGTACTA
ATTACTGCCATTACTGTTGCTGACCCAGAGGTCAATGTCTCACATGGC
CTCTACTGGCACTGTCTGGGCAGAACTGTATATCCAACCTGGTGAACCTG
AAAGCCCTATGACTACTTGGTGTCTCTGGTGCTAACCTAGTCGTTGGGG
CATCTTACTGTATCCTGGTAAGGAAAGACATCCAGGCTCCCCACTTAYMK
WWACYRGYWMRGMYCAKGSYMGRGCRYAAWKTKCTGTRRMRTCTGGCTGGC
ATAGAGACATTACTATTGAAAGTTTTGTCTTTCTAAATCCTTGGACTAAA
GAGAGCACAAGATTTTCTGGAAGATCTTGCTTTAAATTTTTTTTTTATTC
TTTTGAGATGCTACATATAATTAGAGGCCCTGCACATGGAGGCGAGAACC
CCACCTCTGGGCTACATCCTACGTCTTTTCTTAGGGTATTTTTTTTCT
TTCTTGACCTATCAGTATTACTAAGTTGCAAATGTGCTCAGCAGTAAAT
TTAACATACATAGGCAAAAAGAAAAGTCTCAGGACACCCTGCCTCACACT
GTTTACTGTGCTCAGGAGTACTGAGCCATACTGTTTTCTTGCTGCTGCTT
TTTTTCTCTGGTTGTTTACACACAGTGTTCAAGGTGTGTTAATCATAGT
TAGTATTTCAATTTTTTCTTAGGTCAGCAAGAAAGCTCACAGAGGAAGAG
TGCTTTGCTGCCAGCCTGATGACCTGGGTGACCCAAGTGATCTCACCTAC
AGGGTGGGAGCACAGCACAGCATTCCAAGTCTTTTTCTGACCACACAGGC
ACTATGGCACACAAACACACAGGATACATAAATGTTAAAAAAAAAAAAAG
ACTTTTATATTTTTCTCCATATAATTTAAAAGATTCTCTTTCAACATTC
CTTTTGCAAAGCAGTATCATTGTGTTTGTATATGTGTGTCCTTCCACATT
TTGTCTTCAATTCTAAATTTTTAGAATTGTTAGCCTGGTCCTCTCATTTTC

FIG.3B(1)

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TACTACTTTCTCTAGTAAACTGTCCTTTTCATATTACACATCGCTCTCCTG
TCACCTGTTTTAGAGCTGTCATCCATTTTATAAGGTTACTTCACTGTTCT
ACACTACTTTGTGTCTTTTAATTACTATGCCTGGGGTGATTCAAAAAGTG
TCTGTGATGGGTTGGTTGAGGATGGCTCCAATAGGTTCAACACTTGGTCC
TGATTGGTGGAAGTGTGTTGGGAAGGATTAGGAGGTGTGACCTTGTGGGG
GAGTGTGTCAGTGGGAGTGAGTGACCTTTGAGGTTTCAAAGCCCATGCT
AGGCCAGTGTCTGTCTGCCTGTCTGTCTGTCTCCTCCCTTTGCTCTTTC
TTCCCTCCCACTTGCTTGCAGATCAGATTCGAGCTCTTAGCTACTGCTCC
CGTGCTGTGCCTTGCTGCTACCATGCTTCTTGCCATGATGTTCATAGACT
TACTCTCTGAACTGTAAATAAGCCCCCTAATAAAATGCTTTCTTTTAAA
ACTGCCTTGATCATGGTGTCTCTTCAAAGAAATAGAACATTAACAAAAAC
ACTATACCAAAGTGCCTAATAGTCCTACTAATTTTATGATGAGTGCTAGT
GCTTTATAATCACTAGAAGAAAAAATTTCCAGGCCATAAAATTAACATGG
TTTTAAGTATGTATAAATCTTGTCTTGAAATCTGTTTTCTATACTAACT
CTAATATGATAATGTATATTCTACCTTCAAAAAGCACAAATAAGACTTC
AAACCCTGGGAATTGTTAGACAAAGGCCATTTAATACTAATAAGCTATAA
ACTGAAACCATCTGATATATGAAAAGTATTAATAAAATCAAGATAAAATA
ACCCCTATTTATATAACTTACTATATACCTAAAGCAAAATATCAAAGAAA
GTACCTTAAAAAGATAAATTATTCTTATTTTGACAATGAATTCTTTGGGG
CGTTAAATTGTAGAATATCAACACATATCAAGAAAGTTTAGAAGAAAAGT
ACCAAAGTTTAAACAGACTTTCCTCGGTAATTACTGGTGATTTCTTGGCT

FIG.3B(2)

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TTTTTTTTTACACTGCAGTTTTTTCAGGGTGGAACTTAAGCTTTGTACA
GAAGCACTTACCACCACTCTCAGAGCTGGAAATGGCTCAAAGGGCAAAGC
ATTACAAGCCTGGCAACCTGAACCAAATACCCAAAACACTTGCAAAGGTG
AAAGGAGAAAATACTCCAGGAAGTTGTCCTTCGAGCTCCTCTTGACA
CCACTGTATACACCCCCTTATATACACTCAGTTACCATAAATAAAATGTT
TCATTATAAAGACACTTACGCTAAAACCATGCTGTAATCTGAATGGTTGA
ACATATATCCGCCAACAACCCACATTATATTCCATTGACCACAGCTTTA
TGAGAGGCTCTGGGAAGCTTTAAATCAGAATATTCTTCTCGAGTCCAAAA
AGACTGGTTAGCTGGCACAGGAATTGAGCATCCAGGACCTAATAAAAAAA
AAAAAACAACAACAACAACAATAGCTTCACAAAATGCAGCCTGAAAGT
TTATAGTATTCCAAGTTCCAATCTAAGTGCAAAGAATATTTAAAGACTTG
TGGGGCTAGAGAGATGGCTCAGTGGTTAAGAAAACGACTGCTCTTCTTG
GAGGTCCTGAGTTCAAATCCCAGCAACTACATGGTGGCTCACAACCATAT
GTAATGGGGATCTGATGCCCTCTTCTGGTGTGTCTGAAGACAGCAACAAT
GTAATCACATGAAATAAATAAATTAATTTTTTAAAAACAGACCAGAAAA
AAAAAAAAAAAAAAGACTTGTGTTTCCTTTAGCACTTAAGGGCAAACATC
TTTAACTTGTGGGGTTTTAAAGGTTTTTACATGTACAGGTATTTTGTTTA
CATGTATGCCTATATACCACTTGCTTGCTTGGTACCCAATGATGTCAGGA
AAAGGCATTGAATCCCCTGGAAGTAGAGTTACAGATCTTATGAGCTACTT
TGTGGATGCTAGGATCAAACCTGAGTCCTCTGGAAGAGCAACCAGTACTC
TTAACCAAGAAGCCATCTGCTTAGCACCTAACATGAGTTTTTAACTTACT

FIG.3B(3)

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CAAGATACAGACCAAACCAATCACTCCCTTATAAAATTTAATACTACAC
ACTTTCTGATAATTTGGCAATTTCTGATAATCAGGTAAACTTTTTTAGA
GGTAAAAATCTTGCTGAAGCAACATTTAGTAGAAAGGGTAGACCAAGGGG
TTATTATATTAACATCATGTGGAAAAGGCATTAGGGTTGAAATATAATGAC
AGATCAAAATCGATCTTCTGGCAAGTCCAGGCGCTGAATAGATGAAAGAG
ACAAAGGGAGAATTGGACAAACTAAAAACATTTACATGAACACTTACTTT
CTGAGGACCTAAGCATAGAAGGAAAATCACTAAACCAACGATGACTGCTT
CCTCAATACCCCAGGGAATTCCTACAGTACCTTAGTACCCGGTTGTGTT
GGGTAATGGCACTAGATGACAGCACTGAGACTCTAAGGAACGCTTGTCCT
CCTCTCAGCTTGAGTCTCTGCTTCTCTATCACCAGACCATGTTCCCTAAT
TCCCACGAATGAGTTGCAAAGGATTTGTCAAACCTTTCACAATTCTAAG
CACATAGATAACAACCACATATATGTAAATTCAAAGAATCTGAATAAATG
GAGATGAATGCTTAAATGCCACCTGATACATGATTAACATAAGGCGTATG
GCTGCTAAAATAAACTCCCTACAGTTCACTAACTCAGAACTTTCTGTGAG
GGAAAGGACTTTGAAGGGCAGCTCCTACCCTGCCAGTGAGGAAAGCAGGA
GCACCCTCTGGTATCGCTTGCATTACAGATGCCTCGGTGAGGAAAGCCAC
AGTTGTCTGTACAGTGAGGAATGTCACACGACTCCCCTTTCCAGTTTTCA
GAACATTCACACTCAACAGCGCTGCTGCTGTTACTGCTCTTACACTCTCC
TCGGCCTGAGCAATTATTCGGACACATGTCAAACTACAAAGACAGGAGA
AAACGAAGTCAACAATTTCAACTAAGCAACATTGCAACTAATGCAGACCT
TCCTCCTTCAGTTTAAGTTCAGTTCATTTGCAAGTGTGACTGCAGGACTT

FIG.3B(4)

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ACCAGTTAGCCCAAGTGTGCTCACAGAGCTCTGTGTAGCTAGAGCCCCAG
GCTCAAGTAATGAAATCAAATCAACCTTGCTGCATTACATATGAAGAAG
GAAGAATAAATAACTCACAAAGTTAGAGAAATTACAAAACAATAGACATT
TGTGCAAAATCACTTAGACTTAGCTCAAGACTGGCAACCAGGATCCTACT
CTTTCTGGTAGCTCATTAGTAAAGAGTTCTACAAAAGCAGCAAGGTCATG
CTAGGAAGTGGAGGAAGGAGAGGAAGCCAATGAGCTGCCAACATTCACGG
TATACATTTCTCTGTAAAGATTCTGAGAATTAACAGAATTTAAGATTATT
TTCCAGTGATGTAGTTAAAGGTCTTTAGTAACTTTTATCAGCTTAGAAGG
AGAAGAGCAGTTAACTTCATGTATGAGTTTAAGTGTCTCATGACTTAAGA
TAACAGTTTTGCTACAATTTGAAATGCCATACTTCAGACTTTTTAAAGGG
GTGCATTAGTGGACTATTACAATAGCTTAAAAATATAGATTTCTCCTACT
GATGATTATTACTGAGACACTACTAGTCTTTATTAAATTCAGTTAGCAAA
ACTCCTGACATTTTCTTCCAGCAGCGGAAGAATGTCTCTCTCTCTTAGGA
GATCCTCAGTGACAAGATCTAGAAAGACCAAGAACTGTGGTCCCAACCAG
TGGGGCTGATATTTGTTTAACCTTTTAGCTCCTGTTTCTTCAATTATGAA
AAAAAAAAAAAAAGAAGAAGAAGAAAATCCATGTTAAAATTTAGCAAGGAG
CCTGACTAGCTAGAAGCCTCCCTCCAATATATTAGTGTTATTAAGTCATT
TGAGTAGTATCACAAATATTAAATCTAAATATCTTACTTGTAAGTGATAT
TAAATCCAGTCAGATTATAAGCAGCATCACTGAAAAAATGCAGCAGTGCA
TAACCTGAAGTGACAGTGACCTCAGGAGCCGTCTCATTGCCATCTCTTTC
AGGAACAATGAGGCCACTGAAATGTAAACACAGACCAGATTACAGCAACT

FIG.3B(5)

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TCACAGAACTGTCTATATGTTACTATTTGATCCTGCTGCTCCTGTTCC
AACACACACTGTAAATGTGACTCTAGCTGGCCTCAAATTCACAGACCCAC
CTGCTTCCACCTCCTGGGTTATAGGCATGCGCTACTATGCCCAACATCTA
AAAGGATTTGAAATCTATGACTTTGATTGAATTTTTGGTTTTTTGTTTT
GCTATAAACTTTTTATTATAATACTCTCAAGTCTCTACAATAACATTATT
AACAACTTTATGAATTGACAACTGTCAAATATATACTGTTGAAAGAAAA
TACTTTACATATTTTTGTAATATGTATCATATAATCTTTTTAATGTATTT
TATAGATGTCTTATATAAGTAAAAATAGAAAAGTTTACTGATTTATAATC
CTTATACTATTAGCTTTCAGACGTATTTTTGTTGTTAACTGGTAACACA
TTTTATGTTTATAATTCACAATAAGCACTGCCACTGAAGGTGCCAAAGGC
TCCCTAGAATCTCAGTAAGAACCTAGTGGGTAATATTTGAAGTTTTGGAT
GCCAGTAAATTCATGTGTAAAGATTTATTGAGTAAGTGACTIONACCAGCGGG
ACAGTGGTGGTGCACGCCTTTAGTCCCAGCACTTGGGAGGCAGAGGCAGG
CGAATTTCTGAGTTCGAGGCCAGCCTGGTCTACAGAGTGAGTTCCCAGGA
TAACCAGGGCTACACAGAGAAACCCTGTCACCCTGTCTCAAAAAAAAAA
AAAAAAAAAAAAAGAATATACCATTTTTAAGGCATTTGATCCACAAATCA
TACCACCTTGTTTTACAAAAGATATATATTAACCTGAAGGCTGGAAATGG
TGGCACATGTCTTTAGTCCCAGTATTGGGAAGACAGACCCAGATGGATCT
CTGAGTTCAAGACCAGCATGGTCTACATAGTGAATTCCATGTAAGTTTGT
CCGTGTGTGTAACCTGAAACCTCATTATAGAATGGAAGTGTCTACCCAC
CCCACTTACCAACAGTAAGGAATATTATGTTGGTCCCGCTCATTTAATAC

FIG.3B(6)

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ATGGTGTACTCCCAAGGTAAATCATTTTTCATGTTTAGTCGCTCCTATTAT
TTTTTCCATTATCAATTCACTACAACACTACCACCAATCACATTTAGCC
ACTAGAAAAGCCATGTGATTTGCTCCACACATACAACCTTCACTCAATAAA
TAAACATCTTATCAGTACTACTCTCTCTTTCACTCACTCAATCCCTAGTC
CCCTAAGTTTTTGGACGATTACACCAGGTAAATTCCTACTTCAGGGTTAT
GACCATCTTAAAACTACGACCTAGCAATTCTCTTTGTATAAGAAATACT
TCCCCGTATATACACAGAAAAACAAAGAACACTACTACAGCACTATTGAG
ATGACAACCTGACTAAAAGTCACCTAATTGCTTATTTATGGGAGTTGATTA
AATTAGTCATTACAAATCTGTAGGTCTGCAAGACTAACCAAGAGCTTCGT
GAGGACAATAGGTAGGGCTACCCAGAGAAACCCTGTCACCCTGTCTCGAA
AAAAAAAAAAAAAAAAAGGGAGGCACAGAGAAAAACAACAGGCCCGGGGT
CCTGTACATCTATGTAAGCGTAGGTACATGCACATAAAAGTGACTACAAG
AGAACATAAACAGAGAGCGCCGATGAGAAGAGGATGGGATTTTTTCATTTA
ATTTGCGTGTATGAGAGCACCTATATGTGCATGTTATCCGCACCAAAGTG
TGTAGGGTACATTATGTGAGTGTGCCTGCAGAGGTCCTGTCAGGTGTCT
TCAATCACTCCCCTCCTTTTTCTTCTGGAGATAAGAGTTTCATGAAGTAG
TACTGGCTGGACTAGAACTCACTATGCAAACCAGGCTGGCCTTGAATTCT
CAGAGAGCCTCTTGAGTGCTGGAATTATATGCATGTGCGGCAACACAGCC
CACCTCATTTTGGGGGTAGGATCTTTCACTGAACCTGAGCTCACTGATT
GGTTAGACCGGACTGGCCAGTAAGTTCCAGGACCTCTCTTGTCTCCGCCT
CTTCAGCACTGTGATCACAGGCTCACAACCACACCTGGACTTTTACTTGA

FIG.3B(7)

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GTCTGGAGATCTAACTCAGCTCTCCATGCCTGTGCAGAAGGAATTAA
CTGAGCCAGCTGTCTCAGTATCAAGAGAGAACATAGGAACTGTAAGATT
TGACAGTACTCTAGGGCTTACAGAACACCGACACATTTTCTACTATGTAT
TCAGTTAATAAAAGAATAAATACAAACAAAAAACATGAGAAACATATAG
AGGCAGAGACAGACAGACACACACACACACACACACACACGCACACAC
ACACACACACACACACGCACTTAGACGGGTGTGGGGGAAGAAAGAGCAAG
GCCACCTAGAAACAGGTACGTTCCATGCAAATGATCACAGGAAAGGATTG
GGGATTTTAAACCACTTGTGGGAAATGCTGTACTCTCCTATTCTAGCACA
GATTTGAGGAAAAAGTAGACCAGAGAGTCTGTCCTTCCACATATCCTGGA
AAGTCACTGACATGTCCAAGTTTTGATTTCTTCATAGGGACAATGAGAGA
AACCAGACTATCTCACAGCAGCACAGCAAGGACCAACCAGCAGAGCAGG
AGAAGTGCTTACAGCAGTGTGCTGCTAGAAGGTGCAACAGTCTTCTTACA
GAGGGCATTAAATATGCAGGATGGATAAGTTTGCCAACTACAACCTACAG
AGGCTGGACAAGGTAGGACAGCTTCTTCACTGTCAAAGACGTTTGGGCAG
TTGCTTCTATTTACCTTAAATCAAACCTGTGACAGCTGTGGCATATATAG
ATTTCTCCCAGAATGAAAACACATTAACCTCACTTATGTCAATAATATGGA
GTAAACACAAACATAGTCTATCTAGCTCAGCATGCAAGACATGTGAGGAA
GAGGAGCTACTGTGAGTCCCTATCCCTGTCCCTAAGGAAACCAATATATG
TAAATGTAGTCTAAGCTGCAGGCAGTTCTTCAACTGCCTACCCCAGGCTG
CTCACCCTTCACATTCTAAGCACAGACTAGAAAGTATGATCAACCTCTG
AACACTGTGCTATAATGTTACCATCAATCTCACACACAAATTTTCATAACA

FIG.3B(8)

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TTTTAAGTAAGTCTATGATGATTCTATGTTGTGTCCCAGTTATATAAGAT
CCATAGGTCACAGGGTAGACATTCAAGGACACCAACATTTGGAATTTTGG
GTTTTTTTGGTGTACTGTATATACTTGCTAGTGCAGGTACCCATGCTCAT
GTGTGTAGAAGTTGGGCGTCTTTCTTCTATCACTGTCTACTTTATATTTT
CTTTATTGTTTCATTTGATATGTATAGGTGTTTTGCCTGCATATAATGTGT
ATGTTTGTGCCAGAAGAGGGTATTGAATTCCTGGGACTAGAGTTACAG
GTGGTTGTGAGGCACCATTATGGGTACTGGGACTCAATCCTGGGTTCTCT
GGAAGGGCAGCCAGTACTTTTAATCACTGAGCCATCTCTTTAGCTTCCTT
CGTTCATTCGTTGTTTCATTCTTCATTCTTCATTCTTCATTCTTCAGAGG
ATTGAGATACCTTCCTCAGTTAGGCTGGCTAGCCAATGGACTCTGGGAAT
CTATCTGTTTCAGCTATTCTCTCCTTCCCCATCCAAGTGCTGGGGATACAG
GCAGGTCTACTGGGTTCATTTTGAAAAATTACAGAACTATGTATTTTCT
TCATAAATCTGAAACTCAGCATAACTGTCTCAGGCTAACATGGAATCCCT
AAATATATATGAGGCACAACCTGACTTTACCAACTGTACTATGTAAATTT
GCTAGTATATTAGTCAACACTTAATGGAAAAACATCTGATAAAAACAAC
TACAGGCCAATAGGCAAGGAGACACTTGGGGAGGTGGATTCAAGGCAGTC
ACTGGATTCTTGAATTTAAGTCCAGCCTAGGCTACATGAGATTCTGCTTC
AAAAAATAACAATTAAATTTATGGGGGAAAGAATGATGTATTTTGGTTT
CAGAAATTCCATCCTATCATCCAAGGGAGATATTGTATAACAGCGAAGTT
CCTCAGCTCACAGCAGTCAGTAGCATATAGACAATCCTGGCTCCAAGCCT
ATGAAAACACAGCCTGTACTAAAGGTGTGTTCTGTGTTTTGAGTGAGAT

FIG.3B(9)

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GTGCCCCCTAAGTCTTGTGTATTTGAATACTTGGCACTCACTTGGTGGCG
ATTTGGGAGGAATTAGGAGGTGTGGCCTTGGTGGAAAAGGAGCATCACTA
GGGTCAAGGTTTCAAATCCTCCTGCCATCATCCCCAATATGTCCTCTCT
GCCTCCTGCTTGCAGTTCAAGCTATGAGCTCTTAGTTACTACTTCCACCA
CCTACCCCTGCTATCTCTGCTCCATCATCATGGACTCCTATTCTGGTGGA
ACTGTTAGTCCAAAAAGTCCTTTCTTCTACAAC TTGATTTGATGCCAGA
TCTAGCCCCCAGCCTAGCTAGCAATATACCAAGGTATACCATCTTGAAC
TCTAGGTGTCTCTCAATCCAATCAAGCTACATAAGATTAACCATCATACC
TAGTCATCCCCAATCAGTGTATCTCTCTCCTCCAAGACTATAAGCTCC
TCAAGGGTCAAATATGTAGAAAGGAAGAAAGATTCTCAAAGGTCAAGGA
TCAGACCTTGGTGAGGATTGAGCACTGTCTACACTTTGCCTGGTAAAGAA
GGGTCCACAATGTAAAAGAGAACTGACCTGAACAGTTTTCAATTAGGTGC
TAACAAATGTCTCATACGTATTGAGTTTCTTATAAATAAATAAATAAATA
AATAAATAAATAAGCAAGCAAGCAAGCAAGCAAGCACTTAAGAGCACTAGCTGC
TTTCTTCTGAAGACCTGGTTTCAATTACCCAGCACTTATACAGAGGCTC
ATACCAATTGTAACCTCCAGTTTGATGATATCCAACATCTTCTTCTAGCCT
TCAGACACCAAGCACCAAGCATGTAATGGTATAACACATGTATACCAAAC
ACCCATACAAACCAATTTTTTAAAAAATATTCGAGCCGGCGTGGTGGCGC
ACGCCTTTAATCCCAGCACTCGGGAGACAGAGGCAGGTGGATTTCTGAGT
TCGAGGCCAGCGTGGTCTACAGAGTGAGTTCCAGGACAGCCAGGGCTGCA
CAGAGAAACCCTGTCTCGAAAAACCAAAAAAAAAAAAAAAAAAAAAAAT

FIG.3B(10)

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AGTCATTTTAGGGCTGGAGAGATGGCTCAGGGGTTAAGAGCACTGACTGT
TCTTCCAGAGGTCCTTAGTTCAATATCCAGCAACCACATGGTGGCTCACA
GCCATTTGTAATGGGGATCCAATATCCCATTCTGGTGTGTCTGAAGACAG
CTATAGTGTAATAAAATAAAGAAATCATATAAATAAAATAAATAAATCT
TTTTAAAAATATTAATTAACCCAGGCTGAACCTAAACTTACAACTTCCC
ACATTAGGCTCTTTAATGCGGGTGTTATAGGTCTGAATACCAGCTTAAGA
ATAATATTCTTCTGAAGAATGTGCCCTGGTCAATCACCATGACCACACCT
GCCAACAGGTCCTTCATAAAATACTTGGTATATGTTGAATGTTCCATAAA
ATTATGGAGCTAGAAAAGGTAGTGAGCTAGAAGGATATTAAAGATATAAA
CCATTGCCCCAGTGGTCCTCACATTTGTCTAGTAATAGAACGTTGTAAA
CTGTTTTTATTTAGAATTTCAATATATAAAAGACAAATATGAAATAGTCC
GGAAGCAAATTAAGCTACAGCTTGCAGCAAAGCCAGATAGAATGCAGATT
AACTAACACAGTACCTTTGTCTTATGTTTTAGATGCTAAAGTCTAGTCT
ACAACCCCAGCTGCCCTTGAACCTTAGCAGTCCTCTTGCTTCAGCCTCT
CATGCTGCTAGGGTTAAAAGTATGTGCGACCACACACAGTTTTGAAGTTT
AGAGCACTTAAATGATCTATTCAGCAACTCAGGCAGGATTTACACTGAAA
GTAAATTATCTTATGAATCCTTTTTGGTTTTCTTTTATTCATTTCATTC
ATGCACCTTACATGAACTATCTATTGCTAGGCTGTCTCTATACTGGATGC
TCAGCACATCACCAACATGCCGATTCTTCTACTGGTACAATGGCAATGCT
GAGAAAACCAACAACCTAAGACAGTAGGGAGGTGGTGTCTCTGATTGTTG
GTGTTGTTGTTGTTGTTGTTTTGGTTTTTCGAGACAGGGTTTCTCTGTGT

FIG.3B(11)

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AGCCCTGGCTGTCCTAGAACTCACTCTGTAGACCGGGCTGGCCTCAAAC
CAGAAATCCGCCTGCCTCTGCCTCCCAAGTGCTGGGATTAAAGGCGTGTG
CCACCACGCCGGGCTCTGGTGCTCTGATTTTTAAATACAACAATTTTCAG
CTAGCAATGTAACCTCAGTAGTAAATGCCTGCCCAGCATGCACAAGGCTC
CAGACTGGACCCTGAGCACCACAACACTTTTTAAAAGATGTGTTTATTTT
ATTTTATGTGCATGAGTGTTTGCTTACATGAATGTCTGCACTGTGTTTA
CCTGGTGCCTGTGAAGGTTAGAAGGCAATGGAGCTATGGAGAGTTGTAAA
CTACCATGTGGAAATGGAGCTATGGAGAGTTGTAACTACCATGTGGGTA
CTAGGAATTGAATCAGGGCACTCCTCTGCAAGAACAACAAAGGCTCTTAA
CAGCTAAAATATTACTACAAACCCACACCACAAAATTTTAAATTGATAGA
CATTATCACCTTAGTTCTAGATAGAGAATGTGCTTGGCATTGTAAGTACT
AAAAAGGTTTTGGGGTGGATCTTTTATATTATCTCACTATAATTTTATAA
AATTAATACTCAAATATGTTATAAGTTAAGGTTTTTATTTTTGTTTTTCA
TTTCTGTATTTTGTCTATGTAGCTCTGCCTGGCCTGAACTCATGGGAAC
TTGACTGGCCTCAAACCTCAGAGAGACCTGAACGGCCCTGCCTCCAAAGAG
CTGGGACTAACCATGCCCAACAGTAGGTAGCTTTAATACCTAACCAGTGT
ATTAGTTCATGCTCTCAATTAACCAACATTCTCTACATACAGAAATTTT
ATGCCTATTTAATCAAATACACAGTCTAAGTAACTCTAAGTACAACTGC
TTGGCTCATATTCTTACAATGGCTATGGCTAGCTAATTCAAAGGCCAGTC
ACATAAAAGGGTCTCTATGAATTCTGATTAACAAATGCAGTTAAATAGAT
GAATTCCTAAAAAGTAGTATCATAATAATATCATATTTAGTTTTTGTGCT

FIG.3B(12)

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TCCATTATAGTTTGAGGTGCCTCCTCCCATATGCAAGGTATATTTCAAA
TAATAGATATATACATGGTTAACACATGGCAAATGCCATTTTAAATGCTT
AGCACAGCCTGCTCTTTGGCTCCATTAAGTGAACTCTTAAGTTCTCAGT
TAAAATAATTGTTGGAGAGCTATAGGAGCAATGGGTGGAGAACTAGTCTT
CTAATTTGTCCTTTGCCTCCTTGCGTACTAAGTAGTCCCTCCCTCACTAT
GTGGCATTCCAGCAGACTACCACCAAGAGAAGAACAGAAAAGTGTTGATT
TCTTTCTAAAGTAAAGAAATAAGGGGCCAGTGAGATACCTCAGCAGGTCA
AAGCCATTTGCCTAGAAACCAAAGTTCAATCCTTGGAAGCCCTGTAAAGG
TGGAATTAGAAAACAGACTCCACAAAAGTGCCTCTAACCTCCACTCGGG
CACACATGTGCCAACCCTCCATTCTCCCTCCCCACATACAAAGTAACA
ATAAACTTTTCAGAAAATTTAAGTTGCTACGCATGGTGATTGATGAATGTC
TTTAATTCTAGCTCTTGGAAGCAGAAGTGGGTGGATCTCTGTCAGTTCA
AGACCAACCTGGTCTATATAGTGTGTTCCAGGCATCCAGGACTACACACA
CACACACAAAATTACGTGAAGGAAGTAGAATGTTTGAAGGAAAGAAGTCT
GGAAATGGGGATGGAGAGAGACCTCAGCAATTAAGAAAAGGTCTTGCACC
GGACGTGGTGGTGCATGCCTTTAATCCCAGCACTCGGGAGGCAGAGGCAG
GCGGATTTCTGAGTTCGAGGCCAGCCTGGTCTACAAAGTGAGTTCAGGA
CAGCCAGGGCTACACAGAGAAACCCAGTCTCGAAAAAACCAAAACCAAAA
ACAGAAAACCAAGTATGATAGGTCAGGCAATTGGATCGAGACAGGACACTC
AAGATAGCTAGCCTGTGCAATATAGAAAGAAGTCTCATGGAAGAGAGAGG
GAAAGGAAGGAGGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA

FIG.3B(13)

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GAGAGAGAGAGAATGAGAGCGAGAGAGCGAGCGCACCTCAGTTGATAC
AAGATTGGGGCCCTGAGTTCCATCCCCAGCATCCCATAAATTGGGTGTAG
CAGCACACACCTGTATCCCAGCAGAGAGGGCAAAGACAAGTTCAAAGTCC
TATATGGAAAAAGTGTGAGATCAGCCTGGAGACCTGGTGTGTGGCAGTGG
GGTGAGGGGTGTCATCAAGGAGAAGGCTTAGTAAGTAAAGGACCTGCGTT
GGTTCTTGAGTTCAAGTCTCCAGCAATCAGAGAAAGCCAGAACCATTGCA
CAAACCTGTAAGCCAAGTGTGGACTGGACAGAGACAGGCAAATGTTTGA
GGTCCAGGTTCAAGTAAAGAGACCCTATCTCAAAAAATCTGATGGAGAGTAA
CACTGGAAGAACTCAGAGTGAGTCACACATGCACACACAGGTGAATGTGT
ATACAAAGGGGGCAGGGAGGGAGAATGAGAGGAGACTGGGAGATATCTGT
AGTTCATGTCTGTAATTCTAGCACTTCAGAGGCAGCTGGAGCTACACAGC
AAGACCCCGTCTCAAAAACAAACCCAAGCCTGACAGTGGTGAGGTACACC
TTTAAGCCCAGAGGCAGGAGAATCTCTGAGTTCAAGGGCAGCCTGAGTGA
GTTCCAGGACAACCAGGGCTCCACAAAGAAACACTGTCTTGAAAAAACC
AAAACCAACCAAAACAAAAAGAATCAAAAACAACCACCACCACTACAACA
AAGCAAACAAGGGAGAAGGTATAAAATGCTTAGGAGAGTCTTCCTTTAGT
CTCCATCCTTTGGGTACTCCTTCCCCACAGAAAGCCACTACTACCAATTT
CTTACATAAGCTGCTGTTTTAGACACAGGTTTTTTTTTTTTTTAAATATA
GTAACATATTCATGTGTAGCTCATTTTTCTAGTGAGTGGTTGGTCCTTCT
TTTAACAGTTTAAAGGACCTCTATGTTTAAAGGCGATTGGCCCTTGTCTG
GAGTATGGGTGTATTTTCCCAATTTGTGAGTTTTACCCAACCTATTGCC

FIG.3B(14)

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TATTACCTATGGCCATTTATTCTTGTGCGATAAGTAGTTTCCAATTGTATG
ACTATGGTCACAGTGTTCCATGGACTCTTCTGCCGCTAGACAGCCCCTGG
GTCTGAATTTGAGATGGTTACAAGGGTGATTGGCTCTGCTCCCTGGGTGC
TGGGATTAAAGGCGTGACCTCCACACCCAATTTGTTCTGTTTTGTAAGA
AATGAGGTTTTATTGTGTTGCTCAGGCTGATCTCAGTCTCCTGGCCTCAA
GGTATCCTCCCATGTGCGATACACAGCACAAAGGCGTAGGAAAAGTGGCAGA
TTTTTTTAAATTAAGTTTTCTTCCAAAATATAGATTCAGAAATGTGAGA
TTTTCACAAAGTGAACCTGCTCACTTCCCTGGCTCTMGAATCTCCATTGT
GGCTCCCGCCCATCCCTTTTGCCACCAAGTGGCTGTTGTATTGACTTCTA
TCCCATTCCTTAACTATACTGTCTTGGTCTTCGCTGTGAACTTGCTTG
GGCTGAGAATCACCTTGTTCCGGGCACATCAGGTCAGTGAGGGTGTTTCC
AGAGAGTTTTAACAGAGACCAGAAGACCCACTCCAAATGTGGGTGGCAAT
ACCTGATGTTCTGTCATCCTGGACTGGGTAGGAAGAGGAAAGTAAGAAGC
AAACGGCACCCCCACCTCTCTGTCTGCTTCCTCGCCGACACAAAGTGACC
AGGGCCTCCCACTCCTGCCCCCTCAGCTAGAGACACTTGCTGCCATCTTT
CCAACCACTCTGAGACTGTGCCTACTAACCGTGACCCAAAATAAATGTTT
CCTTCCTTAAGGTTGCCTTTGTTAGCTCCTTTAATAGAGCGGTAGGACAT
GTAAGTCCACAGGCAGCCATCGCTGCCAGCCCCTCCCACTGACCGTCTG
AGAACCACACTCAGCTGTAGGCACAGCTCTCATAGCTGTGTGGGCGTAGC
TCTGTCTACTGGGTCATTCCCCTGCTGCCGAGCATTATGTTTTAGTT
CCTGGCTGATGGGTAGCACTGTTATGAACATCCTAGTACAAATCTCAGGG

FIG.3B(15)

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TGACACGCGCCTTCATTTTTCTGAGAAAATGCCCAAGGATAAAATGCTA
GGGCCAAGGGAAGAATATTTACCATTAAAGAGACACTGGTCAGGACTGGA
AAGATGGCCCAGTGGTTAAGAGCACTGACTACTCTTCCAGAGGTCCTGAG
TTCAATTCTCAGCAACCACATGGTGGCTCACAACCATCTGTAATGGGATC
CAATGTCCTCTTCTGGTGTGTCTGAAGACAGTGACAGTGTACCTACATAC
ATGAAATAAATAAATAAATATCTGAGAGAGACAGACAGACAGACACTGGC
TAGTCATCTCACAATGTTCTCATGTTTAAATATGATACCATTGTATAA
AGCAGAAACACAGGAAAAATAAATCTGTGGTATTATATTTGATTTTTAA
ATTAAC TTGATTAGTGAAGTTAGCAGCTACACTGGGCAGGGGTTGGGAGT
GGGGTACTCTGAAGTGCTGGTATTTCTGGTTTTGTTTTTGTTTGTGTGT
TTTTTATCTTATTTATATTACATAGAAAGCCATTTTGCTAATACACTTA
CCATGTGTATATATTGTGCTTGAATTACAGCTAAGTAATTATTTCTGAGG
GGCTTTAGACTACTGAAGATTGGGCCAATGAGCCCCACCCAAGTAGTC
TCCAACATCCCTCTTGGAAGTACTTGAGAGCAAAGATTCAAGTCACATGT
CCCCAAACCCTCAGCAGCCACCACCCTTTAGGTGTGGCTTTTGCTCTCGG
TCATCCTGGAACATCTTGCCATCTTTGGTTTGTTCTCTCCCTGTCTTGCC
TCTGGTAGAGCTGGGTTTCTGTGCTTCTATTCAACCATGTACAAGAACCA
TGTGCCACCTGCCATGTGCCAAGCCTGTGCCAGTCCCTGTGAGCGAGCAG
CCCACCCCGTGAGTTATCATGTGAGGAGCTATGAGGAGCAGGAAGGGGCC
CGGATGACTTCAGCAGACAGTATGAAGCAAGCACTGTGCGATTTATGCTC
CCTGGCCACATGCCACAGATGGTGTCTGAGACACTAGCGTTTAATATTT

FIG.3B(16)

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GAATTCTCCACATTCTAGCCTAGACATTTTGGTTGCAAGAAGAAAATTGA
CTCCAGTTGTATCCTGGAATGAAATTTATTGGAGGAAAATACTGGACAGG
CTCCCAGAGAAAATACGATATTCAGGCACAAAAAGAAATGGGGACTGAGG
ATCTGAAGTTCAAGGTCATCTGTAATGAGATTGAAGTCAGTTTGGGCTAC
ATGGGACCTGGTCTAGGGGGAATGGGGAAGAGAAGGGAAGGGATCGAGAT
AGGGAT

FIG.3B(17)

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CAATGTGCTCTGACGATTAATGGGCTAGAAATGTGTGGCTGTTGATTAGT
GAAAAGATGTCATGGTTCAGGAGATTGGTAGTCTCTGTGGGAAGACAAC
CACTGAAAGGGAGGAAATAGCCTGGAAGAGATAAAGAGACAGTGATCAGC
TAGGAAGCTTAAAATTTAAATTTTGTGGAAGTACTGTTAGGAATACTAG
CAGAGGCCAGATGAATGTATGGTTAAGTTATAGCAAAGGAAAAGATTGTT
AATGGTGAGGTTAGGAATGCAGGGTGACACCAACCTGTAATGTCAGCATT
AGCGAGATAGAAGCAGGTGTTTAAGGCCATTCTCTGCTACTTAGCAAGTT
GAGGCCAATCTGGACCACATGAGACCTTTTTTCAAAAATAAATCTCCTTA
AACAAAAGAGGCTGGGTTTTTTGATAGATTCTTCAAGATGTTAATGTAAA
TAAATGGAAGACCAAGGATGGCATGCTAATATCCTCAGTGTCTGAAGAAG
GACTATGTAGTGTTGGCTGCTGACTCTGAAGTAAGTGCTCATTACTGACA
GATAGTGTATCTTAGAGCCTGGCAGATGGGATGGAAGTGAGGAAGCAAGT
AGCACCTTTGTATATTATGTTCTAAGTAGCCAGAGATACTTGACACAAAA
CAAAGTTGAGAAAATGTATCTTCTAGAAAATACAGACATGGAAAGGTGTC
CTTTCTATAAAAGAGGTATTAAACATTAACCTGAAAAAAAAAGTTAGCAAA
TTGGGCTTTGGCAAATGAATATAGTCAAGTTTCATTTTTATTTTGTTTT
TGTATATGACTGTTTGGCTTGTTGTACCATGTGTGTTCTGGTGCCTAGG
AAGTCAGCTGGAGTTACAGATGGTGTGAGTTGCCATGTGGGTGCTGAGAG
ATGAACCTAGGTCCTCTGGAAGAGCAGTTAGTGCTCTTAACCACTGAGCC
ATCTCTCTAGTTCCTTCTGTAGAATTTTCATTAATTTACAAAGGAGAAAG
TATAAATGATAAAACCATGAGAAGATAGACCGGCACTAGAATTAGTGGAG

FIG.3C(1)

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TCAAAATGTTAATGATATGTCAGATACGCCCTTATATGAGGAAGTTGCAAA
ATTATGAAAATCCAGGCACTCCACTGAGTTAGAAATCTAGGCTCTGATGC
ATACTGCTATGGTAAGGTAGCAAGTGGCCATTGAGTGCAGAAGTGAGTCT
GGATGGGTCTTCTGGTGTGTGGAGCACACAGACTGCTGTCTTCTGCATT
GCAGTTTCACCTGTATTTCTTGGAACCTACTTAGCTTTGCAACTAGGCGT
TAAAAAACTTTATATTTATGGTTTTAAGTTATTTATTTGTTTTATTTT
ATTTTATGAGACATAGTCTCACTCTCTAACCTAGGCTGGCCTGGAACCTGC
CTAGGTAACCTGAGCTGGTGATTCTCTTGCCATAGCCTTCTAAAATTTTA
GATTGCAGGCATAAGCCAGACCACTCCTGACTTTTGTAGCCATTTTCTG
ACATGAAGTGTAACCTTGCTTTCATAACTAAAATGATTAGTTGTTTTGT
TATTGTTTAATCCCTTTTGCTTTGAATGTATCCTTTTGTGTGGGTGGCAG
ATATATAACCACAGACTTTTCCACAGGCATCCTACCCTAGGTCCAGAAAT
GACTCTGAGACGTCTTATATATGAATGAATGCCTAGGCCAATAGCTTTGG
CTGATTTCCACGGGTTCATAGCTCAGTTATCCCATTTAACTAGTCTAAG
TCATGCCATGAGGCTACATACCCCTCCTTCAGTTTCAGGGGACTGTCTTC
TCAGTTGTGTAATGTCCTATCCTCTGTTGCTGCTCCCCAACCCCCATCCT
TGCGTCATAGTCGGTCTGTCTCGTCTCCCCCATTTACTTGCACAACGG
ACTCTACTCTAGAAGTCCTCTCTGTGCTGGAGCTTGCACCTCGGCTCTCC
CCGTCTAAGCTAATAGGCAACAGCATTGTACAGACAGGTGATGCTTCCAT
ACATCGCACAGGAGATTCTCCCTACACAGATACTTATTCATCCAGCGTGA
ATGCAACCGTCCAGGGGTGTCTCCTAGTTGTAGTACATGCTGTGTATC

FIG.3C(2)

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AGTCTGATGAATTTCTTTGTCTTTACAACCAAGAAAGATAATACTGTAAG
AAATTTTGACTAACATTTTTCTTTATTTAAATTACAGACTAACTGGCTC
TTCTGGATTTGTAACAGATGGACCTGGGAATTATAAATATAAGACGAAGT
GCACATGGCTCATTGAAGGACAGTAAGTTATAATGGCTGACTTTATTTTA
ATTTATTATAAGAGCACAGTATAGCACAAAATACTTCCATGTGTGTTATT
GCTATTTCTTGAGACAGGACCTTTCTGACTGAGTAACTCAGGCTGACCTT
GAATTTTGCTATGCTACCTCTGCTTCCCAAGTGCTAGGGTGGTAGGTGTG
GACCACCATGCCCTGCTGCTAAATACCGTTCATTGATGCTTTTCATTTG
GATAGTGTTCCTTGCTTTTTTAAAATTTACTTTTTGGGGGACCAGAGAGATG
GCTCAGTGGGTAAAGTGCTTGCTGAACAAGTCTGGTTATGTGAGTTAATC
CCTGGCTCCACAGTGGAAGAGTGACTCCTGAAAGTTGTCTTCTGACTCC
CACGCTTGTGCATGCACGCACACACACAAATAATAAAAATAAAAAATTAAA
AGGAAATTTTCTTTTTTGGGTGATAGGGATTGAACCTATGACTTCACTAA
GCAAGTGCTCTATTGTTAAATAATTCCTTTAATTTGTGGGTTTTTTTTT
TTAGGTTCCAAGTTGACTTAATGTTATAAATGAAAGATACATACCAGAAA
TTTGCATATTTCTAATAGTTTAAAAAAGTTAGTTAAATCTTTTTAATAG
TTTGCTTAAATCTTTATATAATAATGCTATTATATCATTTTTCTAAATAT
TGATTTTATTATCAGCAAAACAGTAAATGAGCCATCAGAATAACCACTGT
AGCCTGTTTCCCTGGCCCTCTGTCCTTCCATCTGTCTATCTTCTCTTTT
TTTCCTTTTTTGTGCCTGTCATTTAGGGCAAAGCATTTTAGTCTCTGAAC
AAAACCTTGAAATTTCCAAGTAACTCTTGTTTATTTGTTGTGTCTCATAT

FIG.3C(3)

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TCAACCCAAGAAATATTATTTACTAACTCATTTAAAAGCAACAATTATAA
CCCACTACATGTTAGCAGAAAAACCTATTTGTTTTTATTGAGACGGGATC
ACACTAGTAAGCACTACATGGCATGGCGTTCCTGTGTAGATCAGGCAGG
CTGGCTTCGTGCTCTTGACAGTCCTCCTGTGTTTGTCTCTCACTTCTGAG
TGCTGGGATTATAGACATTACCAACACACCGATTTGGGGGGTTGGGGTAC
TGGGATCAGTCCAGAGTTGCATGGATGCTAGGCAAGCACTCCACCAACTT
AGCTATATCCCTGGTCATAAATGTCATAAGGAAAAAAATTCCTTATATTT
AAAGAAATTTTAAGAATTGCATTGTTTAAGATTTACAGATCTCTTTGCT
ATCTGGCAATCTTTTTTGATATTTGTTTGTGTTTTAAAAATATGTGGTA
TGTAACAAACTTAAATATGAATGGGACAGTTCAGATGAGAGTGAAAAG
TTAAATATTTGGGAGAAAAATTGATAGGTTTATCTATTATGGAAAATTC
AGAGATTTTAGTAAAATTTGAAAATGGAGCTGGGAGGTCTGAGGTAGTCA
TCTAAAGCTGCCAGTTGTAGAGCGTGTTGGAGTGTGGAGTCAGAGGGAGT
TACTGATACACTTGTTGAAATTGCCCAGGCTTCATGGGAAGTGATGAGGG
GCTGTTACTGTGACTCTGGGCAGGGCTTGTTAGTTTCCTTTGGATTTAGT
CTCAGTCAGAGTTGATACATAGTTTCCTGAGGACGTGGCTTTTTGGTACA
GTGCTGTGAAAAGGCAGAGAAGCAGGTAACTTAGAAAATGTGTGTTTTT
AAAGTGATGTGTTATGAAATCTTACGTAAGATGAATAAAGAAAGAAGTGG
GGACACTGAGGGCTCCTGTTTCTAAATGTTAAAAGCAAGGCTGGAAACAT
TCTTTGAAGGCCCTGAAGTCAGAGCCCGTGTCTCTTTTGGTTCCAGGA
CATTTTTGATATTCCTTACACATAGCAAATACTAACTAGATCTCTGACA

FIG.3C(4)

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AATGCAGGAAAGCTGTTTATATTTATATATATTTATATTGTATATTTTC
TCCTTATAAATTCTTTAAAAGTCTGTTTTAGTAGTTAATGTTATGATTAT
TATAAATTACTTAATTATTTTTCTAGGCCAAATAGAATAATGAGACTTCG
CTTCAACCATTTTGCTACAGAATGTAGCTGGGACCATTTATATGTTTATG
ATGGGGACTCAATCTACGCACCTCTGATTGCTGCCTTTAGGTAAGCCCTG
CTGCATTTTATCTCAGGAAGTAAGTGTGTCTCCAGGATGGAGTCCGTGCT
GCATTTACTTTATTCTGCAGTCACACTCATCTCATGGAATTAGTTCTGTT
CTGGTGAGCTACAGTTCACTTGGTTTTTATGTACTGGGTCGTTTTCCATG
TATACTAGTATGTAGCCACGGTTAGTCTTGAACCTCTGGTTCTCCTGCCT
CCACCTTCCAAGTGCTAGGAGTATAGGCTTGTGCCACTGTGCCTGACTCA
TTTCACATTCTTGAACGTGAAGTTTTGATAACACTATTAAATTTACCTG
CTATTTGTGATTTTGTTAAAGTTTGCATTAAAAAGTTTTTGA CTATATTG
ATAATATTTTTGTGACAAATTTAAATCAGAAACCATAACCTTTCTTGTTCT
TGTATGTATTTTATTCCATAGGCCCTTAGGAATAACTTTTTTCAATAGTA
TATAGTTCTCTCAGTTTGTATATATGTATTATTAGGGATAGGAGGAGCTT
TCTGGAAGACTATTTATAAATTGGACAATGGCTAGCTGTTGAGAGTGAGG
AATTTGCTAGTTTTGTTTTGTAAATCCCTCCCCAATGCATCTGTATTAGT
GATTTAATAAAATAATGCAATTTTGTGAGTTATATGGGTTGCACTGAATT
TTTGCTATTTTATTTTAAGAAAGATTTTTGTGTGTCTACAGTGTATATGA
GTGTATGATATGTGTGCGTGTGCATGTGTGTGTGTACTTCTATGCAGGTA
CTCACATGCTATGGTGTGCACGTAAGGTTGGAGTGCAGCCTCACATGTTG

FIG.3C(5)

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ATCATTATATTCCACCTTGTTAGAGATAGGTTGTCCTTGTTGTTGCTGC
GGCCTGGAGCTGGAGCTGGAGCTAACGAGTCTCAGCCACCTGACATGGGT
ACTGGGAACCAAGAGCAGCAAGACCTCTTCTTCTTCTTCTTTTTTCA
TTTTCGGTTTTTCAAGACAGGGTTTCTCTGTATAGCCCTGGCTGTCCTGG
AACTCACTCTGTAGACCAGGCTGGCCTCGAACTCAGAAATCTGCCTGCCT
CTGCCTCCCAAATGCTGGGATTAAAGGTGTGTGCCACCACCACCCAGCCT
AAAAGATTTTCTTACTAAAATATATTTCTAAATTAATTAGTTGGAATCTG
GTTCATACTTCTTTTTGAAACAAAACCAGCATTTTTTTTTCATTCTACATA
CAGAGACATTGACACTAGACACTGGTTATGAGTAGTTACTATAAGAATGG
GAAATTATTCCACCCTTGTAACCTTAATACAACCTCTTATCAGGCTCTG
AAGACTTTTTAAAAGCAAGAATTGTATATAACACACAGAAATGATTTAGA
CTATTTAGATCTTTATTGCATGGGATTTTAAAATTATTATTGTATTTCGT
GGGCATGTTTTGTCTATGTAGCATATGTGCCTGTAGAGGCAACCACCAAG
TAGGTCCTGGGAATCAAACCTGGTACCCCTGCTCTTAGGTGTTCTTAACT
GCTGAGCCATCTCTCCAGTCCTC

FIG.3C(6)

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AGGCAAGAAAGAGCCAGCGAGCCTCCAGACAGACCATTAGAAATTCCACA
GTCAGCACAATAGGGAGAACAGTAAATCTTACATTAAGAAGGCCAGGG
CCTGGTAGCAAAAGGTTTTAATTTAAGCACTTGAGAGGGAGAGGAGGCAA
ATCTCTCTGATTGGGGGTTGGGGTTAATGGTGAATGCCATGACACCCTGC
TCAGAGTTAGCCTTCTCCCCTAAAAAATTTTAAATTCATTTTCAATGCT
GACACAGTTAATCATAGACATTGTATCTCAGACACCTCAACATACTCCAG
ACTGCAGCACCAGCCCACTGCTGAGGCTGTCGTTCAAGTTGGTAGAAGGCA
TGCTCAGCATTGCGAAGCACCAGACTTCATCCTTAGCACTACATAAAAC
TGGGTGTGGTCATGCACACTTATAACTTCAGCACCATGGAGGCAGAGGCA
GGATGATGAGAACTTGAGGATCATTCTCAGTTACATAGGGAGTTTGAGGT
TAAGCAGGGGTACAGGAGGCCTGTCTCAAACAAACAGACAAACAGACAAA
CAAACAACTTCAAAAACTCTTGAAGTACTAGGCCTAGTACGTGCTGAG
ATTGTAGGTATATGTCATCATGCCTGTTGTAGAATGAGTGAGAGCGGACT
CCATAGGCTTATAGATTTGAATCTTGGTGTCTGTCTATGTCATGTCATCC
CTGCACAAAAGCCACACTAGGCCACACATTCTCTGTCTGCTGCATG
TGGGTTAGATGTGAGCTCTCAGCTGCTGCTCCAGTGCCATGCCTGCCTGC
TGCCAGGCTCCAGCCATGACGGTCAGGGACTAACTCTCTGAACTGTAAC
CAAGTTCCCAATGAAATGCTTTCTTTCATAAGTTGCCTTGGTCATGGTGT
CTGCTTCACAGCAATAACACGGTGACTAAGATACCTGGCTCCTCCCCTCC
CCACCCACCATTATTTACCATAAAGTAAACAATACACAGTTGGATAACA
TGATACTGAAGTTATTTTCCTGTTTCCTGATGTAACCCAATTTTGGACAA

FIG.3D(1)

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GATTAAGCCTTAAATAGCAAGCTGTGAGGCAGGATAAAGAAAAAGCTCGC
AGGCCAATGTCTGCTTTACCAAATCTGTTCAGCAGTCTAAAGCTGCCGT
CACCTCGACTCCTGTGATGGCATTTCATCACTATCTTAGATATTCCTG
GGTCACAACCTTTTAGTACACAGATTGCAACTCTGATGGAATGGCTGACT
GCTTGGCTAATTAAAGCAAGCTAGAGTTTGTCTGGCTTCCTTGTCTGAAT
GGGGAGGTGGTATTTACAAAATTTGTAAATAAACTACTATATTTGCATG
ATGTATATAAATTTGATGTGGCTGCTTTTAAATCATTTAACCTAACTGT
CCACAGAATCATCTGTTTGATTGGAAAGATTGTAGCTTCAAGAGAATTT
CTGCTGAACCTGAAATGATTCATAATGATGTGTCTGAAGAATGTGTGCTA
TCACCTACGGTTTTTGTTTTAGTTGATATTTGTACTTTAAGATTTCTTT
ATGTATGTGTGTGTGTGTGTATTTATGTGAATGTATACCTCATGTATGTG
GTGCTCAAGGACACCTGAAGAAGGGCTCTGGAGCTGGAGTTACAGGGAGT
TGTGAGTGCTAGGAAAGAAAGCTGGGTACACTGGGAAATCAAAGGTGCT
TCTAACCCTGAGAAATCCTGCCAGCCCCCTGGTTTATTA AAAATATCAA
ACAAAACCAACACTAGTTACATAAGTATCTCTCTCTCTTTCTTTCTCTCT
TTCTTTCTCTCTCTCTTTCTCTCTCTCTCTCTCTGTACACACACACACA
CACACACACACACACACACACACACAAAGGATCCATAATAGTTCTTCTGT
ATCCGGGTAAATATAAGTTCTTAGGGGCTAGAGAGATGGCTCAGCAGTT
AAGAGTGCTTGTTGTTCTTCCAGAGGACCCAAGTTCAGATCCTAGTACAC
ACATCAGGCAGCTCACAGCTACCCATATCTCCAGCTCCAGGAAGAAGCAA
TCAATGCCTATGGCCCATGCAAGCACCAGCACACATATGCTCCACAAACA

FIG.3D(2)

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TCCATATATATAGCTAAAAGTAATAAAAAATAATCTTCAAAAAATTAATT
CTGGTTGAACTGAAAAAGATCACCTAACATTTAGAAAAAGCAGTTTACTA
GTGAATAGGACATAAATCATGGTATCAAATATTCTGTTGTAAAGGAAGC
AACTAGAAAAAGCATGTGTTTGAAATAACCAATGGATACAAAACAAATGA
GGCAACCCCAACATCTGTCAGTACCTTGCAAACCAACACAATAAATTTGA
TTTTATTTAAATCGTAGTTATTTTTTCATGCTAGTAGTTTTGAAACACAAT
AAATTTGATTTTATTTAAATCGTAGTTATTTTTTCATGCTAGTAGTTTTGA
AACCAAGATCTAGATTTTGTATAGCCACATAAATACACATTAGAATTGCA
AACTGATACGAGCTTCATCTTCATCAGTCTCTCTTCATGAAAAGCAGTTA
CAGGGACTGAGACATGACTCAGCAGTTACGGCATGGGCTGTTCTTCCATA
CGACATGGATTCAATTCTCAGTGCCCAAATGTTGGCTCACAACCATTGT
AACTCTGGTCCCAGGGGATCTGACACTCTTCTTGGCTTCTATGGCCACTG
TATTCATACGGTACACAGACACATATGCAGGCAAACTCAACAAAAAAAAA
TAAGGTTTAAAAAAAAGAATTAGAACTTAAAGGCACTTCATTCCGTCAGC
ACTAAATCAGCCTCTCTGGAGTCTTCCCACTTCATGAGAAAATCGTCAGC
TCTCCACTGCTGTCTGTGGCTGAGGAGCAGGACCTGGACAACGTTTCAGAG
ATTGTCAGTGCATCTCTTTCTTCTTTGGTTTGCTGTCATCAGGTTCACT
GTCACATTCCCTTTGTACCATCCTTCTTTAACAGCCTTTTGAAAATGCA
GAAATGTTGGATGCTGCCTTCAGTTCACACAGGCTGTCTTTTTAGCTCCT
CATCTATCTATGCTTAATTTGTTAGTGGTGCTCACCCATGTATGTGTTTA
TGTCATGAAGCCACAAGATGAGCCTTGATTGAGTCTTGCTGTCAGTGTGG

FIG.3D(3)

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ATCACAGAAATGACACCCTATCATCTTTGCTTCCTTGCTTGTAGAAAGTCA
TTGATTCTGCTTATACTCAAGGCCACAGTATTATACTTGGGTGTGAACC
CCAGGAAGCAGGGAGGTGGGGGGTGT CATGGATACTACTCAGATATCTGA
CTGTTGTGATATTTTCATCAGTTCTCATTGGTCCTATCTTTAAAATCTGCC
CTACATCTAGAGCTGGCTGTGGTGGTGTGTGTGGTGGCATCAGTATCAGA
ACTTGGATTACAGAGGCAGGAAGATTGTGATTTTTGAGGCCAGAATAGGT
GCATACAAAGATCCTGTCTGCAAAAGAAACAAATGTGCAAATAATTATAA
CTACTTTACTAATAGCCTAACTAATAACCACTGCTAGTGCTGTGTCCACG
AAAAGGTGAAGTAACTGTGAAAATGACTTCCCCTTCTGTGTGACACACG
CCGTCATGTGATTTTACTTGTGTCTCATCATTGTTTTTCTTCTGTTTGC
ATGTGTGAATGTTACATGTGGAAGCCAGAAGTCAGTGTTGAGTGTCTTC
ATAATTGATCTCTATTCTCTTTGTTTTGAGACAGGGTTTTGAGACTAAGC
CCAGTGCTCAGTGATTCATCCAGTAACTGTAGGGAGCTTCCTGTCTCTG
CCTCCACAGTGTTGGGATTACAAGCATGATCCAAATTATGTGACAAGCGC
TTTACTAACTTAGCCATGTCCTCAGCTCCCCACTCCCCTTTTCTTTCTT
CTTCTTTTTTTTAGACTTACTTGTTTATTTTTATGAATGTCTTGCCTGCA
TGCATACATGC
AAGCAATTCCAGAAGAGGGCATTGAATCCCTGAAACTGGAGTTCAGTTA
ACTGTGAGCCTGTCATGTGCGTACTGGGAGCTAAATCCGGGTCTCTGGA
AGGTCAGCAAGGTCTTACCTGGGAGCCGTCTCTTTAGCTCATGTGTTTCT
CTCTTGAAAGCAAGAAACCTAGGAATCATTTTGAAACTTCTTTCACAGCCT

FIG.3D(4)

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TTATCATAACTTCACGTCAATTTTACCTACTCTTTCAACAAATACATGT
TATATTTACTTATTTTTATGTTTAGCCTGCTATTGGTTTCTACTTAGCCT
CTTGCAGTAGAGTTCTGTCAGATTTATGTTTCTATTGCTTTTAATTTATT
TGTAAGGTGAATGGGAAAATATTTAAAAATTACAGATCCCATCATTTAC
TATATTCTTAAAAGCCATGGCTAGCCAGGCTTGGTTGTGCATGCTTGTAC
TCCCAGGACTCTGACAACTCAGTAAGGAGGAGAGTGAATCAGAAAATAGC
GCCAGCCTGTGCTGCTTAGCAAGAAACAGAAACAAGTACAATCACACACA
TAGAAAATCCCCATTAATACCATCCCATTAGATATAATGGTCCTGTATG
ACCATTCAACCACTGTTTGTCTCTGTACTGCAGTAACAGTCTTCTGCCC
TTGCCCGTGAAGCACGTGCGCACCCCGCCTCCAAGTGCTTTTGCCTGGT
GTCCTCCGTCTAGATGTCCTGTTACTATATGTAAGGACTGGTTTCTCCTC
CTCTTTACAGTTCAATCTAATTGTCTCATGAAAAGATCTTTCCTGACCAT
CTGGTTCAGACAGGTTCTCCCTGTTGTTGTTTTGTTTTGTTTTATAGT
TCTAAATTCCTTTCAGGAACTTTTGCTTATTTTAAATCCCTGAGTGCAT
ACGTGTGCTTGTTGTTGCTCATGCTCGTTGTTGGGCTTACTTTACTATC
AGCTCTGGATGTGGTTCACAGAAGGTGCTCAGGGGAGCACTCTCAGCCAC
TCATCTCACACGGGTTATAGATATATGTATTGATGCTACGTTTGCTTGTG
AGCCATGTTTTAAAGATTAGAATATCTTTTCTATGTGTA CTATCAAAA
CACATGTTAGGGCTTTATCTATTTTATACAGATATTGGTGTTCTTGCTTT
ACTAATTTTCATGGAATTTCCGGTGAATATTAGTATTTTAGATAGGAAGAC
TTGTCTCAAAATGTAGCTCAGCTGGTTGAGTGCCTGCCTGCATGTAGAAA

FIG.3D(5)

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GCCCTGTATTCACCTCTCCAGCACCTCAGAAGTGGGCCATGGTGCATATGC
TGTCATCTCAGCACTCCGGAGGGAGAGAAAAGAGAATCTGGAGTTCAAGG
TTATCCTTGGCTATATAACAAGTCCAAGATCAGCCTGGGCTACATGGCAT
CCTGCCTCAAAATCAAACACCAAATCAAAAAGCTCACATCTTGATCCAAA
AGAAGGTAGAGAGAATACACTGGGAAAGTCTTTGAAACCTCAAAGCTAAC
TCCAAGTGACAGTGACACCTCCTTAGCAGGGCCATAAATTCTAATCCTTC
CCCAAAGCCCACCAACTGGAGACCAAGTATTCAAAGATAAGAATCTATGC
AGTCCATTCTCCTTCAAACCTACCACAGTAGGTTTTCTTAAAAAAGAAAA
AAGAATATTTTAATTGATTGTGATTATTCAGTATTATTCATGAATAATCA
TGAACCTACATGGCAGGACTATAAACTATTATTTTTTTTAAAGATTTATTT
ATTTATTTTATGTATGTGAGTACACTGTAGCTGTCTTCAGACACACCAGA
AGAGAGCATCAAATCCCATTACAGATGGTTGTGAGCCACCAAGTGGTTGC
TGGGAATTGAACTCAGGACCTCTGGAAGAACAGTCAGTTCTCTTAACCAC
TAAGCCATCTCTCCAGCCCCTATAAACTATTATTATTTATAAAATATA
AATCCGTGAGTCTGTGCACCCCTGTGTGCACATGGATGGGACATCTTTGA
ACTGGATTATATCATACTTAGAAGAATACAAGATACTCTGTTTTGTCATT
TGGGTGAAAATATGGTCTGTTTATTTTGCAGGTATGACCTGACTTCTAGG
GAATGGCTTCCACTAAACCATTCTGTGAACAGTGTGGTTGTAAGATATGG
TCATTCTTTGGCATTACATAAGGTAACTATCTCAACTCTTCACCAAGCA
AGAAGTTCAACTCTTCCTGTGTCTTTATGTCATTGAATACTATCGAGCTT
TGGTTTTAGTTGGTATAAGCTTTGTTTTGATGTCATGGAGGTATATAATT

FIG.3D(6)

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CACCAAGTTGTCACCAAGTTGTAATTGGAAATTGAAGTTAGAACGATTTT
AATCCATGGTGTCTTGCATTTGGATACTCTGATCACAGTTAACAATGAAG
ATTAAATAGTGTGAGCAAGCCTATGCCATTATCAAGTCTAGCATACTGC
ATGCGTGTGACTGAGTAGCCATTGTTATCTCCTTGTTTTGAGCGTATATT
GTAGAATGAGGCAACTGTATTTTCCACACCATTTTCGTTCTGTAACACGT
TTCATGTAGAGAAGGTGATTTAGAGAGGGGAAGAATGTGATTGTATTGGT
TGGTTCTTTCTCTATGCTATTCCTAGCAAGTCACCGAAGAGCTCATGTTA
CTCACACTTCTTAAGCTGGGATCACAATGAGATTGTGAACCACTCATTGT
TGTTTTCCAATATAATTTTTAAAAAGATGATTTATTTTTATTTTATGTG
TGTGGGTGTTTTGCCTGCATGTATGCCTGTGTATACTGTTCTCCAGAGG
TCAGAAGAGGATGGCATCAGAACTGGTGGCTGTTAGCTGCCATGTGGGTA
CTAGGAACTAAACCCGGGTCCTCTGCAAGAGCAGCAAGTGTTCATAACT
CTCTCTCCAGCCCTAGAGTTGATTTCTTAATGGTTTTAAAAATCCTGTTT
ACATCTTTCTTATAGGATAAAATCTACATGTATGGAGGAAAAATTGATTC
AACAGGGAACGTGACCAATGAGCTGAGAGTATTTTCATATTCATAATGAAT
CATGGGTATTGTAACTCCGAAAGCTAAGGATCAGTATGCAGTGGTTGGA
CACTCAGCACACATTGTTACACTGGCATCTGGCCGTGTGGTCATGTTGGT
CATCTTCGGTCATTGCCCACTCTATGGATATATAAGCGTTGTGCAGGAAT
ATGACTTGGGTATGTATTTTTTCCAGTGGAGGCATCTTGAATATCATACT
GAGAACCCCTGCCCTTATTATTAGGACACCGTAACAAAATTCAGCATGAT
CTTGATCCAGTACCTTGTCTTGAAATAGTATCAGTAGATAACTGGTGAGA

FIG.3D(7)

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TTGAGGTTGTTGAAGTCCCTGTGCAACAGCTGTTTCTTACTTGTCAAGGT
CTAGTCTTGGCTTGGGAGGGGTTCTGAGGAAAGGGGTGTCAAAAACCCA
AAAAGTCCAATTGTAGGTCCAAGCTGGCAGCTGTATATTGCATTAAGGAA
AGCTGAGGGAAATTTGGGATATTTATTTTCATCTATTAGTCTACATCAAGC
AAGTCAAGCGCTCACAGTCAACGTTTGCACCCTCAAATTAGTAACAAAAG
AGGGGGAAGTCTGAGGAGTCCAGCATGGTCTGGTTGGGACAGAATGACATG
GTTCCAGCCCTGAGACAGGGGCAGCAGGTCCGGGCCTCCATGGATGTCAC
ACTATGGACATAAACCTGTTTGTATAATAATGTACATATTTTCATGCTCCT
CTTCTGAGTAATGTCCTTCTGTTAATGTGAATGACTTCATGATAATCAGA
GCCAGTGTGAGTCTGGGAAGTAAATGGTGGGACCTTCAGGACAGCTCTTA
AGGCTGTGGAAAAGAACATGAGTTCAAAACCATATACTTCCTCAACTATA
CAAAAATAGAAGGATGCAATATGAATTGTATGAGGGGCTTCACAGATCTA
AAGGAACAAAAGCAGCTTCGCTGTGAGCCAACCTTGTGAGAAAGATATTGA
GTAAGCAGTTAAAGAGATTTAGGGAGTGCTGATTGCTAGAGGAGGCCACC
CAGCTAAGTTTGTGCTTACAAAGGCAGACAAAGTCCTGAGTTCAGGGTGG
GCCTGGAACAGAGCAAGGTTAGTTAGACCTTGGTGTGGTAGAAATGGTAA
TTTCCAGACAGGATACCCAAGTATTTTGTGCTTAACAGAGGCAGGTAG
ATCTCTGAATTCTTTTGTAAATGTTAAAAGGAAATGTGTGCTTGTGTCTC
CCAAGGGGCCTGAGTCCCAGGATGCTGATTTATAGGAAACCTGGAGTAAC
TGGGTTTATGACCTGCAGGAGACGAGCTATCCAGAATGTTTTTTGCAATA
GCAAGAGAGAACTGCCTGGAGAACTGCCTTCAGCAAAGAATAGCAAGAGA

FIG.3D(8)

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AAGCTGTCTAGAGAGAGAGCTGTCTGTAGAGAAAGCCGGTCAGAGAGAAA
GTAGACTGGAAACTGTCTCCAGCTTGGACCCACAATTTGACTTTTTTGT
TTTGTTGACAAGTTGCCCTCCCCAGAAACACCTTCCTCAGGACCCCTCC
CAAGCCAAGGCAGGGCCTTGGCCCTTCTTGTCAGCTTGCAAGGAGCCAAA
GATAGCATTAAATGCTTTGGATATCAAATAAGCAAAATGCAAAACAGTA
AACACTCTAAAATAATTCTGGCTAGTCCTTTAAATATTAGGCCAGTGCAC
TGTTATTTTACCTTAATGTATAATCTTGTTACATTTTATTGTTTTAT
TGTATAATAGGAATGTCAGAATTATAATTTTGTAACTTTGTTTGACATT
CCTGTGAAAATGCATCTAAAGATCATTAAAGTGCATCTGAAGATCATAAG
GACTCACTGAGGAGCACAGGGAATTAAGTGTCTGCTTAAGAGAACTTTGA
ATCTTTAATCTTTAGAATTTGTTTTAAAAATTTGAATCTTGCCAGTGTGG
TGGCGCATCCCTTTGGTCCCAGCACTCAAGGGGCAGAGGCAGGTGTATCT
CCATTAGTGTGAGGCCAGCCTGGTCTACAGAGCAAGTTCCAGGCCAGGCA
GGGTACACAGAGAAACCCTAGCTTAACAAAACAAAACAAAATATGAATCT
TTAAAACTTGTTCTGTGAAAATTTACATCATGTATACAATATAGCTTGT
TCATATCCACCGCCATTCTTCCAGCTCCTCTAGGCTTTCCAGTGCATC
TCCTTCCTAGCCTTATGGCCTCCCTTTCAGGGTGAAGGTTAGCACACTGA
GTCCAGTTAGTGCTGATCCGATGCAGTCTTGCTAGATGGTCTTCTTTAT
AATAAGGTGAAAGTATATCCTAACTTCCGTCTTTTGCTCTAAGGTGTTT
AGACTTTAACTAATGTTTAAATCGTTTAAATAATTTATTATTTATAAG
AAGAGGAGCCTGCAACATTGACTTTAACTATTGTCTCTTATCCAGAAAAG

FIG.3D(9)

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AACACATGGAGTATATTACATACTCAGGGTGCTCTTGTGCAAGGGGGTTA
TGGCCACAGTAGTGTTTATGATGACAGGACCAAGGCTCTGTACGTTTCATG
GTGGCTACAAGGCTTTCAGCGCCAACAAATACCGGCTTGCAGATGACCTC
TACAGATACGATGTGGATACTCAGATGTGGTGGGTGTTTTCTAGAGCTT
TCCCTTGGTAGTCTAGAATCTGCAGAGGCAATTGATTAATAAATACTGTGC
TATGGTTTGACTTTTGTTTCAGCATTGTATGTAACAAAGTTAGGAGATCAA
TACAGTAATAGAGTTAAGGTACTAATGGTGCTGTTGCTGTCTGTTAGTGC
TTAGTGCTTTAGACCTGATTCCTGAACCTCTAGCAAGGTTTCCTCTCTTC
AGAATTCTCAGCAATAAAAGCTGTGCTGATTTTATCCATACTTAAAAAGC
ATATCCTTCCTTTTCTCTTTTTGGTGTTGGGGATCAAACCTTGTACATGA
ATAGGCTATACCATCTTTATCCATTACATCACCAAACAGGATGCTCTCG
TGCCTATTTGATAGGGTTTTCACTCACTTCGAACTGAAACTTGGGTTGTA
AGAGTATGGTACTTTTAGCAAATGGAAATAAATTTGAGTTATGATGCAAT
TATAAAGCACTGGTCTCTCTGTATTTCCCTCCTCCTTCTACTCCCTCCCT
CTTCCTTTCTGACCCCTCTCTCAACATACATTAGAGACCATGCTTTGAC
TGTCATTTTATGCTGTGCTGAAGATCAGGTCTTTAGTGGCTGTGAACCAC
GGAGCCTATGCAGTGGAAGTTCTGGTCTCTGGCTTTTGCCTTACTAATAA
AACACTGAGCATAAATTTTGATTTGTATTTACAATTTCTTACCTGGAATT
CTTAAGTGGAATTATGGAGCCATAGAGAATGAACATTTTAGGGCTTTTAA
TATAGTTTCCCGAAATTTTAACAGATTTTCATGATTGTAAAGGAAGTGG
CTTACGTATAGGGGGAAATCAAGTATTGCACATTTGAATCTAAAGTTATA

FIG.3D(10)

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AAGTAATTACATTTAAATTGGCAAATAAGTATTCTTTTAAACTAACCTT
ATATTTATTATTTCTAAATAAACTCAAAGGACCATTCTTAAGGACAGCC
GATTTTCCGTTACTTGCATACAGCTGTGATAGTGAGTGGAACCATGCTG
GTGTTTGGAGGGAACACACACAATGACACTTCCATGAGCCACGGTGCCAA
ATGCTTCTCCTCAGACTTCATGGCTTATGACATTGGTAAGCTTTCCAAAG
ATGTTTGTAGCTTCAGGAATATTTTCTTTGCTGATGGAAAGATCACTATGT
TAAAATAATTGCACCATTTAAAAGAAGTCCAGGTGGTAGAATTTGCATTT
AATTTGAGTAGGGTTACACATCTATTGAAAAGCATTATTTTGGATTAAAC
TACATTAAATTCTTTGTGAAATCACTCTTCTTAATTGCTTTAATTCTTTT
TTTAGGTTGAGTTAATTGGTATCTTCTTTCTTATAAGTGCCTTACATAGT
AGTGGTGGTAGTTGTAACCACCAGTGTTATGTTAAGTTTGATGGGATATG
CTGTTTCCTAGAAACCTGGTTTTACACATGCTGTTGATGTCAATATACAT
GTGGCCAGAAGAGGGCAGTGTCTGTTTATTCCTGGAAAATAAACATCAGC
TGCTCTGTTGTGTAATATCACCCATGTGATGTTCTTTCTGTTTATTTGT
CTTTGCATTTTGAGACAGCCTCACTATGTAGTCTAATTGGCTGAAGCTCA
GTATATAGATCAAGGTGACCTTGAACCTTAGAGAAATCCTCCTGCCTCTTC
TGAGTGCTAAGATTAAAGATGTGTACTACGAATGAAAAAAAAAATGTGT
ACTACCACACCTGACTAGAGATTCATTTTAAAAATTATTCTTATTGTGAT
AAAATGCTCAGAATAACACTCACCATCTTAATGTTTTAAGTAGTTTAGAT
TTAAATATATTCCTAGTGTTATTCATGTTATAATACCATCTGCTTGCCGA
CTTCTTGTAAACTGAACTCTGCCCTTAAACAATAGTTCCTCTCTTCAT

FIG.3D(11)

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CCCTCACTCCAGCCTCTTGAAATCATTTTCTATATCTCTATGATTTTGAC
TAGTCTAAATTAGGCATTTTTTAAAAAAATATTTTGTCTACTTGTATGT
GTATGAGTGTTTTGCATGCATGTATGTTAAGCACACCATGTATATTCAGT
GCCCATAGAAGCCAAAAGTAGGCATAGATTCCCCAGAGCTGGAATTACAG
ACTTTTGTGAGCCACCATGTGGGTGCTGGATACTGTGCCCAAATCCTTTG
GAGGAATAGTGAGTCTTCTTAGCTGTTGAGCCATCTTGTGAGCCCTAGAT
GTTTGTTTTTAACAAACGTGTTTTTGCCAGCCATTGAGTTTTTAAATTGA
GAATGGGGGGTACACTATAGTTAGTCCTTAGCTTCAAGCTTGTGGAAGCA
GAAATGAGAAGACAATATAATCTTAACCTCAGGAGGATTCTTGCTGGCTGA
AACAAAGATGTGAAATTACCTCCGAGCACTCCTAAGCCACTGGGGTGAGC
AGGGTGGTCTGGAGAGGCCTTGAAGAGAAGCTGTCTGAGCTTGTTCTGG
GGCACTGGGAGTCAAATAGACCTCCTGGGCAGGGGGATTAGTGCAGAC
AAGAGGCAGGAAAGTACATGTCAAATATTTAGGACTTTTGAACCGCTACC
TTTCTTTTGTCATGGTAACACAGAAGGTAGCAGGTGACTGTTAGACTAGA
ATGTTGAGATCTGATTCAGAGTGCCAGGGATCGTTGGTTGGTCTGTGTGA
AAGTCTCACAAGTGATAGAATCATATGTGTGTCTTAGACTTTTTTGTG
TAGGTATTTTAGATTTTTCTTGTTTTTCTTTTTTGTAAAGTCTGGCCCTCA
CACTATGGTCCAGGCAGGCTTAAGACTTATGGTAACCATCCTACTCTGCC
TTTATGGGCCACCATGACCAATTTAAGAAGCTCTCTTGGGTGGCATTGTG
ATAAGTGATCTGGAAGGGGCATATTGACAGTTAGCAGGCTGCTACTGCAG
AAGTCCTAATTAGGTTTGTATCAAGGCCATGGAAGGAGCAGTGACTTCTA

FIG.3D(12)

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GTACCTGGCTGTTGTGTGTCTTGACAAAAATATAACTGCCCTTTCTTCCC
AAGTGTCTACTATGGACCACCTTTGCCAAAACATAAGCAGATTCAGAGA
AAAACATATCATGATTGCACATGGCTATAATCCCTGAACTTAGGAGGATG
AGAAATATGGCAAGATTGAGACCAGTCTGAACTATCTAGTAAGACCGTGT
CTTTAATAAAAAATAGTAAAAATTATAAAATCAGGGAGTAGGATCTGGGAA
GAAGAGAATGAAGTAAGTGTGGGGCATATCCAATTGGAGATGTCTTTAGG
ACAGAGCTGATTGCTGAGAGGTGGTTGTAGGAGAGGTGAGTTATTGTGGG
GCATAAAAGATGAGCAAGAGTCAGAGACAGTTGGAGAACAGAGTCTGAAC
AAGAGTAGAGACTAAAGAGAGTGTGAGAGAAGCAGGGAGAAAATAGGTGA
GATTGATGACCTGTGAGATATGTTAATGGCCAGAAGAGTGGCTAAAAATG
ACTGGAGAATCCTTCAGACTTGTCAACAAAGAAATCCTTTAGCCTAATTT
AGGGTGCAGGCGGCTGAGGAAGGACATAGGTGAAATATGTGCTCTGTGTG
TTCATTTTTATTAAAGCTTATCTGCAAAGGCCTCAGATTTGCTGTGTACT
TGTAAGCTGAGGCTCTTTTGAACCTCGGTTCTCCTGGCTCCACCTTCCCA
AGTGCTAGGATTACAGATGTGTGCCCTAGTTAAAATAGCTGTATACCTAG
CATTAAAAATTTAAGTTAGAAAATACTGTGGTGCTCCGGGGATGCATCT
CAGCAGTAGAGTGCTTGCCTGCTATACACAAGGCCCTGGGACTGATCCCT
AGCACCACAAATACTAAAGCAGACATTCTGGTAGGGAAAACCTGGTAGACA
GCAGAGTGGTGACCATCAGGAGGGGGGTGTGGGTGATGAATGACTACAT
TAATTAGAAGTTCTGTGCAGTATATTTATTTTCATGCCCTGAAACATTGCT
GCTGCTGTTGCTGCTTTTCTTTACACATAATAACATAACTAAAAGACAGA

FIG.3D(13)

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CAAGCATGTGGTATGAGGCTGTGGATGAGGCATTCTTTGTTTTCTTTTT
TTTTTTTTTTTGAGACAGGGTTTCTCTGACCTGGCTGTCTGAAACTCAGT
AGGTAGAACAGGCTGGCCTTGAATGCACAGAGACCCTCCTGCTTCTGCCT
TCTGAGTGCTGGGTTCAAATTTATGTTTTTTCTATAAAGACTGAGAGT
TCACATGGACTATATATGACAACCTACTCTGAAATGTGTTTTTCTCCCC
TTAGCTTGTGACCGATGGTCAGTGCTTCCAGACCTGAGCTCCATCATGA
TGTC AACAGATTTGGCCATT CAGCAGTCTTGTACAACAGGTAATTGGAAA
GCAAAGGCTCTATTACTGTCTTACATCTTATATTCATTTTAATATCAAC
TTCCTAACAGTTGTATCTGAATGGTAAGAGGTTTGGGGAGAAAAAAGGAG
AGAAGGCAGTTCTAAGTGCACGATAAGGTAAGGGGAATAGGACTGGGAGG
TTATGGGGTCAAAGAGCAAGTCTGAAGTCTGCACTATATCCAGGTGTGTG
CTCAGGAATACTTTTCTGACCAGCAGAGCTCTTTTCCATTTGCTCCAGG
AACCTTAGTCCTGTAAAGGACATGCAAAGGACTAGGGTTGTGGGCCAGCA
ATAGAGTGTTTATCTAGCTTGCACAAGATCCTGAGTTCTGACCTCAGCAT
TTTGCTTCTGCAAACACAGCATTGCGCATAAGGGACATGCAGAATGGCC
ATTTTACCTAGTCACTTGAAAGTGTGCTTTAAGATTGAGAACTTAACAG
CCTGCTGATGCTGACTTTTCTTATTTTGCTTCTGTTACTGCTTCTGCTT
CTTCTTTAATACTCTAATGCTTACATTATATAGTCCTACAGGTATTCAA
ATTTTCTGTTGGAGTTTCCTAATACAAGTAATTTAACTTGCATTAGGAAA
AGGATAAAAGTGCCATTCTGGAGTTGTGAAGAATGACCGTTTAGAAGCTA
GATAGTGGGGAAAGATGATACTTTAATCATGTGATTATTTAGTGTTTTA

FIG.3D(14)

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CAAGTATATAGGGGATTGTGGCAAGACCATTGTATGATTAGAGACTAAAG
TGGAAAGATTTTTTAAATATCTTGTTAACTTGAGTGTTATCTTAAATTAC
AATCTGATGCTTTCCTTCAGAAAAAGCCCTAAATGCCTCTTGAGGTTTTTC
ATCTGGCAAGTATCATGTCACCTGGCCTTGCTGGTGGAATCTGCCCCAGC
TCATGTGTGTTCTTAGTGTTCTCCTAGCACAGAGTTAGGCACGTGTGGGC
ATTTGCATACTAATGTATAGTAATAGTAACAATTGAATGAATTGTCTATT
AAACATTCTTAAGTTTTACCCAAACACAGAGAGGTGACAATTTGTCAT
AAAATGTAGTTTATCCATGAATCAAATCAGGAATGACTGTCTGAACAGT
GTTTTTATTTTTTATTTTATTTTATTTTGTGTAATTTCTGTGATGTGTTT
GAATATCTCAGTTTTAGGCAGGATTGGAAATGTTAGAGGTTGGTAAGAGG
TCATGGTTGCAGTTTGATCATGAGAGAAATCGATGGCTCTCCCTTCATTG
CAGTGTTGTCAGTCAGCAGTGTGGGATCACCTATGTCTAACAGTTGTTCT
AATTGAGAGAGGATTACAGGAGGGAAAGCAGTGAGATTGTGAGGTGCTAG
ATGAGGAGATGGCATTACCTAGCAGCCTTCTCTCCCGCCCTCCCATCAT
GTGACCTGAGAGATTCACAATTTCTGAAGATATCAGCTGTGCTTAGTTTA
AGCAATAGTTTTATTAATACTAAATCCAACCTTGATTCATGTTATTCCCAGGG
AACCAGTGGTAGGATTAATAATGAATCCTAGTGTTCTTTTTGGTTATTGG
AATGTCAAGTTTTTCAGACACTGTAACGAATACAGAGCCATACAATCACTA
TATTTATTTGGTCCTTTGTTGACTTAGAAAAATTGAAGCCCAGTTTAGGT
GAGCTACCAAATTTCTCATTGTGGATTAGTATTAACTTGCGTGGAGTTG
TGGGATCTTGGAAGTGGGGGCTAAGCATCCGTGTTTGTACAGCCCAGAA

FIG.3D(15)

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GGAACAGATGAGGTTCTTTTGAGGAGTCTTATGTCTTTATGAACTTGGA
CTTAGAAATATTTGATGTGTTTAATTCTGCTGTAGTTTTTTAACTCTAG
CTAGTGAGCATCTTTTCACAGGAGCGCTTGAGTCTGACCTACAGCCATTG
TCTGTCTCTGGTGTGCATATTACAAATGCACTGGGAGCGTTTCTTGACCC
AAACATATAATTAGATTTTTCTTCTAAAAAGGTCTAGTTTGGGAAGGAAT
GAAAGGGATTAGAGAAATGTTGTGGGTTTGGTATTTATTTATTTATTTAT
TTATTTATTTAATGTATATGAATGATCTATCTTCATGTATACCTGCATGC
CAAAAGAGGACATCAGACTCATGATGGTGATGAACCATCATGTGGTTGCT
GGGAATTGAACTCAAGACCTCTGGAAAAACAGCTGGTGATCTTAACTGCT
GAGGCATCTCTCCAGCCCAATTGTTCTGTTTTAGTTTGAGGATGAACATC
TAATTTAGAGATGCCCTGCTTTTCCAAAAGTGAGTTTTAAACACTAATTT
CCATTGTCAGTGGATTGGTCTTTTAAGAATATAGGTAGTGGTGGCACAGG
CCTTTAATCCCAGCACTTGGGAGGCAGAGGCAGGTGGATTCTGAGTTCTG
AGACCAGCCTGGTTTACAGAGTGAGTTCAGGACAGCCAGGGATACACAG
AGAAACCCTGTCTCGAAAAGCAAACAAACAAAAACAAACAAACAAACAA
AAACAAACAAAAAGAATATAGGTTGGAATAGGTTGGAAGCAGCCAATGAT
AGTGCATACCTTTAATCCCAGCACTTGAGAAGCAGAGGCAGGTGGAAGTCT
TGAGTTTGAGGCCAGCCTAGTTAGTCTACAGAGTATTTTCTGGAGAGCC
AAGGCTATATATAGAAACCCTATCTTGAAAGGCCAAAAAAGGAGGAAAAA
AAAAAAAAGAAAAGAAAAAAGAAAAAAGAATGCAGGTTGGGCAGTCAG
GGTAAGTGTCTAAGGTAAGAGGAATTCTTCAAGGTGGAAAGTCATGAGTT

FIG.3D(16)

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CTGCGCCAGCCTAGGCTACAGAGTACTGAAAGGGGAAGAGACTGTCCATG
TGTCAGACCCTCATTTCTCCAAAAGTCACATGACTATATTTTTTCTGTAT
TGCCCACTCTTCCATACATGCACCTAACAATAAATATTGAAGTTCACCT
GTGGCACTATATCTATGTGATAGACTTCTAGAAAAGTGATTTAAAGTTCA
AAAGGTAAATACGTAGTTTTGTTTCAAGTTGCCAAAATCCCTTTAGTAGA
CTCCTACAATCTTACATGCCCAGTAGCAGTATAGAAGCTTGCTTGTTGCC
TTGAAGCCTCACCAATTCAAATATTAGGTAACATTTGTTACATTTTTCTT
TGTCAGCTGGATAGGTAATGAATGACACAACAATGTGTTCCCATTTTCTC
TGCATTACTAATTGAAGTCCTATCACCCACAGCAGACTGAAGAGTTCCTT
TAATATTTTATGGACTTTGACAAACCTAGGATTCATAGCTTCCATACAGA
GAGGAATTTACAAATAGCAAAGTTGGGCTGTTAGAAGAATAAAAAGAGA
ATTCTGAGTACAGCTTCTCAAAGAAGAGTCCCACGTAGGTGTCCTCTGGG
ATGTGCCTAGATGCAGGGTTATTGTACAGGAGCTCTTCTGTCTGCTCTCT
GATACTTGAGATTATAGGGTTGCAGGGAAATGCATTAGATGGCATTACAA
ACTGATAAGATAAAGTTAGGAGCTATCAGAGATTTAGGACATGGTTTTTC
TCTGTAAATGGGGCTTCTGGTGAGATTCCTAGAAAATGCTGTTTATAGCT
AGGAATGGGGTTATAGCTAGGAATGGGGAAAGACCTTAAGCAGTTGTGAG
CTGTGGTGGAATGCATGTGTTTTTCAGTTTGCTAAGGCTTCCGGGAATACT
TTTCTGTGCGATAATTTTCTTTCACCTCTCTTTGTAGCCTTCTTTGTATTA
AAATCCTCTCTGCTTGCTTTTGTGTGTGAATGTGTGTATGTGTGTGTTTG
TGTATGTGTGTGTATGCATGTGCATGTAGGTCCCTACATAGGACAGAACA

FIG.3D(17)

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TATTTCTGGAGTTATAGGTGCTTGTGAGCAGCCTTTTAGGGAACCAAAC
TCTGTCCTCTGGAAGAGTAGCCCCCTTAACTGCTGAGTCATTTAGCCTC
AAGAATCTTCTCTTTTCCCTATTAGTAGAAGATGTCATCTTAGCTCTAGG
AACTACACCACCTCTGGCCTCAGTGGACACCCATTTACATATGCACATAC
AGCAGACAGACATATAACTAAAGATAAAATAAATCTTTTTAAATGTCAT
TTCCCTGTGTAATAATTTTCCATGTACACACTCACAGGTAGATTTTTAAA
CTATTCTGAGTGATCACAAAGCAGAGCAGAAGGTGAAATTTGAGAGAATA
GATGATATTAGTGGATTTTGAGACCTTGAAAATAATGTCTCAGAGCATT
AATTAATCACTCATGTATGTATGTATGTATATAAGTATGTATGCATGTAT
TATGTGGATGGGGGTGCTGTAGCACATGTGTGGAAGTCAGAGGACAACCTT
TGTGAAGTCATGTTTCTCCTTCCATCTTTATATGGTTCAGTGATTGAGC
TCAGATTGTCTACCTGTGTAGCAAGTGCCTTACCTGCTGACCTGTGGCAC
TAGCCCTCTCAGAGGACTTTTAATATTTGGAATATTTCTAAGGATTGACA
GTCAAAGTTTATTGTGAGCCAGGCACTTAAATCCTAGCACTTGTGAGA
CACAAGATGGAGGTCAGTCCAGTCTACTGAGTTCTAGACCAGCAAGGGCT
ACACAGTGAAACCTGTCTCAAAAATTTCAAAGCGGAGCTAGAGAAATTA
CCCAAGGAGCTAAAGGGAACGCAACCCTATAGGTGGAACAACAATATGA
ACTAACCAGTACCTGGGAGCTCTTGTCTTTAGCTGCATATGTATCAAAG
ATGGCCTAGTGGCCATCACTGCAAAGAGAGGCCCATTTGGACTTGCAAAC
TTTATATGCCCCAGTACAGGGGAACGCCAGGGCCAAAAAGGGGGAGTGGG
TGGGTAGGGGATTGGGGGGGTGGGTATGGGGAACCTTTGGGATAGCATTG

FIG.3D(18)

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AAAATGTAAACGAGGAAAATACCTAATAATAAAAAAAGAAATGATATCA
GAAAAAATAAAAAATAAAAAATAAAATAAAATTTCAAAGCAA
CAACTCAAACCAGCCCTACGTCGTGCCTCTGAGTTCTCAGTAAATTCCTT
CTCTCTCTCCTCTCAGCACCATGTATGTGTTGCGCGGCTTCAACAGCCTC
CTCCTCAGTGACGTCTTGGTCTTTACCTCGGAGCAGTGCGATGCACACCG
CAGTGAAGCTGCTTGTGTGGCAGCAGGACCTGGTATCCGGTGTCTGTGGG
ACACACAGTCGTCTCGATGTACCTCCTGGGAGTTGGCAACTGAAGAACAA
GCAGAAAAGTTAAATCAGAGTGTTTTTCTAAAAGAAGTATGTTTTTCT
CTACTTAGAATTTAAAAATCTAATTTTATCTGAATTGTGAAGGAACCTAG
TCTCTGTACTTTCTGTTCACCTTACTCTCTAGTTATTTCTTAATAAAAA
AATACACAAGATCTTTGGATGGGAGGAAGCATGTGGCTCCTGGAAGCTGT
TAGCAGGTAATAAGTTGTCTTTGAATTACACAGGCTTTGTGTACCAACTC
CTGGTCTGGCTGCAGGTGATCTGAAGCCATAGCACAAATGAAATTTGTTTT
CATTTTGGTTTTATGAGACAGGGTCTTGCTCTATAGCTCATACTGGTCAA
GCTCCTTGTCAGCCTCCTCCTTCAGCCTCTTGAATGCTGGGGTTATAGGC
ATGCATCACTGGCCCTACTTGGGAAATATTTTGATGACAGACATGCTATA
TATTTCTTTGTTCAGTTTAGTAGCCACTAGCAATCTGTTATTATTAGATA
TTTGAAATGTGGCTATGTAAC TAAGGGGCTAACTGTTTTCTTTCTTTAG
TGTATGTAGTGAGGCAGATGTAGTAGCACACGCCTGCAATCCAGACACTC
ACGAGGCTGAGGCAAGAGGCAGTTCTAGGCCAGCCTGGGCTGTGTAATGA
GACCTTGTCTCAAGAGCCAAAACATCAACAATAAAAGAACAGTATGTGGC

FIG.3D(19)

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TATTGGCTGTTATGTTGATGATGAAGGTCTAGTGTTAAGGATAAGAGCCT
CTAATGGTATGATCACATATAGCAAATTGCTCTGGTAGACAGCAGAGAGC
TGCTGTTCTTGAAAAGTATTTCCAGCCCCCTTTAGCTGTATATAGCAAGC
AGTACAGCATAACAGACAACTATGGTCCCTTCTTCTAGAGCCCCCTGGCG
TGCTCTTGTTATTTTTCTCTCCTTTGCTACTTGCTTAGTGTTGCTCTGA
GCACCACTTCACCAACTCAGCGAAGTAACGTGCAAAAATGTTTGAAAAT
AAGAATGCCTCCAAGATATTTGTCCATATCAATCTTTAAAGTATGAACT
ACTTCCTTATCTAGTTGTTGCAGTTACATGAGAGTTATATTAGGCAGAGA
CTACTTCTGTTTTTCTGGTATGTGTTAAATAAAGTTGTGCAGGGACATAA
AGCTCCTGAGGCTGTGCTGTTGATTAGAATTTTGGTTCATTTATGGAAAA
CAGCTTACCAGAACCTGGTAGGATTCATAATTCTCCCGAAACAGTTAGAA
TTGGTAGAATAACCAAATTTAAAGTTAAGCTTAAATATACAGTGCATTG
GAAATAATATTATCTTCTGAGGTTCAAGTATGAGCCCATTAGTTTACCTCA
CTTTCTGGGTAGACCTAATCCTGTCAGAGTAACTTGGCAAGAAAAGCAG
CCTACATGAAAACCTGATCAGGCAGGGAAGTTTCTGTGGCCTCTCTTCTG
CTTGTGTATGTCATATTCATGAAATGATTTATAGATGGCAACATGGCTTT
TAGCTTCTTGTTTGGGGATTTAATGAGAATTATGTTAGGTCTACAAAGAG
TGGAAGTTGTGAAATCCACAGGTTTGGAGTCACATGAGTATATAGAGTTC
GAGTTAGCAAGTGCCTCCTGTGGGGTTGTGGGTCACTGGGTATACCTGCA
CCCAGGTAGGCCTTGCAATTTGTAACAAGGACAAATGTATTGGTCTCTCAT
ATTGCTTCTTAGGCTTCTGCACAGCTTCTGGTGTTAATTCGTGTGCTAG

FIG.3D(20)

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TTGATGTTTGTCTGGGAAGAAAAGCATCCATTACTTCTTAGAAGCTATA
AAATTAACAGACCTTTGCTTTTCACTTTCTGGACACTATGGGAGGACAGT
TATAAAACAGTGTTTCTCGGATTGTCTGCTTATATCTGTTTTATTTTAAC
CTAAACATGGCACTGCTTTTTTCTTTTCAGTTTGACTATACACTTTGCTT
CCTGACTATTGTTAGGAGCTTTCTACCTCAGATTATACATAAGAGAGGC
TGCCGCATAGTTGATGGGTTTGTCTTCTCTGTAGCCCTTGACCATGAC
AGATGTGACCAGCACACAGATTGTTACAGCTGCACAGCCAATACCAATGA
CTGCCACTGGTGCAATGATCACTGTGTCCCTGTGAACCACAGCTGCACAG
AAGGCCAGGTCAGATGCTGTTTTTCACGGATTTTAGGGAATAGAAAAATG
CTAGATGAGTGTGAGTGTAGGGCAAATAATGAGTAGAGTTCTTTTTAAAA
TGGGATATCGATTTGAATTCTACTGTTGCTCAGGTTTTCTCTTAGGAAGG
GATGCTATATACATCCTGATTCCAAGGATCGCTCCTGCTGCTGAGGTCTT
TGTGCAGTGTTTCCGAAAGCATGTTTTACAGAATGCCCTTGGCCCATATC
TGA CTCAGCATGACATCTGGGCTAATCATGTATGATTTGTTATAGGTGAT
AATAGGCTATGAGTAAGGTGATCCAGCTTTTGCTGTCTTTGATGGCTTAT
GACATTTTTTTCTCAAAGTTTAATGCATTTTCATAAGAAATAAGACTTGAG
ATTGCTATGGTGGGCACGGGCTGGGAGGAGCTCTGGAAAAGCAGCAGGTT
CAGCTTTCACGTTTTACAGATAAGCATTGGCTGAGGCTTGGTGGTGCCAG
TGGTTCCGTTGGGCTGCTAGCTTGCCAGCTAAAAGCATGTTAGTGAGAAT
ACACACTGTGGTATTCACATTGCAGTGCTGCTTCTGTTCAATTCTAATTC
TATCATTCATCCATCTACCTATCTCTATCTATCTATCTATCTATCTATCT

FIG.3D(21)

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ATCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCT
TATCTAATTCTATCTGTCTGTCTGTCTGTCTTTCTGTCTATCTATCCTCC
ATCTAATTCTATCTATCTGTCCACCTATCTATCATCTAATTTTATACATC
CATCCATCTATCCATCTATCTGTCTGTCTATCATATATGTAATTCTAACC
ATTCATCTATCTATCCACTTATCTGTCTGTCTATCTAATTCCATCCATTTA
TGTATCTATCTATATATCTAATTCTATCTATTCAATTCTTTTCTTTTTT
CTATCTTTCTTTCTGTCAGTTACCATTCTCAGTTAATTCTCACTGAGTTAT
TTGTGTGAATAACAAAACACTTCTCCCCTGTGTTCCAGATCTCCATTGCC
AAGTATGAGAGTTGCCCCAAGGATAACCCCATGTACTACTGCAATAAGAA
AACCAGCTGCAGGAGCTGTGCCCTAGACCAGAACTGCCAGTGGGAGCCCC
GGAATCAAGAGTGCATCGCCCTGCCGGGTAGGCCTTGACACAGGGATGTCC
TCTATAAGGTCCAAGCTTGGTCCTCCCTCCTCAGATCAAGGTGGACCTAG
GAACAAGATTGCTTATTCTGTCTATTTAGCCCTCTCACTATTGGGGGGGG
GGGGGGGCGATATTTTGTATGTTTTTAACTTAAATGTGGTTTTTATGTAT
GTATTTACTAGCCTTTGAAAGAAAGTGAAGTGTGAGCTCATGTTCTGGAG
AATTGGGGGGTAGCTTAGATCCATGTTACAACTGTGTCCCACTGTCCTT
CCTTCTGCTGTGAAGGAGAACCTGGCACTAGAGCTCTGTGGTCTCAGCAG
CAGTCAGGAACCTGCAGGAAGCACTTACTGACAGTTGTGTGAGAAGAGAT
TTCTGTACCAGCATCATCTCCCATGTGACCTTCCTTCCGGACTATTTAG
CAGAGGTTGTTAGGGTATTAACCTTAGGTCCCTGAGGCCAGCTAGCCCTGA
CTAAATCTCTATGATGTATTTGCTTGATCAGGATATGCAGGAAGGGGAGC

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TTCTGTGCTCTCCAACATCGAGGTTTGAGGGGAAGTTGGTCTGACTCTTT
TGAAAGCATTTTATTTAGTTTGCTGAATGGGCTTTAGTTTAGCCAGTGTT
CTATTGCTGTGAAGAGATACCATTTCACGCTGTAACTTTTATGAAAGGA
AACATTTAAGTGGGGGCTTGCACTCTCAGAAGCTATTATCATCATGACAG
GGAGCATAGAGGCACAAAGGCAGGCATTAGAGTGGTAGCTGAGAGCTACA
TCCTCATCTGTGAGCAGAGGCAGACAAGGTGTGAAAAAGACAGAACCTGG
CCTGGGCTTTTGAGACCTCAAAGTCTACCACCCCAGTGAGACACTTCCT
CCAACAGCTCCTGCAACAAAGCTCCATCCCCGATCCTTCTCCAGTCTTG
CCACTCCCTGGTGAATGAGCACTCACATATATGAGCCTATGGGGGTCATT
CTTACTCAAGCCACTACAGGCTTTGTTTTGTGTCTCAGACTTTATGTCAA
TAGAATACCTAGACACCTTGTTACAAGACAGGCCTGGAAAGCCTGCAGTG
CTGACTCCCTGCCAGTAGCACATTCTGAGGAGCAAGTCCCTTAAGTCGCT
TACCTGCTCTTACATTACGCCTTTCCCTGACCATTTAGTGAGCACTGTTG
GTGTCCCCAACCTGAACCTGGTTCTGGGGAAACACTTGCTTATTCACCTC
CGTGCTAATGGCCAGGGAGCAAGCATGCTTTCATGCAACACTGTGAGTTC
AGTACAACCACAGGAGGAGATTGCAGACTTCCTTCGTGTAAGTGTATCACT
ATGAGGTTTTCCAAACCAGTCTCCCTTTCACCTCATTTTTTGGCATGCCT
TATGTACTTGCTTATACTTTCTATCTTATGACATGAAAACAGAGTGGCAT
TTGGAGGCTTAAATTTATCACATTCCCAATTCAATTCCATTTTCAGTTTA
CTCTTTCTGTATATACATCAGTGTGCAGATAAATATCTCTTTGTGTGAGC
ATTGGAGGCCAGAGGTAAACCTCTGGTATATTCTTCCTCTATCACTCTTC

FIG.3D(23)

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ACAGGGTCCTTTGATGAATGTGGAGCTCACTGATTACATAGACTAGCTGA
CTCAACCCTCAGGCCTCATAACCCTGCCTCTAGCCCTCAGATGAGATTAC
AAGCAAGCAAACTACGCCTGGCCTTTTATGTGGGTGCTTGG AATTTGAA
CTGGGTACTTATGCTTGACACAAGTATTTTATGCACTGAACCATCTCCCA
AGCCTCCATTTGCAGTTTTTTACCTCACCTTCCAATATATATATTTATT
TGTATGCCCTTTGTTCAAGATTTTAGTCACCTTTTACATTTTTCTTCAA
AATAATTGCACCAATTTCTTAATAATGGCACCCAAAAGTAGGAACATTAG
CCTAGAGTATACCCTGTGAGCCAGGAAATGTGACTGGTGAGACTTGTA
AGGGTCTTTTTATTCTGGCCCTCAGCGGAGGCTCAGCAGTGGAGCATGCA
TGCTGTTCTCTGGAGGACCCGAGGTCCCCAGGGGCCAGGTCACAACCAC
TTGTAACTTTAACTCTGATCTAATGCCCTCTATGGCTTTTGTGCTATAGT
CTCTTGCACTAACCACACTCAAGGCACACATACACACATTCTTTAAAAG
ATAAATTATTTATTTTCAAAGGTTTTTTTCTGCATATAGAAGTTAATAA
TTTGTCTGTTATGCTCACCAGATCCTAACAAAGCACCTGAAATTCAAATC
AGGATGAGTTCAGATGTTCAGTATTTTGAAGTAGTAAACCGAACTGCATA
ATTCCTAAACTTTGTTTTCTTCTCTTCCCCTTTAAAAAAGAAAATAT
CTGTGGCAATGGCTGGCATTGTTGGTGGAACTCGTGTCTGAAAATCACTA
CTGCTAAGGAGAATTATGACAATGCTAAATGTCCTGTAGGAACCACAAT
GCCTTTTTGGCTTCCCTCACATCCCAGAAGAAGGTGGAGTTTGTCTTAA
GCAGCTTCGATTAATGCAATCATCTCAAAGTATGGTGAGTTAATGTGTTC
AGAACTTTGGTTTCTAGGGCACAAACAGCAGCTCTTATGTAGAAGGCCACA

FIG.3D(24)

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GTTGTATGTTATTTGCCTGGTAAGAGAAAGAATTACAATAAATGATTAAT
AATATACTGTGGGCCTCTATTTTCAGAGGCTCTTCTTTTGATACCTTTCTT
CTTGTCTTAAAAAGTTCAGTACTTTGCATATTTTATTAGTTGTTATTATT
AAGTAAATTATAAGGTATGAACATATGGAATGAATGGTAATATGTGTACA
TATTCTGGTGACATCAGATTATTTTGTACTTGATTTATATCTAGATTCTG
CTTGGGAAAAGGGAGAGTAAATGTTAGTTACCTAGGTGTCATTAAAGCC
ATCTACAGCCCCTGGAGGTATTATTATAGCACATAGTGAATCGTCAGTA
AGAAATGTAAATCTGCCCAGGTTTTATAGCCTTCTTCCTAAGGCTTCTG
AACTCAGAAAGTTCTCTTACTCTAGAGCCAACTCTCAAATGGCTTG TAG
T TACTATATAGTCTCATTGGTATTTTCTTGGTAAGTCTAATTCTAAGA
CTTGTGATTTGACTGTGATGCTTCAGTCAATTAGATATTCACAGAGCAGC
TTTTCTGTCTATGCTGGCTGTGGTACAGAGAGATGTGAGGGACATGTTTT
TGTCTAGCCAGGAGAAGACAGAATGCAGCTCAGCATCTCTCATTG G CAC
CACCTTCATGTGATGGGATGCCGGTATGGTGTGGGTCTGGTTGTTAAAT
CTCAGGAAGTCCATATATCCAGAAATGACCTCAACTATAGGTGGATTCT
GGCAATTAGGTAAAAGTCAGCATTCTTGGGCACTTGGGAAACTGGTTAC
CATCTGCATAAAGGAGTCATTTCCCTTCTATCTGGCAGAAGGGACATATG
GCTATCTATTGTGCCTGTCAGCATGGAAGCACATGCTAGTCTCCAGGTCC
CCCCAATATCACAAGTACCTATAGCAGTGAATTAGTTAAACTGATTG G C
TCCCAATGGGTCAAGTACAGCTGCACCTGCCCAAGAGCTCTTTGGGTTTG
CAAATGAGAGACACATAGTTAATTTTTATATGCTTTGACTAGTTCAGTTG

FIG.3D(25)

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CTGGACATTTCTAATCCTCCCTGCAGTAGCATACATTAACCCCTCCAAC
TTCCTGAGTCAACTTACTAACTCAACATTTTCATCTCTGACACCCCAGACC
TAATGGCAGAGTGGCCCTTAGAGCCACTTTCCCAATTTTTTTTTTATCAG
ATATTTTCTTTATTTTCATTTCCAATGTCCCCTTTCCTAGTTTCCCTGTC
CTCTCCCCCTGCTCCCCAACCCACCCACTCCCTCTTCCTGGCCTTGGCAT
TCCCCTATACTGGGGCATAGAGCCTTCACAGGACCAAGGACCTCTCCTCC
CATTGATGACCGACTAGGCCATCCTCTGCTGAATATACAGCTAGCACCAC
GAGTCCCACCATGTGTTTTCTTTGATTGGTGGTTTAGTCTCAGGGAGCTC
TGGGGTACTGGTTAGTTCATATTGGTGTTCACCTTTCCCAAATTCTTACAT
GGCTGGTTTAGTTCCTTTCCTGCAGCTCTTAGGTCTAATCCCTTTCCTTCC
TCTGTCATGGTGATTGCCTTCCTCTCCTATCTCAGTTCCTTGCCTGCTCA
ATCTAAAAGTCCCACCTCCATCTTTCTGCCCAGCCACTGGCTGTATGCAG
TTCTTTATTATCAGTTGAAGCCAGCTAGGGGCAGAGACCTTCAGGTCTGT
AAGTGCTTTGGGGAGCAGAATTAAGACAAAGCATTAGAACCAATTCCCAA
CAAGTACCTGCTATACATTTCAAAGTCCATATTAGTCTCCTGGGTCTTCC
CTTCCCCAGCTACTTGTCTCCTTGTAATCCAAATGACAAGCTTTTTTAC
ACATCTCTTTATCTCACATTTCCCTAGCCCTGGCCATGTCCACTTGTCT
TTACTCTCTGCTCTGCTCTCTTTCCAATGCCCTCTGGATATTTCTCTCT
CTTATTCACAATAAAAACCAAACCAAACCAAACAAAAACCTTACCCTAA
TAATGGAGTGGTCAGGCCTGAGGTTTCTTACTGCTCCCCCTTGCACAGG
TCTTGTGTCTGACACACTGGCAGGCTTTTATTAGCAGCAGGCTCTAGGAG

FIG.3D(26)

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CTGAGAGAAGCAGCAGGCACCTCTGAGGTGGTAGTTACTAGAGTGATTAG
AACAGACAGTGGAGACGTGGCTGGAAATATGGACTCTGGTGTGTTGGAGCC
AAGTATGGTAGGCGGCAGAAGCCAGCAGAAGCATGATCCACACCTTCACC
AGGTTGCTTCCATTGGGAAAGGCTGGACCCCTTGGGAAGGGGTCCCTTTG
TGCCTTCCTAGGTGTTCTGGAGCCAGGTGTGTGAGGGATACAGTAAAGGGA
CTGACTGCATGACTGCTCCATTAGGGTGAAGGGTTTTGTTGTGAATAGGA
GAAACAAAATGTGCAGAGGCATCTGGGAGAGAGCAGAGCAGAGTGAAAAG
GAAGCAGTGTAGGCATGGTCAGGGCTAGGGACAGCGGAGACAGCAAGATA
GCGAGTGGGTGATAAGGTGAGAGAGAGTGTGTGTGTGCGGTGCACACATC
ACGTGCATTATAAGGAGGCTGAGTAGCTAGCTGGGGGGAGGGAAGGGCCA
GAAACTAGCATGCACTCTGAAACGGGTACTTGTGATGCTGAGGGAGCTT
GGGGGAGAAGGGCATGCCTCAAGACCAGAAGAGGGAGTTGGAGTTACAGT
TTGTAAGATGCCTAATTTGAATGCTGAGATCCAACTCTGATCCTTTGGC
TGAACATCATATCTGCTGAGCCATCTCTCCAGCCCCTAGAAAGGTGGTGA
TGGTGGTTGTTCTTGTTTTGTTTTATTTTGTTTAAATGGGGAGCCAGGTA
CAGTACATCATGCCTTTAATCCCAGCAGGAGATTCAGGAGATAGAGACAG
GTAGATCTCTTTGAGTTCAAGGGCACCTTGGTGTGTATAGGAAATTCCAT
CCACCCAGGGCTACAGAAGGGTACCTTGTCTTTAAAAAAAAAAAAAAGAA
AGAAAGAAAGAAAAAGAAAAAAAAAAGAGAATGAAATTTAGAGTTATGC
AAGATAGGAGCTCAGTGGTAGAGTGTGTGCCCAGGAAGTGCTGGGTTTGA
CTCCTCAGAACACAGCAGGGGCAGAACTAGTCTACAGGTTTATGAGTG

FIG.3D(27)

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GTGTTTTGTTTTGTTTTACATAAAATGTGTTGAATTAGATAAGTAGATAA
AATGTGACTCATACACAGATAAATAGATAAAATGTGATACATGTACCTGT
ACATAGAAGATTATGATCTCACCTTTAAAAAGGAGGAAATAGAGAGTTTT
GGTAGTTACACCACAGGAAAACCTGGAAAAGAAAATGTATATATGAGGCTG
TGCCCCATGGCTAAAGGAACATGTTTTTAAGTCATTTGAATTCACCAAAC
AGTTTTAGGTAATGATATATGGTTTTGCATACAACCAGTATTTTATAAAT
ATTAGCAAGGTCACATCATTTATGAACCAACATTTAAACTAAATTTGTAA
ATCATCATTTCTTTATAGCACTTGTCATAGAACATAAGTAGTTTAAATG
TGATTATTGCTTTGCTCTTGATGTCTGAAAATCTTCATGTATTCTCTCT
TTGAGCCATTTTTATGCTTTGCAGTACTGGATGCATATTGAAGTGATCAC
TTATTTTAATCTACCTTGCCTGAGTTTGGGGAATAGATGGTTTCCACATG
TCTGTGGGTTATGCCTAAGCTAGTGGTTTTTATGTTAGAGCTTGTTTTGG
GGAAGGCACTGGTTGCATTCATAGCTGTGTTTCTTTTGCCTGTAGTCCAA
GCTCACTCTGACTCCATGGGTTGGTCTTGGGAAGATCAATGTGTCTTACT
GGTGCTGGGAGGATATGTCTCCATTCACAAATAGTTTGCTGCAGTGGATG
CCATCTGAGCCCAGTGATGCTGGCTTCTGTGGGATCTTGTGAGAGCCTAG
TACTCGGGGATTAAAGGCTGCAACCTGCATCAACCCTCTCAATGGCAGCG
TCTGTGAAAGGCCTGGTAAGGACATGGGTGCATATAGTGCTCCAGGAGGA
GCCAAGACAGCAAAGGAGGCACAGCTGAATGAGCGCTGAGGTGATGAAGT
ACTTATGGCAGCAGGGAGAGGAGCACCAATTTAGGCATATGTATTTCAA
CAGAACCCGATTCCAGATAGTCTTTCTTGGCCTCTGACTGCTTTAAGCCA

FIG.3D(28)

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TACTGAAAACCAAAAATAAAATTGCTGAAAGAACCCAGTTTATATTGAGC
TGCACTGTTTCGTTGGTCTCAAAGTGTTGAGAATTGTTCTAGAAGATTAT
TTCCTTGGTGTTGGCAGAGAAGTGCTATGGAGGAAACAACAACCTGAAAC
CAAAGAAACATTTAGAAAAGCAGCAAGTCAGGACACTATTCAGACACTGC
TGGGGTGGGGGGAGAGGGGCATGGCCAAAGAAGCCGACAGAGCCAACACC
AGGCTGTGGCAATGTCCTGCGCTGAGGTAAAGTTAGACTCCATGAGGCC
AGGCCCAGAACAGCCATACACAAATGAGGACTCCAAAACAAGAGGTGCAA
GTGTAGTGGAGACTCCATCCCTGCAGGTCTGTTTCAGGAAATGATTGTA
CTTTGCCTGAGTAATACAGCCTAGGAGCTACTTTCTGATAGGGTTTTTTA
AATACTTACAAAGAATTATTTATCTTTAATCATGTGGTTTTGTATGTGTG
TGCTTGACATGCAGTGCTTGTGAGAGAGAGTATGTGTGAGAGCATGCAT
GTATGAGAGTGTGAGAATATATGTGAGAGAGTGTGAGTGCATGTGTGCGT
GTGTGCATCTGTGTGTACAGGTGTGTGTACATGCATGTGTGTATAAGAGT
ATGTGAGAGTGTGGGTGTGTGTGTGAGAGTATGTGAGAATATATGTATGA
GTGTGTGTGAGTATGAGTGTATGTGCGTGCCTGCATGTGTGTGTGTGTGT
GT
GAGTTGTCAGATCTCTTAGAGATATAGTTGCAGTTGGTTGTGAGCCATCT
CATATGAGCGCTGGAAGTTGAAATTGGGTTCTCTGGAATCCTCTGGGTTT
CTTGTTGAAGCCTGAATATTTTGATAAATATTTATGTCATTATCCCTCAA
AATTGTAAATGTAGAATTTAACAACCTCAGGTCTTGAGTCATCTTTGTCC
CAAGGTTTGTTTGTTTGGTTTTTTGTTCCCCACCTTTTCTTCAGTGCTT

FIG.3D(29)

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TTAAAAAAGAGAGTCCATTTTTCTCTAAATGTTTAAATACAGTTGAGGAA
TAGAACATCTGACTCCAATTTCTGGGTTTCCCTCCATGTAGTGTAGTGC
TGACCTGATTTCAAGTGTGCATTGAAAACTTTGATCACTTGGAAGGCAGCT
ATGCTCACCCTATACTACCAATGTCTGCAATCCTATAGGAGAAACAACA
ATATGAACTAACTAGTACCCCCAGAGCTGTGTCTCTAGTTGCATATGTA
GCAGAGGATGGCCTAGTCAGCCATCATTGGGAGGAGAGGCCCTTGGTATT
GCCAAGATCATATGCCCCAGTACAGGGGAATGCCAGGACCAGGAAGCAAG
AGTGGGTGGGTTGGGGAGCAGTGCGGGGGGGGGGGTATAGGGGGTTTTG
GGGATAGCATTGAAATGTAAATGAAGAAAATAACTAATAAAAATTGCCT
TAAAAAAAACAAAAAAGAAAAGTTTTTGATCTTAGCTGACCAGTGTCTC
TTTGGGTCTTAATTTCCAGCAAACCACAGTGCCAAGCAGTGCCGGACACC
ATGTGCCCTGCGGACAGCGTGTGGCGAGTGCACTAGCAGCAGCTCGGAGT
GCATGTGGTGCAGTAACATGAAGCAGTGTGTGGACTCCAATGCCTAGGTG
GCCTCCTTCCCTTTTGGCCAGTGTATGGAATGGTATACGATGAGCAGCTG
CCCACGTAAGTGGAAGGAGCTTTTGAACATTTGCAGGCAAGTTGGGCTTG
ACTTTCTGCTCAAGTCCATGCAGAAGCTGGTCGGGCGGGCCCTTCCAGAT
TAACATGTATGTATAGAATGCAGCACAGTGTTCATGCAGTAAATCAGTT
ACATCAAGGAGAAGGCACAGGGTACAGAAATACCTTTTCTTCTTCAGGGT
AATATTATAATTCAATCTGTATAATGTTTCTACATCTTAATCTACCACTA
TGTAAGTGCTTTCTAGTAGAGGCTCCCGAGCTCCCTTTTTTCATCCAAC
ATCCTGATATTAAAAGGTTGGAAAAGTCCCTGTTATATATTATGTAAAT

FIG.3D(30)

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GTGGGGCCCTTTAAATTATTTTCAGTTCAATAATCACTATAGGGTACTATT
TTTAATTCATGGAAGTTAAATCATCTGTAAAAGAAAAGGTAATAACAGT
AAATTCAAATCTTGTGATAGTGAATTACAAGTTGGATTGTTTTGCCTTGT
TTTTTAATAGCTGAAAATTGCTCTGGCTACTGTACCTGCAGCCATTGCTT
GGAGCAGCCAGGCTGTGGTTGGTGTACTGATCCTAGCAATACTGGGAAAG
GAAAATGTATTGAGGGCAGCTATAAAGGACCTGTGAAGATGCCGTCACAG
GCCTCTGCAGGAAATGTGTATCCACAGCCCCTTCTGAACTCCAGCATGTG
TCTAGAGGACAGCAGATACAACCTGGTCTTTCATTCACTGTCCAGGTAAGA
TGCCTGTGTATCCTAGTTCAAATCTCGTACATAAACTAGACGCCCAGATC
CCTTGGCTCACTTGTTTTCTTGACTGTGTTTGAGTTCTTCTGTGTTCTG
CATCACCTTGTTGGATCATAGCTGGCAAAGGTGCTCTCCTTTCTGTGGGC
TTTTTCTTTACTTGATTGATTGTTTCTTGGTTGCACAGAAGCTTTTTAG
CTTCTGAAGTCCCATTTGCCAGTTGTCCTTAATTCCTGGGCGAGTAGAA
GCCTCATAAAAAAAGTTCCTTCCTACACATGTATCATGTAGGGCACTGC
CTATGTTTTATTCCAGAAGTTTCAGAGGTTGCGGTATGTCTTTGATCCA
TTTAGGGTACTTTTTGTGAAAGGTAATGGACACAGTTCTGTTTCATTCA
TTATTCTACATGTGGACATCTACTTTTCCAGCACCAGTTTTGAAGATGT
TATCTTTTCTGCAGGTTGTTTGTTTGCTTGTTTGTCTCTTCAGAAAATC
CCAGATGGCGGTAGCTGTGAGTGCTTAGGCTTGGCCTACCTGTTTCATTA
TGTTGGCTTGCATGTCTGTTTTGTGCAGTGCCACCATATTGTCTTAATTG
CTATAGCTCTGCAATCTATCTTGACATCTGTGTTGGCAATCCTGCAGTTT

FIG.3D(31)

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CGACCCTTCTGCTCAGCAGTGCTTTGGCCATCTGGGGTCTTTTCTGGGT
CATAATGAATTTTAGGATTTTTTTTTCTATTTCTGAGAAAGTATTGTTGA
TATTTTGATTGCGATTGAATTGAATCTGTAAATTGCTTTTGGTAGAATGG
TCATTTTCACAATATTAATTTTACTGATCCATGAACATAGGATGACTCCA
GTCTCTCATGTCTCCCTATAGCCCTGTCTTAAGAGATTTGGAGTCTTCAT
TGTAGAAGTCCTTCACCTCCTTGGTTAAGTTTATTTCTAGATATTGTATT
GTCTTTGGTATTATAAATGGTAGTATGTCCATGATCTTGTTCTCAGTGTT
TTTTTAGTTTAGTTTTTTTTAATTTATGTGTATGAGTGTTTGTTTTATAT
ATGTGTATATGTGCATTCATGTCTCTGGGCATCAGATCCCCTGGGACTG
GATTTACAGACAGCTTTGAGCTGCCTGTAGGTGCTGAGAATTGAACCCAG
GTCCTCTGCAAGAACAGCCAGTGCTCCTACTCCCCAGCCCCAGAAGTACT
AATTTTTAAGAGCTGATTTTCTACCTTTGCTGACATTGTTGATTGTTTCT
AGAAGTTTAGTGATAGAGTTTTTGAGATTTCTTATATATCTTATGTTATC
TGTA AAAAGGGATAATTTGACTCCTTTTCCTATTTATATCCTTTTATTTC
TTTCATTTGCCATATTGTTCTAGCTAGTGCTTCCGGCTCAGTATTGAAAA
GAGTGGTGATTGTGAACAGCTTTTCTTATTTCTTATTTTAATGGGATTAT
TCACCCATTTAAGATAATGTTGGTTATGGGTTTGT CATACACAGCCCTTC
TTATATTGAGGTATGTTCCCTCCAGTCCTGTTCTCTCTAGGACTTTTTTT
TTTTTAATCAAGAAAGCATATTGGGTTTTTTGTGTGTGTTATTTTGT
GTTTTTCTAGACAAGGTTTCTCTGTGCAGCCCTGGCTGTCTCTGGAATTCA
CTCTGTAGACCAGGCTGGCCTTGAAGTCAGAAATCCACCTGCCTCTGCCT

FIG.3D(32)

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CCCGAGTGCTGGGATTAAAGGCGTGCACCACCACTGCCTGGCACATGTTG
GTTATTTTGCAAGCCCTTTCTACATCTACTAAGATGAGCATGTGGTTTCA
TCTTTGTCTGTTTATATTGTCTGTTGTATTTATTGACTTATGTGTGTTGA
GCCAACCTGAAGTTCTGGGATAAAACCCACATGCTTTGGATGATTTTTGT
GCTATGTGCTTATATTGTGTTTGTAGTGCTTTATTGAGGACGTCTGCAT
CCGTGTTTCATCTGGGGTACTGTCTGTAGTTTGCTTATTTTGTGTCTTTA
CCTGCTCTGCATTTTAGAGTAATCCTGGATTTATAGAAAGCATTGTTGGGAG
TAGTCCTTCTGTTTATTAATAAAAAAAAAAATTAAGAATGATTGGTTGTTGTG
TGGTGGAATTCTGCTGTGAACCCATCTGGTTCTGGACTCTATTCGGAAGG
CTTTTTATTACTGTTTCAGTCTCCTTGTTTGCAGTGATCTATTTAGGTTG
CTAATCTCCTTATGATTCATTTGGATGAATCAAGAAATTAATCCATCTCT
TTAGATTTCCAGCTTAATGGAATATGAGTGTTAAAGTATTTCTTTATAGC
ATTCTGTATTTTTTGGCATCTGTTGTAATATTTCCCTGTTCTTTCTGTTA
ATCTCTTTCTTTCTTGTTGGTTAGTTGGGCTAAGAGGCTCTTGGTTTTTTT
TTTTTTTTTTTATCTTTTTAAAGGACCAGCTCTTAGATTCATTAATTCTT
TGTATTATTTTCCTTGTTTCTTTTCACTGATTCATTTTAGATTTTATT
ATTTCTTGCCATCTACTGCGTTTGGGTTGGTTTTAGTTATTTTTCCAAGA
TTTTCAGTTTCATCACTAAGTCATTCATTTGGGCTCTTTTGGGTTTCTTC
ACGAGAACCCACTTGGGACTGTTACCTTCCCTTTTAGACCTGCTTTTAAT
GTGCCCCAGAGATTTGTTACATTGTCTTTTCGATTTAACTTAGTTTCAGG
AATATTTTGATTTCTTCTTTGACCCATTTCATTCATTCGGTAATGAGTTGTT

FIG.3D(33)

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TAATCTCTAGTGAGTTTATACATTTATTAGAATTTTGTTTACTGATGATT
TTAAGGTGTTTGGCTTTGTTTGTGTTGTTTGTGTTTGTGTTTGGAGACA
GGGTTTCTCTGTTGTAGCTCTGGCTTTCTCTATGTAGAACAGTCTGACCT
CAAATTCACAGAGATCCACCTGCCTCTGCCACTGAAGTCTGGGATTAAA
GGTGTGTGCCACCACTACCTGGCTGATTTTAAGTTTTATTACATAATAGA
CAGGTAGGGTACATAGATTTTCTACATTTGTGAAGGTTTGCCTTGTGTTGT
CAGCATGTAATTCTGTGTGCTGCTGAGGGAATGTATGTTGTTTTGACAGT
TAGGTGGAAAAGTCTGTAGACATCTGTTAGATCCATTTACATTTCAAGA
AGCCATTTAATTCTGAAGTTTCTCTGCTTATTTTTTCCCAGGTGACTTAC
CTATTGGAGAAAATAGGGTGCTAAAATCATTTACTATTATTGTTTTTTTT
AAGAAGAAAATAATTAATTTAAAAAACCTGGAAAGAAAGATACCAAATG
TGAATCATGTTTCTGGATAGTGGGGTTATATTGATCATTTATTTTTCC
TCTCAAATACTGTGAGTTTTTACAATGAATAACAACATAAATATTTTTAT
GTTGCTGTGGACTTTAACTTTGCTTTGATAATATATTGGTTTTTTGAGA
CTAATTTCTTTTTGATATTTTATTTTCTCATACTAGTTTTTAGTAACTT
TGGTTTTGTTTTGTTTGTATTTTTTAGACTGGCCACCAACTTGCTATGTT
GTCAAGGGTGGCCTTAAAATCCACACCCAATACTTTGTCCTCTCTTTCTT
CTTTCTTTTTTTTTTTTTATTGGAACAAAATTTCTAGGTGGGAATCTCAC
TATGTTACCCAGGCTGACCTGAAACTTCTGGGCTTAAGCAAGATGGGTGC
ACATGATCAGAGACGCTGCGCTGCCCGCCTCAGCCCCCTGCTAGTTGGAAC
TATAGGCACAGACAGCTGTACTTCACTCATTTCAATGATTTAACATTTAG

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ACTATATGCAAATAAATATGAAATGTATTCACCAAGTTCTCCTATGGGAG
AAACAGAGCCCTTAAGATTTTTTCTTTTCAGCTTGCCAGTGCAACGGACA
CAGCAAATGCATCAACCAGAGTATCTGTGAGAAGTGTGAGGACCTGACCA
CGGGCAAGCACTGCGAGACCTGCATATCTGGCTTCTATGGTGACCCGACT
AATGGAGGCAAATGTCAGCGTAAGTCACACAGGTCAAGTTAGTCACAAGT
CAGGTACAATAGTACAGTACCTGCAGTTGACTTAAATATCTTAAAGGGAA
AAGGCCTCTTGGTTTGGGATATTGCCTTTCTTAATTATGTTAAATTGTTA
AAAGTTTAACTGAGGGGCTAGAAATGTGGCTCAGTTGGCTAAGAACACTG
ACTGTTCTTCTAGAGGACCGAGGTTCAATTCCCAGCACCCACATGGCAGC
TCACAAGTGCTTGTAACACCTGGGATCCAACAACCTCATACAGACATACA
TGCATGCAAAACACTAATATACATAAAATAAATCCATTAAAAAGTGTTTG
ATGATGCTGGAAGAGGAAAAAAGGCTCAACTTGTGGGTTTGGGAGCAGTT
AGTTAAAGCAACAAACCGACAGTAAAGGAGCTAAGCTTTTATTTCTTCAG
CAGAGGCATAAACAAGGGGCCGAAGTCACTGAGGCACCAGCTGCCTTTAT
TCCATTTCCCTCCCATGGAAGCACATCAGCTCAAGTCAAGCAGAGCAGCC
TGGGATGGGAGGTCATCTCATTGGAGAAGGAGGCAGGAGGCATTGTGAGG
GGAGGGAGGACAAGGCTGGGAATGGGAAGTCCTGAGCTCAGAATCAGAAT
GAGGACAAGATCTTCAGTTTCCTTCTTAATATAAAGAGGTATCACAGAGG
TCTCTATAGAAGTCTACTGGAAGCCTCACACAGGCACAAGGGTACATTTG
AAAACTGTGACAGCCAGGGAGAGTCCCCTTCTGAAGTGTCTTCCTCAG
AGACTGCAGCACCTGACTGTGCCCCAGTCTGCAAGAGGTTTGGGGAGAGC

FIG.3D(35)

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AACTGACCTCCTGAGGACCCAGATGAATCTTTAAGATGGCCTGCTTTTG
GTTTTGGTTGGTTGGTTTTAGACAGATCTAGGAGAGTTGGTGATGAGCT
TGAATTCTCTGTCCTCCTGCCTGACCTCCAAATGCCAGCTTCACATGGG
CTCCCATTAAGTTGTGAGTTTCGGTGTCTGGCTCCTGCTCTCACAGCCAG
TGCAGTACATTGAGCTCCATAGAGATAGCGCCGGGGCAAATGAGAGCTGG
ACGGGCACTGGGTGACTCTGTGCCTTGTGCCGGAAAATCAACTAAACATG
GGCAAAGGAGATCCTAAGAAGCCGAGAGGCAAAATGTCCTCATATGCACT
CTTTGTGAAAACCTGCTGGGAGGAGCACAAGAAGAAGCACCGGATGCTT
CTGTCAACTTCTCAGAGTTCTCCAAGAAGTGCTCAGAGAGGTGGAAGACC
ATGTCTGCTAAAGAAAAGGGGAAATTTGAAGATATGGCAAAGGCTGACAA
GGCTCGTTATGAAAGAGAAATGAAAACCTACATCCCCTGCCCCCAAACAG
GAGACCAAAACGAAGTACTAGGACCCCAATGCACCCAATGCCTTCTTCGG
CCTTCTTGTTCTGTTCTGAGTACCTCCCCAAAATCAAAGGTGAGCACCCA
GCTTATCCATTGGTGATGTTGCAAAGAACTAGGAGAGATGTGAACAAGG
CTGCAGCAGATGACAAGCAACCCTAGGAGAAGAAGGCTGCCAAGCTGAAG
GAAAAGTACGAGAAGGATATTGCTGCCTACAGAGCTAAAGGAAAACCTGA
TGCAGCAAAAAAAAAAAAAAGGGGGGTGGCCAAGGCTGAAAAGAGCAAGA
AAAAGAAGGAAGAGGAAGATGGGAGGAGTATGAGGAAGAGGAGGAAGAAG
AAAGATGAAGAAGAATATGATGATGATGAATAAGCTGGTTCTAGTTTTTT
TCTCATCTATAAAGCATTTAACCCCCCTGTATACAATTCACCTCTTTTAA
AGAAAAAATTGAAATGTAAGCCTGTGTTAGATTGTGTTTTAACTTTAC

FIG.3D(36)

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AGTGTCTTTTTTTGTATAATTAACATACTGCCGAATATGTCTTTAGATA
GCCCTGTTCTGGTGGTATTTTCAATAGCCAGTAACCTTGCCTGGTACAGT
CTGGGGGTTGTAAATTGGCATGGAAATTTAAAGCAGGTTCTTGTTGGTGC
ACAGCATAAATTAGTTATATATGGGGACAGTAGTTTGGTTTTGGTTTTAT
TTTTGGGTTTTTTTTTTTCATCTTCAGTCGCCTCTGATGCAGCTTATATG
AATATGATTGTTGTTCTGTAACTGAATACCACTCTGTAATTGAAAAAA
AAAATCGTGGCTGTCTTGACATCCTGAATGTTTCTAAGTAAATACAGTTT
TGTTTTTATTAATATTGTCCTTCGACAGGTCTGAAAGTTTTCTTCTTGA
GGGAAAGCAGTCTTTTGCTTTTGTCCTTTTGGGTCACATGGGTACTGC
AGTGTGTATCTTTTCATATAGTTAGCTGGAAGAAAGCTTTTGTCCACACA
CCCTGCATATTGTGGTAGGGGTAACACTTTCATCCATATTCAAAGAATCT
CCAAAATCGTGATCAGTTGGATAAGAAATATTATATAACCTACTTGGCAA
AGCAAGGTGTGATCAATTCTGTACACCATGGGATCATTAGAATCAAGCA
ATCTGAAAATCTGTCCTTAAAGGACTGATAGAAAAGTATTTTCTAATCCT
TATACAAAGGCTCTCCTTTAACTGCCACTGCTATGTAATGACAGTTATGT
TTTGCAGTTTCCCTACTAAAGAAGACCTGAGAATGTATCCCCAAAAGCGT
GAGCCTAAACTACACAACCTGCAGTACTATTTGTTGACCTTAGTCCCAGCG
AAGGCTATCACGAGAATGCTAGCTATAATATAATGCCTCTGCCCCTCTAT
CTAAATATGGATTGCTCAGGAACTTGACTGCTTAAAGGTATTTTTTTCA
TATTGTTGTTCTCCTATAGGGTTGCAGACCCCTTTAGCTCCTTGGGTAC
TCTCTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATC

FIG.3D(37)

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TATCTCTTGT CAGATTTCTTTTTCTTTCTTTCTTTCTTTCTTTCTTTTT
TAAGATTTATTTATTATTATTCTAAGTACACTGTAGCTGTCTTCAGATG
CACCAGAAGAGGGTGT CAGATCTCATTACGGATGGTTGTGAGCCACCATG
TGGTTGCTGGGCTTTGAACTCAGGACCTTAGGAAGAGCAGTCGGTGCTCT
TAACCACTGAGCCATCTCTACAACCCTTAAAGGTATTTTTAAGTAGTTGA
GTCAGCTTTTTAAAATTATGCCAGAAGTGCAAAAGTTCAAAAGTTTAGGA
CCATCCTCTATTGAAGTACAGGGTCATCCTGGGCTACATGAGACCCTGCC
TTAAAACCAAAATCAAACAAACAACAGGAAAAACAAGAGTTAAGAAAGAG
AAAAAGAAGCACTTGGAACAAAGATCTGTGGAGTATGTATAGGCTTCTC
TACAACAGGTGTATGTAGGATCTTGATGGCTTTTGAGTCTATTACCCTCA
AAGAGGTA CTGAGAAACCTAAATGTGATCACCGTGGTCTCTGAGGGGCAC
CTGGCAGGATTATGGGAGATAACTAAAGCTTGCTAATCACAGAGTTTAGG
GAGGGAGGACGTCTCTAAGGCAAGTTAACTGTCTGGTTTGAGATGCTTAG
GTGATGTCTGAGGAAGTAATAAGGCCTGTCCATTTTCATACACACTCAGG
CCTTAAGTCTGGGTAATGGCTACTTGAACATAAAATAGTCCTCTATGAAA
GGAATAATATCTCTGTGTCAGCAGCCTTCACGGCTAATGTTAATTGTGCA
GGAACCCTGCTTCTCAGTCAGACAGAAGCTCAATCAGGCAGGGGCAGGAC
TTCTTTGCCTTTCCCATGTCTTGTAATTTCCCTGGCTTTTCATCTTGGT
TCAAACATACTTACCTGTTAGGTAATTATAAGAACACCAAATATTACTGA
ATAAAATGTGTTTATGACTTTGTGGTGACTGCCATTCAAGAATTAGATGC
CTTAGCCAGCAATGATGGCACAGGCCTTTAATCCCAGCACTTGGGAGGCA

FIG.3D(38)

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GAGATAGGCAGATTTCTGAGTTCCAGGACAGCCAGGGCTACACAGAGAAA
CCCTGTCTCGAAAAACAAAACAAACAAAAAGATTTGATGTCTTT
ATCACCCAAATCAAGTAACTTTCCAAAGTCTCACAGTGAGATGTAGCCTA
GTTGGGAGCCACATCTAATATATGCTGATGATCTTAACAAGTAGCCTGCT
TGTGTCTTCAGGTGACCACCCCGGTGTCCTCAGCTACCTCTAGAAAGATC
ACACTTTCCTCTGTGGTCTCTGCAGGGTCCCTGTATGATTCTGGAACCTT
GCTGTACTTCTCAGAGTCTGATTCATAAAGCACTGAGTTTTTGCTTGTT
TGTTTGTTTGATACTATTGGTAAGAATATATATTGAACCTTGACATGCC
TTTTTAAATAACATTATTTTACAATAGTACTTTAGCCTTGATTATGTT
AACTGCTTACTGTTTCAGATGACATTCGTACATCTTTTAATCCTCAAACC
AGTCCTATGAGATGGCTAGCATCATTGTCACATCATTTAGGCAAGGAAAC
AGGTCTTGGGTAAAGCTTCATGCTCAGAGCTCCTTGGAACACAGTGGACT
CAAGTGCAAGCAGACTGACGCGACTGGGTTTTACTAATTAGTAAGCCTG
TACTCTATGGAGGAAGAGTTTCTGACCACTGGATGCAGTCTGATGACCTC
TGACTGTTCTGTTTGAAAGGTTTCTTTCAGTGATTTTATTTTCTCCATG
TGGACTTTTTTCCAGCTTTTAAAATATATATATATATCTTATTCGCTTC
ACATCCTGCTCACTGTCCTCCCTCCCCTGTCATCCCCTCCTACAATCCTT
CATATCCCCCTTACCTTCTGAGCAGCTGGGAGCCCCTCTGGGTATCCCC
ACACTCGGGCACATCAAGTCTGTGAGGCTGGACGCATCTTCCCCACTGT
GGCCAGACAAGGCAGCCCAACTAGAACATATCCACAGACAGGCAACAGC
TTTTAGGATAGCCCCTGCTCCAGTTGTTTCAGCACCCACATGAAGACCAAG

FIG.3D(39)

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CTGCACATCTGCTACATATGTGCAGGGAGGCCTAAGTTCAGCCCATGTAT
GTTCTTTGGTTTGTGGTTCAGTCTCTGAGAACCCCAAGGATACAAGTTAT
CTGACTCTCTTAATCTTCCTATAGAGTTCCTATCTCCTCTGGGGCCCACG
ATTGGTGTCCCTATTGCTTCACTGGGATTCCTGCCTGGCTACACCCACTA
TGACCAAGGCAAGTCTTAGAAAAGACAACATTTAACTGGGGCTGGCTTAC
AGGTTCAAGAGTTCAAGTTCAGTATCATCAAGGCAGGAACATGGCATCATC
CAAGCAGGCATAGTATAGAAAGAGCTGAGAGTTCTACAACCTATCTGAAG
GCTGCTAGCAGAATACCGACTTCCAGGCAGCTAGGATGGGGGTCTTCAGA
CCCACACCCACAGTTGGTGTCCCTATTGCTTCACTGGGGTTCTGCCTGG
CTACAGGAGGTAGCCTCTTCAGGTTCCATATCCCCAATGCTGTGAGCCAC
AGTTAAGGTCACCCACTATTGATTCTAGGGTGTCTCCCTCATCCCAGGTC
TCTTTCATTGTGGAGATGCCCCCACTTCCCCACCACTGTCAGTTGCAGA
TTTCCATTCTCGGGACCATCTGGCCATGCCTTCTGTTTCTCCTCACACCT
GATCCCGACAGCCCCGCCCATTCCTTCTCCTACCTAGTTCCTCCCTCCA
TATGCTTCCTATGACTATTTTATTCCCCCTTCTAAGTGAGATTCAAGCAT
CCTCACTTGGGCCGGCCTTCTTGTTTGTTCCTTGGGACTGTGGAGTGT
AGCTTGGGTATCCCATTTTTTTATGGCTAATATCTGCTTATAAGTGAGTA
CATACCATTCGTGTCCTTTTGGGATTGAGTTACCTCACTCAGGATGGTAT
TCTTAAGTTCTATTCAATTGCCTGCAAAATTCATGATGTTTTTGTTTTTA
GTAAGTGAATAGTAGTCCACTGTATAGATGTACCACAGTTTCTTTATCCA
TTCTTCAGTTGAGTGAAATCTAGGTTGTTTCCAGTTTCTGGCTATTACAA

FIG.3D(40)

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ATAAAGCTGCTATGAACATAGTGGAGCATGTGTCCTTGTGGGATGGTAGA
GCATCTTTTGGGCATATGCCCAGGAGTGATGATATAGCTGAGTCTTGAAG
TAGAACTATTCTTAGTTTTCTAAAAAACACGAAATTGATTTCCAAAGTA
GTTGTACAAATTTGCACTCCCTCTAACCAAGCAAGTGAAAGATCTGTATG
ACAAGAACTACAAGTCCCTGAAGAAATAAACTGAAGAAGATATCAAAAGA
TGGAAGATCTCCCATGATCGTGAATAGGTAGGATTAACAAGGTGAACT
GGACATCTTACCAAAGCAATCTAGAGATTCAGTGCAATCCCCATCAAAA
TTCCAACACAATTTTTCTGTAGACCTTGAAAGAGCAATTCTCAGTTTCAT
ATAGGAAAACATAAAGCCCAGGAGAGCCAAAACAGTTCTGAGCCATAAAC
GAACTTGTGGAGGAATCACCATCCCTGACCTTAAAGCCGCACTACAGAGC
AGTCGTGATTAAACAACAACAAGGCTGCGCACTTTTGGTACAGAAACA
GACGTGCTGACCAATGGCATCCAATCCAAGATCCAGAAAGAAACCCACAC
ACTATAGTTTTTTTTTAAATATAAAGTTCTTCAGCTTAATGCTTCTCATT
ATTCATGAGAGAAGAAGACTCAACAGCAAAGAAGGTGAAACAAGGGTGAC
AAGTACCACAGGGCTCTCGAGTGTCTCTTGTGATGGACTAGGGAGCCCGT
CAGTTCTGAATGCTCAGGAATGTGGTTCACAGTGTGGCCACAGTACAGAA
GATCCCCGAGATAAGGCAGAAGACAGTCACCACAGGTCATCTCCACAGGG
CAAGGACTCAGTATATGGCATATTACTAATGCTCTTAAATATTTACTGAA
CAAAGGAACAAAATGCTGAGTCTGTCACAGAGATGAAAATAGCCGTTGCT
TCAGGGGACAGCAGAAGATAGCCTTTTTTTCTCCTTGAATGGTAGTTAAT
TTAATGTTGCCTCTATATTATTAGAAATAAATTACAAGCTGAAAAATAAT

FIG.3D(41)

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GAGTCATACGCAGTGATTTCTCTTGCTTTAGGCTGTCTTTACTACAAACC
CATTTTCAGGCTAAATGATTTTGTCTTAATCACAGTCTATGGTAATCTGTC
AAGCCAGTTGTGACCTGTCTTCCTTTCTTCTTCCCAGCATGCAAGTGCA
ATGGGCACGCATCACTGTGCAACACCAACACGGGCAAGTGCTTCTGTACC
ACCAAAGGTGTCAAGGGGGACGAGTGCCAGCTGTGAGTACCACACACACT
CTGTGTCTCCAGTGGGGGACTGGGCCTTGCAGCTGCCTGGGCCCTGTCGG
CCACCTGCTTGCCTGGGCATTGTTGCCCTTCACTCCCAGGGTCTTTGAGT
GGACTAGTGTGGAGGTTTACCTTTTTTCTTCAGACAGGTTATCTCAGTT
ACTTTAATATTGCTCTGATAAAACATATGACCAAGGCAACTTACAAAATA
AAGCCTTTAATTGGGCTTATGACTTAAGAGCATTGGAGTCTACATTGAGT
TCCAGGGCAATAGAGCTACATAGTAAGACTGTATCAATCAATCAATAAAT
AGGACTACATAGTAAGACTGTATCAATCAATCAGTAGATGAAGAGAAAGA
AAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGGAAGGAAGGAAGGAAGGAA
GGAAGGAAGGAAGGAAGGGGAAGAACAAAACAAGCTTAGATAGGAAGAAC
AGGATAGAATGAATGACAAATGCTTGAAAAATGTTTTAGCTGTACTTTTA
GAAGCATACTCAATCCACACAGAAGTAAAAATGTTGTTCCCTTATGAGTAG
TACCTAGCATTATTACATATGTACTTGCCTGTGTCCTTGGGCAAGTATTT
GTTTATTTGTTGTTTTTATACTGTTGCTGGTGTAATTACTGAGCAGTTA
GCAGAAACATTCTGCAAATGGGATAGTCTCTCTGATCTGAATAATGATA
TAGTTTATGTAAAAGGATTTACTTGGTTTAAAAATAAATATAGAGTCTGT
GCTTTAAATGTCAATAGAAGATAATTTCTTTTTTCCCTAGATGTGAGGTA

FIG.3D(42)

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GAAAATCGATACCAGGGAAACCCTCTCAAAGGAACATGCTACTGTAAGTT
TTTGTAAATTGTTCTAGAGAGTAATTGAACAAAACGACATTGCTTTTTTT
TTTTACCATTTGTCTGAGAATGATAAATGCTTGGGGGATGAAGCAAATACT
CATAGCCATGCCCCTGACTTGGTGAACACTGTTCTAACTGAGGCATGGTC
TCTGCTGGTCATCCAGAGCAGTTAGCAGGGGTGCTGTCCTGCCTGTCCTT
GTTGAGCTCCCGCGGAGGCGTGCTCATTACCATTGCCAGTGTAAGCTTA
TCATGTCCAATCTTCAGACAGCCAGGAAGGAGTTTCTAAGATAGAGGTGC
GTTCCACCATTCTCTCTGCAGCTGATTTGTGCTCACAACAAGTAAATAA
AACACCAAATTAATACCTTGGTGTGAAAGTGAATCTGGTAAGCTTACAGC
TTTATCATAAATATATTTTTTGTCTATGAGAATCTACATAGTAGGTTCTA
GACTATAGAACAATAAAAAAAGGAATTAACATTTGGCATATGCAGCATAA
TGGTATATATAAATTGTAGAAGAAAATGGATGGTTCTAGACCTGAAAAGA
CAAGAAAATTGCTTGTGTGTAATCTGGGCAGGTCTTAAGTTGTGACCTTC
AACATCTGCTTCCCAAGCAGCTGGAACCACCAGGCCTACAGAATTCTTAG
CTATGATTCTAAAGGTCATTCATCAATATAATGTTAATGTGTATTTTAT
TAAAGTTTCAAACCTTCTATCTTTAATAATCTGCAAATGTAGCTCAGTAGA
GGAGAGCTCTCGCTGTAAGGTCTGTGTTCTATCCCAGCACAAACAAAC
AAGACATTTAAGAAAAAATTAACAAGTTGGCTGTATTGTCTCAGTATC
TCATCCTTGAGATAGTGAGGCAGGAGGACTTTTAGTTTGAGGCCTATGTG
GGTTATGTAGTGTGAAACCTTTCTCAAATAATTTACACTTTTTTCTTT
AAAAACAACCTTTTTTCTTAATTTATGTGTTTTGCAACATGTAAGTCTGT

FIG.3D(43)

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GCAATGTGAACATATCTGTTGCCTTTGAATGCCAGAGAGGGTTTCAGTTT
TCCTGGATCTGGAGTTACCAAGGGTTGTGAGCTGCCATAGTGGGTGCTGG
TAATGAACTGAGTCCTCTGGAAGAGCAGCCAGTGCTCTTAACTGCTGAGC
CATCTCTGCTGCTAGGTACTCCCCCTTCCCCCTTAAATTTAAGACAAAG
GTCTCACTGTGTAGCCTCAGATGGTCTAGAACTCAATTTGTAGAATGGTT
GACCTTTGAACTCACAAAACCTCTGCCTGCTTCTGCCTCCTGAGTGTTGAG
ATTAAAGTTGTATGTCACCACACCTGCCCCTATGATTTCTATATTTAATA
AAGATCATGACTAGGATATAGAGAACACTTTTGAAGCTGAAGAAGAAGAC
AGTTACAGTTAAAAGCAAAACAAAAACAAAAACAAAACCCAGAAA
AAAAAGAATGAAAACCTAGCACTGAAGAAAAAATAAATTTTAAAAATAGG
CAAAGAGTCACTATTATATTGTGATGGATGTGTTATATGTTTAAAACCAC
AAGTGAGATACAGGCCTGAAATGACTTTAATCGAAGCTACACCAGCCTGG
GGTGGTAGTTCAGTTGGTAAAGTTCTTGCTATGCAAGCACAAGAAGCTGG
GTTTGATGCCCAGGACCCATGCTGAAACCCAGGAGTGCTGCTGAGTGCTT
CAGCTCTGGGGTGGCAGGGCTCACTGGCAGGAAGCCTAGGCTAAGAGAGA
CTCTGTCTCGAAAAACAAGGCCGATGGCACCTGATGAACGGCATCTCAGC
ATGACCTTTGCTCGGCATATAATGTGTACACACAAATTCATAGTTTAGTA
GAAGACAAGTATGATCTGCTTTTCATGAAGTCTGTTGTAATAGCCTTCT
TTAGTTAACCATAGTTGCTTAAAAAAGAAAAAATGGACCTCACTGGAC
AGAAAATGGATAGAGTGTTCTAATAGCCAATTCAATTCATCATCATTATC
AAAACCTATAACTTAGGGGGCTGGAGAGATGGCTCAGCGGGTAAGAGCAC

FIG.3D(44)

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TGACTCCTCTTCTGAAGGTCCTGAGTTCAAATCCCAGCAACCAGATGGTG
GCTCACAACCATCCATAAAGAGATCTGATGCCCTCTTCTGGAGTGTCTGA
AGACAGCTACAGTGTACTTACATAAAATAAATAAATAAATCTTTAAAAAA
AAACACCTATAACTTAACTTATCAATAACTTTAACTTTCTACCCCATG
CTTCCTAGTTACCCATTCTGCTTTCTGTTTGTATGATCCTGGGTATGGCA
TCTTAATGGAACCACAGTGTGTTGACTTTGTATCTACTTAATATTAGGCAT
GATGCCTCTGACTCTCATCCCTGATATAGCACAGTTCAAAATTGCCTTTC
TTTGGTGCTGTACATATAGCTGAGCGTTTGAGTGCTTCCCTGCATGCACA
GGTTTCTGAATTCAATCCCCAGCACAAAAAATGATAAAAAGAAAGCAAAA
AGGCTTATTTTACAGCTGGACAGATCATCCTGCATTGTGCCTGTCATGT
TTTGCTTGTTTCTTCTGTCAGTGGACACTGTGTTACTTCTACCTTTTGGT
TGTTGTCAGGAATATTGTAAACATGAGTGAATATACACCCAGAAGTACAA
CTGGATGTGGTAATTCTATGAGTGTTTTGTTTTTGAGGGATGGTTATTA
TTGTTTCCATACAATAAATTACATTTCTTACAGTTCATTACATTTCCAA
AAGCCATGCATAGCATTTCTGTTGTTCTACATTCTTATTGACACCAGTTT
TCAATTTACATTTATTTTGTGAGTTTTTTAATTGGTAACCATCATAATGG
ACATAAAAAATAGCTCATTGTAGTTTTGGTATTTGTATTTAGTAATGCT
TGGTGTGATTATCTTTTATATTCTTATTAACCATTAGTGTGTATCTTTT
TTTGGAAAAACACCTCTTCAAGGGTTTTACTATGTAGCTCTGGCTGGCCT
GGAAC TTGTGCAGACCAGGCTTGCTCCGGTCCCACTGTCTTAGGTAGG
TTCCATTGCTGTGAAGAGGCACCATGACCAGAGCAACTCTTACGAAGGA

FIG.3D(45)

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CATTTAATTGGGGCTGGCTTACAGTTTCAGAGGTTTAATCCATTATCATC
ATGGCAGGAAGCATGGCAGCATCCAGGCAGATGTGGTGCTGGAGGAGCCG
AGAGAGTTCTATATCTTGATTCAAAAATAGCCAGGAAAAGACTGTCTACA
GCAGGCAACCAGGAGGAGACTGTCTTCCATATTGGGCAGAACTTGAGCAC
TAGGAGTGTTCCAAAGCCACCTACACAGTGACACAGTACATCCAAAAGG
CCACACCTATTCCAACAAGGCCACACCTCCTAATAGTTCTACTTCTCATG
GGCCAAGCATACTCAAACCACTACATCCACCTACTTCTGTCTCCCGAATG
CTGGGATTAAAGGCATATGTTGCCATTACCCAATTTTAAACCAGATTATT
ATTGTTTTTTGTACAACAGACTTTTAAGGTTAAAGTTTGCAGCAATAGG
CATTCTTTGAAGCTGTATCACACTGATATATGTCTGTTGTTTTCTTCCTT
CCTAGATTAAAATAGTACAGTATATTCAAGTTTCAATTGTCCCTTCCAT
AAGAAGTCCTGGTTTCTGTTCATTATTAGTTTATATCTTAGTGTTCTTA
AGTAAAATACTCAGTATTTATAGATGAGTTAGATTAGAGCCAAACCCCA
ATCAGGGTATTGGTAATGAAGGTTTGTGGATAATTCAAAGGATACTGCA
AAGATCTGGTTTCTAATGGAAAGAACATGTAAGTTGGCCATTAGTGGACC
ACACATCTGTATTTCTTATTCTTTGGAACCTTGGGCAGGATAGACAGATG
AGCTAAGATTCCCTTCATAGCTATTGAATTTGTGAGAAAAACAAATTGTGT
TTCCAGAAACCTGCTTTAGTTTGTATCAACACTTACTTCTTTCTGTGTG
TGGTGTGTGTGATGTGCCTGTACCATTTTCAAGTTTTTCTTCTTCTTTC
CATAGATACCCTTCTCATTGACTATCAGTTCACCTTTAGCCTGTGCCAGG
AAGAGGACCGCTACTACACAGCCATCAACTTTGTGGCTACTCCTGATGAA

FIG.3D(46)

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GTAAGCTTTTCTTTTAAGCTGTCTTATTTTGTGTTAAATTTTGTATAGGT
TTTTTCTTGGTCATCCTGGACAAAAGTACTACATAGAAGCAGACAGTAT
CAGGGTGGGAATATAAAAGGCAACCAGTTTTTAAGTATTTTTTTATTTAC
TTGTTGACAGTTTTATATGATTATATAATGTGCTTGATGATATTCAACCT
GTGACCTTTTGTCTCCCTCATACTTAGTTCCTTCTCTCCCCACCAAGTCA
CCTTCACTCCCTCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
TGTGTGTGAA
AGACAGACAGACAGATAGACAGAGAGACAGAGATTGATTGATTGATTGAT
TGATTGATTGATTGATTGATTTACCTACCTAGTTTACCAGCTGACTGCAG
GAGCATGCTGGGTGGGAAGTTCTTACTGGAGCATAGACACATTACAGTGA
CTACACCACTGAAGAAAGTGACTCCCTCTCAGGTAGTCTTCACTGCCACT
AGGTCCTCAGGGATCAAGAGAATGTTTGGAGTCTACATTTTATCTTTTTT
CCACTCAGAAGGCAAACATTACTGAATGTTTTTAAGTAGTAGAATAATGT
TCATGATAGTCTGTTTAATATTAATAAAGAAATTTGTTCTAATTATAAA
ATTTTTAGAAGATAGACAAGAAGACAAAATTTTTGAGTTAACAGTTTGAA
AGGTTTATTTTTATTTTATTTTATATGTATGAATATTTTAGCTTCTTGTA
TCCCTGTGCATCATGTGTGTGCAGTGCCTGTGGAGGCCAGAAATAGATAT
TGGATCCCTGGAAGTAGAGTGATAGATCATTGTGAGCCATCATATGGGTG
CTAGAACCAACCCAGGGTCCTCTGCAAGAGCAGTGAGTGCTCTTAACTGC
TAGGCCATTTCTTTAGCCCCTAAATGTGAACAACCTTTTAAATAAATGTA
AGTGATCTTAAATACTCTGGAGAAAAATCTGTAGCTATACCTTACTTTTT

FIG.3D(47)

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AAAAATTATTTTGTATTATATTATGAGTGTTCCTACATATATGTGTG
TCTGATGCCTGCAGAGGTCAGAAGAGGGTGTGGATCCCCTAGAACTGGG
GTTACAGATGGCTGTGAGCAGCTATGTGGTGCCTGGGAGTTGAACCTGG
TTCTCTGTTAGGGCAACAACCTGCTTTTAACCATCAACCCATCTCTTGGC
ACATGGGTGCATTGTTGGTTTGGCTGCTTGAGTTGTGTGTGAGGGGTGTG
TGTGCATACATATGTGGGTCCATGCTTATCCAGTGGAGGCCAGAGGTCAG
AGTCATGTATCTCTCTGTTACTTTCTACCTTATGTTTTGGAAGCAAGATT
AGATAGACCCCTGGGACCTTCCTGTCTTCTCCTCAGCACTAGGACTACAA
GTCCACACCTGACTTTTTACATGGGGCTTCAGATCTAACTCAGTCCCAAC
ACTTGTTTCATTTCTTAGCACCTTGGCTAGATTCTTAGGATTTTAGAAG
GAGCTTATAGCAAAATACCACAAGTGAAATTTACTACTGCCTTAGTCATA
AGCAAATATTGAAGGCTCAGTCTTAAGGGTATAATTGATAGTGTTCTTT
TTTTTTTTAAGTAAACAAATAGCCTGTCAAGGTAACCTATCGCTGTAGTCC
CATTACTTGTGAGAGATGTCAGCTCAAGGCCAGCCTCCGCTACATAAGTA
AGGGAAGACCAGCCTGAGCTATATGGGACTCTATCAAAACAAATAAACAT
TGTAGAATTTTGTAACTTATTAGAAGGTAGCTGATGATCATGAGAGT
CTTTAGACATTTCTTCATTCCACTGTTTTGTGTGTGTGTGTTCATGACA
GATTTCTTACTAGATTTATCTCTTGTGTGTGTGTGTGTGTGTGTGTGT
TTACAAAATGACAAAGATTTTAGTCCTTCTCGTGGAAAGTAGTTGCTAGT
GGTCAGCAGATACTTGCTAGTATAAATAAATGAGCATAGATCTGCGCTTG
CAAAGGAAGACAAAGGGAAAAAAGGTTTTCTTGAACATAATTCCTACTTT

FIG.3D(48)

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GTGAAAGAACTTCTCATTTGGAAATTACATTTTGAAAATAGGTATTGTG
AATGTTTCCATTGTGGTTTGTGGTATAACTATCAAATAACACTTTTTTAA
AAAGAAAAATCTTAATTTTCTAAGATTTTAAATACCCTTTTAAAATGAG
CATTTCCAGCATGGTTTGATTAATTTGTAAAATGTAAGAATATAGTATCT
AAGGCTACAGAAATGACTCAGTGGTTAAGAGCACTGGCTGCTTTACAGAG
GACCCAGGTTCCATCCCCAGCACCCCTCATGACAGTTCACAGCCATCTGTA
TTTCTAGTTCCAGGGCATCTGATGCCCTTCTCTGATTTTCTCCAGTACTA
GTGACACACAGCATACATTTGAACAAAACCACTGATACACATAAAATAAA
TTGTTTTCAAGAAACAATATAGCATCTAATTAGCTTACAAAATAATTAT
TTGTTTCTGTACTAATTACGTTTCTATTGGCATGACTAAGGCAACTTATA
AGAGAAAGCATTTAATTTGGGGTTCACACTTCTAGTGCCTTAGATTCTAT
GAGCATCATGGTAGGGAGTGTGGCAGTAGGCAGGCAGGCATGGTGCTGGA
GCAGAGGCTGAGAGCTCACATTTGATTTTCTACTAGAAGACACAGAGAGA
GCTAACTGGAAAAGGCATGGGCTTTTCAAACCTCAAAGCCCCCTCTAGG
AACACACACCTCCACCAAGGCCATACCTCCTAATCAAACAGTCCTACCAA
CTGAGGACTAACCATTGAGAGATAGATGAGTCTATGGAGGCCATTGTCAT
CCAAACCACCACAGGCCCCAAGAAAGATTTGTTAGTGAAATTTGAGTGAA
AACTAAACAGCATTAGAATTTACCTGGCATAGCCAGCAATGATCTCTTC
TGTTGAGTGCCACAGATTTCTTTGAGTTAAACTCAGTTGTTAAACCAA
AAATCAAATGTAATTGGCACTTTAAATTGCTATAAGGGGAAACAAGGTT
TTCAAAGCCATGAAACCATATTCAGAATAATTTTAGCGAGAGAAATATTT

FIG.3D(49)

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TTTCTTTTTTTTGTCTTTCTTTTTTTCTTGGAGAGAAATATTTTTATT
ATTTTATATTATTTTAATTACATATTTAATTATTAACCATTTCTGACAGA
GGGCAAAGGTGAGGATCTTCATGGAACATAATCTGATAAAGCACCAA
TTCTTCCCAACTCTGGGATGCAAATGACAGTTCAACTTCAGTTTATTGCT
TGTATTGAAGAAAATTGACAAGAAATGTCATGTCTTAACATAAGCATGGA
TTTCTTTTAAGATGTAGAATAGTCTATAATTAATGTTTTTGAGACTAGTA
AGACCTGATTATTGTTGTATCTTAAAATCTAGAAGGTACTAACAATTTTC
TAATGTGTATTTTTTTTTTTCATCAGCAAACAGGGATTTGGACATGTTCA
TCAATGCCTCCAAAACTTCAACCTCAACATCACCTGGGCCACCAGCTTC
CCAGGTACAGACACACCTAGAGAGATGGATTGGCAAGTTTAGTGTAGGAG
TTGGGGAAGGAGGCTCTGAAGGCTGGTGAGTGAGTTCAGAGCCACCTCT
GCCTCTTAGTAGCCATGGCACCTTGAACAAGCCATGCTTGAACAAGCATG
TACAATTCCCTCTCTACCTTAGGCTACTCAGAGTGAGGAGTCACAGCTCT
TGCTCCAGCGTTGCTGGTTTCAAGTTGGTTGGATGGCTGCTCCCTGCTTT
GCCACCACCTTCCAGCACTATGACTATCTCTATGTTTGTGCTTCACAGGG
GAAAACTAAAGTGACTCATAGTTTTAAGAAATGAAAACTCTTTAAGGGA
AGGGGGATAACTCTAATATGTAGAGGTATTCATACTTTGGGATAACTCCT
AAAAGTACAGCTTTTCCATTCTTGTTTATCTTATAGTGACTATAAAATTC
TGATGGCCCTAATGTAGCAGTTACTATAAATAACCACTCCATAACTTGAT
AGCCCTGAAGATAGACCTAGGTTTGAATTTACCTGCACGGTGTTGAACAA
GTTACTGAAGCTTTCTTTTCTTTTGTTTTTTAAGTTTGTTTTATTTTATGT

FIG.3D(50)

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GTGTGTTTGCCTTTGCCTGTATGTGTATAAGTGTACCATGTATGTGCAGT
GCTTGAGAAGGTCAGAAGAGGACATCAGCTCCCCACCCTCAACGAGTTAC
AGACAATTATGAACTACTATATCTGTGCTGGCAACAGAACCCAGGTCTTC
TGAAAGAGCAACCAGTGCTCTTAACTGCTGAGCCATCTCTCTCTAGCCCC
CAAGTTACCTAACTTTCTGATCCAGTTTCCTTCTTTATAAAATGATACA
GTGAAAATAGCTTTGCTATGTACAGAGATATTCCAACTTTTAATATTAC
AACATGACATCTACAAATATGTTAGCCCTCATTCATAATCTTGCCTGAAT
TGTAGAGTGTTGCAAGGAATAAATGAAATAAAGGAGGTACTTATTATAGA
GTTTGAGGTTTGCCTTCATGCATAAAGAGAAGCTTTTTTGTAGTCTGTACT
ACTCATGTTCTTAGCCAATGGAGTATATAAAATATGGTAGAACCATTTAG
AAATGGAGTCTCACTGGGTACAGGCCTGAATGCAGTGGTAGCAGGTAGCA
GAAAGAAGGCCTGAGTGGCTGCTTGAGCACCTTCTCCATCAAGACTTGAG
GACCTTTCTGCTTAGGAAGTGATGAGCGAGTAAGTGTCCCTGAACAGGAG
CCTTGAGCATATTCTACAGTGTGAAGCAGAAATACAAAGGAGTTGAGGTA
TCATGTGCAAAATGAATGCAGTGTCTGTTTTATATGTATGATTGTTTTAC
ATACATGTATGTCTGTGCATCGCTTATATATCTGGAGCCTCTGAGACAGA
T TACTTAATCTATTGGGACTTGAGTTTTTCCAATCTGTAGATGGAGATAG
GAAGGTGTTGTGTGGGTTAGAGACTGAAGCTCATAAGGCTATATTCTTTT
GACACTGTAAGTGCTCAATAAACTTTTACCCTCATTACTAGTGCGCAAAG
ATTCTTTCTGATTGGCATACCCGCCTCCCAAGTCTTTATTTTTATTCTTG
CTTCTTTCTAGCCGGAACCCAGACTGGAGAAGAGGTGCCTGTTGTTTCAA

FIG.3D(51)

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AAACCAACATCAAGGAATACAAAGATAGCTTCTCTAATGAGAAATTTGAT
TTTCGCAACCATCCAAACATCACTTTCTTTGTTTATGTCAGTAATTTAC
TTGGCCCATCAAAATTCAGGTAAGAACTGCTTTTTAACTTCATTCCTCGTA
AAGATGGTGACATCTCTTTAGTGGAGACTAACTTCACTCATTGGGAATCT
GTGGTGACTGAAAGATAGTGTTGCTTTGCCTTTGAGGGATCTTTGCCATA
GACTGAGTAGCAGGTGAGTGCTGTTCTTAGGTTGGAGAGATGTTCAGTGA
GTGGAGTGCTTGCTACACAAGCCTGAGGACATGCAGTTCATCTGCAGCCT
CTCATACAAAGCGGGACACGCAGGGTGTCCTGTCACCTCAGCACTGGAC
ATGCAGTGTGTGCCTGTCACCCAGCACAGGACACGCAGGGTGTCCTGT
CACCTCAGCACTGGACATGCAGTGTGTGCCTGTCACCCAGCACAGGACA
CGCAGTGTGTGCCTGTCACCCAGCACTGGACAGCAGTGTGTGCCTGTC
ACCCAGCACTGGGAAGCAGGGGACAGAAAGATCTTGCTTGCTGGCCAGC
CACTCAAAGCTGGATCTGTGAGTCTAGATTAGTTAGAGACCCTGTCTC
AAGTAAAATAAGGTAGAGAGGAATTGAGGAAGACACCTGATTACCTCTGG
CTTCTGTATGCATGTGCACATATATACCTTCACACATATACACACTCA
GAGAAAAAATTCTGAGAGTGTATATCACTTGTGAAGAAAGTTTTAAAGC
ACTTTTAAAAGCAAGATGAAAGCTATGCAAGGTATGCAAGGTAGTATACT
TTTGTAATCCCAGGATGTGGAAGACCAATGCAGGAGGATCACCTGAGTT
TGAGGCCATAGGAAGACCCTGCCTCAAAGGAGGGAAGGAGGGAGGGAGG
GAGAGAGAGAAAGAGAAAGAGAAAGAGAGAGAGAAAGAGAAAGAGAAAA
GAAAGAAAGAAAGAAAGAAAGGAAGGAAGGAGAAAGAAAATCAAATTGATT

FIG.3D(52)

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GGCATATAGTTATGTGTTTATTTTTTGAGTAATTGCTATGTAAAAGCCTT
TAGAAATACACAGTTTTAATTATGGAATTGAGTATAAATAAAACAAGTAC
ATGTTTGTAACCAATAAAGTATAAAAATGACACATAAGATGTCAAAGTGG
TATGATGGCTATAATGTGGAGTCCATAGAGGAAGCAGTAGGCAGTATGAG
GTACTGTGTAAAAACACATAGCTTTACTATTGCACAGACAAGTGTGGATT
CTTGTTCTGTGTGTGGTTCATGGAGGCTCTCCAGTTTGCAGATTCTCTGT
GCATGTGTCCTGAAGGATTGGTCTTCCTGCTATGACCTCTGGTGTATTATTA
GCCTGAACTGAGTCCTAAGGAGACAGGTAGTGGAATGTTTGTATTGCAA
AGACAGTATGGGTAGTTGTTTTTAGAAACAGGAGTTCAACAGAATTGATA
GAACTTGTGATCAAGAAGCTAACAGCTGGACTGGGATGTAGCTCAGTTGA
AAGAACGCTTGTCTAACATTAAGAAGCCCTGGGTACCATCACTACCACAG
CATAAACTGAGAGTAGTGACAGACTCATGTGTCCCAGCACTGGGAAGGTA
GAGGTAGGAGGATCAGAGGCTGCCAGGGAGGTTGAGAGTGACTTACGCT
AGGAGATAGATCTAAAAATGAAAAGGAAAAAGAACTTGGTAGCTGCTAGA
GCTACCATGAAGAGAGTGGAGCTTAAGGATTCAGCTGAAGAATGTAACT
GCCTTCTGATGACAACTGAGAGTCGCTGAGTTATTTAAAGTCAGGAAGTG
AACAAAGATCAGTGTTTCAGAAAGACCTCTGTGGCAACAGTATTGACTAG
AAGTAGCCCCTCCTATGTCAGGTACTGGTTTAGACTGTATTTGGAAGTGT
CCTCTTCTTGATGGCCCTCAGACACCTTTCATGGCCACTCCTCTGCATT
TGTACCCCATAGCCACACACTTGATGGTTCCTTATTACATAAATAGCTCC
TTATAGGCAATGATAGATTTTATATTTTTGATAATTTTAAGATAAACTCT

FIG.3D(53)

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ATGTCATTGCATAGAATTTAGTAGTTGTAGGTACTCAGTAAATGTATATA
GGATGAATACAAAAGCTTTAGGGTAACAGTATTTTGTCTTCTTCCCCCG
CATTTTAACTATCTCATAGTAGCACAGACTAACCCATAACTGACCATGA
AGCCAAGGATGACCTTGAACCTCTGTACCTTCTACCTCTTCCCCGAAAGT
GCTGAAGTTACTGGCATGTGCTGCTCACCCAACTAATAGCAAGTTTTTCT
TATAAAGGTGCTGATGCCCTTTCCCTGTTTGTGTTAATTGCTGACACTTA
AAAGCTCTTTATCCCAACCCACAGTGTTAAAGAGTTTAGTTAAATTTTGT
GGAAATTTTGTCCCAAATGAAGTGGTTGATGGCAGGCCTGGTGGCTCCTT
CCTATAATTCCAACACTCAGGAGACAGAGTCAGGACGATGGCCAAGAATT
CAAGGCCTTGGGCCTACAGAGTAGAAGAGAGAAGAATGAGGATTGGAACA
CCTGATTAAATAGATACCATTTCTGCTACCAACCTGTGCCTTAGCTACT
CTTCTATTGCCGTGACAAAACATCATACCCAAGGCAGCTTATAAAAGAAA
GCATTTATTAGGACTCACAGTTTCAAGGGTTATACTCCAAAACCATCATG
GCCGGGAGCAGGCAGCAGGCAGGAACATCTGCTGTGAGGAAGAGCTGAGA
GCTCACTTCTTTATCCACAAATAGGAGGCAGAGAGAAAGCTAACTAGGAA
TAGAATGAGCTTTGCAGACCTCAAAGCCCACCTCCTTCCCAAACATTTCC
ACCAATTGGGAACTAAGTATTCTAATCTGTGAGCCTCTGGAGGCCCATTC
TTATTTAACTACCACACTTTATAAGTTAATACTACATGTGATGAGGAAA
CTGGTATGGGAATTCTGAAAAGTAGTTCACAGGAGTGGGAGGGGCTGAAC
GTGAGTAGATGCTAGCATGTGTGTCAGGAGTGAAGTGTTGAGAGCATTGC
CTGGTTTGACTTCTCTCCAGAGCTGAGGTGAACATGCTTTGTGCCAATAC

FIG.3D(54)

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AAACCCGTATTAAAGCGGTGGTAGTTACTGAAAATCAGTGCAGGGCTGTG
GTCTCAACACAATGTTTGAAAAAGAAAACAGGGCATCCACATCAGGCAGT
GTACAGCTGCTTATAATTCCAGTCCTCTGGCCTCTGCTCACATGCACATA
CCCCCCCATACATACACACATGATTAAACATAATGAAAAATTAAAAATTA
ATGCTATAAAAATGGAAAGAGCCGGGCGTGGTGGTGCATGCCTTTAATCC
CAGCACTTGGGAGGCAGAGGCAGGCGGATTTCTGAGTTCGAGGCCAGCCT
GATCTACAGAGTGAGTTCAGTACAGCTAGGGCTACACAGAGAAACCCTG
TCTCGAAAAACAAAAACAAAAACAAAAAAGTGGAAAGAAA
GGTTCAGTGTTTCACAGGAAACTCTGAGAGGTGATAATCCAATCCCAGT
TTAAATATACTCCATAGTGCACACAGCCTCTCCCATCCTTGGAACCTGA
GGCCTGTGAGAAGACTCAGTCCTCTCCTGGCTTCCAACCTTACAGTGTTT
AAAACCTTCTGCAAGATCCACATGGTCCTACCAAGACCCTGAAGGTCAG
GCATGCTGATTAGGCTGTCTCTGGGCCTGAAGTGAAAGGTAAACACTTCC
GAGATCTCCAAAGCCTTGGAAGATTCTGAAATGTATGGGTGTTGGTTCA
GGTAGACTCTCAGCCTTGGTGAAGCTGCCCCGGAGCTGTAGGGTTATCT
GCAGAAAGTCAGCCAGGTGCACTTACCCTGGAATCCTCTCCATTACAG
ACACCTCCCTGAGGCTTTGTGGCTTCACCTCACTGTGCAGCTAGCTCCTG
TTTTACATGCTTATATAATGAATGGTCTTGGTAAAGAAGATGATAAAGGC
AAGCTAGAGGCCTTTTTTTTCCCCTCTTCAAATTTTGATTGGCCTTTCCC
TACTGTTACACTGTCTACTCAAGGTTTTGAGCATTTACTTTGTGTACATA
GTAAAGCAAAGTACATATTTTTAAGTAGAAAAGAAAGCATCTGTGGTCT

FIG.3D(55)

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TTGATATAGGTGCTTTTCTTTATTTTAATAGTAATACTTATTCCATGCTT
GTTAAGAAATTCATTCACAGCGTGTTTTCATAGAGACTTTCTCTATAGAG
ATATATAGAAATCTAGACATGAGGACAGCCCACTAACCCTCTTCAGAC
ACTAGCTGCTTCTCTTAGAGCCCTGGGCTCTCACCTTTGGAGGACAGCC
ATCCTCACTCATATGTGACAAGCTTAGACACAGAATAATCACAGAGACTC
CAGCCTCCCCCACAACCCACAATGCCAATATCCCATATTCCCAGGAACT
TTTAATAAGCCATCCACTCTAATACTCCATCTCTTATCTCAGGCATAGGC
CCTGGTTTTGGTTTGCTTCAGAGTACTGCCTTTTCTCTACCAGGCCCTTC
CCACTCTTGCTGACCCTCCAGAGATGTCATTTCCAAATGAAGGGGGTTT
TTGGTTCTGTGGGTGTTTTGTTTTTCAGTGCAGTTCCTTAACTGCTATT
AGGGGACGGAGCAGGCAAACCAGATCTCTAACTTCTGAGGCCTGTGAAGA
GAAGCATCAGAACCTCCCAGGGGAGCTGTAGGAGCAGGAGTCAGGCCTAG
ATATGACTGTGAGAGAGTGGGGACCATTACCACTGTCTTACAAATGAGGG
GAAGGACTACCGTGCTGGGCCCTGAAAGATAAGGAGGACCAGGCTTCAGG
AAGGTAGGACACATTCTGCTGACTGTCTGGGATTGAGGACAGTAACACAA
CTACTTAGACATACTTTGAATGAAGGACAGACTTAGTGCTTCAGAACTGT
AAATCCATTATATCTTTCCCAAGTCTTAGGCTAGCCAAGTTTCTCAACAT
TTATCTACCTCATCCCAAAGGGTCCCAGGACAAATATTTCTTACTCAA
CATTTGATGGGAGTTGGAATCAGGTTGAGGAAATGCAGGGGTGTAGATTT
TAGATTTCTGGGAATATGTATAGATAGCTACCTTCTGTGGATAGAAAAT
GAGATTGTAAGTTTTTCAGTGTTTTTTTACACGAGTTTGTGTGCCCATGT

FIG.3D(56)

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ATGCACATGTGGAGGCCACGGGTCTACCTTAGGTGTCTTCTTCAGGAACC
AGCCATCTTATTTTAAAGATGATCTCTCTCCAGACCTCAGGGCTATCAAC
ACACCTCAGGGATCCATCCTCCTGACTGTATGTCCCTAGCATTTGGGTTA
CTGTACCACCATGCTCAGGTCTTTGTGTAGGTCCTGGGGATCACAGTTAG
GTTCTCATACTGCAGGGCAAGCACTTTGTAAACAACTATCTCCCCTGCAT
ATGGAAGTATTACCACTAAATTACAACAAGATTTTCTTCTATTAAAATTA
TATTTTAGAAGCTGGATATAGTAATGCGTTGGGGCAAAGGAGGGAGGGGA
AATGAAGAGGATAGGAAGAGGGGGAGGGAGAAGGGAAAGAGTGAGGGCGG
GATCAGAAGTCCAATGTTATTCAAGGGCAGCCTGACCTAGATAAATCCCT
ATTAAAAAGTTTTCAGTATAGAACTTCTCATCACCTTCATTATCAGAAA
AGCCCCTAAATTCAGAACACTTTTTAATCTTAATTAGTTGACAATTTTAT
AAATGTATTATTTATATATATGAATAACATTTTCTCCTACCTTTTTTTC
CCTTCCCCTCTGATGATTCCCATCCTCCCAACCAAGCCCCCTTCTGCAT
TTGTTTGTTGCTTTAATGACCCACTGAGTTCCATTGGGCTCACTTCCATG
AGTGTGACTAGAAGAGCTATTTATCAGAATGTGGGCAACTTACCAGTAGT
GACACTGATGAAGAAAGTGTTTCCCTCTTACCCAGTAACCATTAATGGCC
AGGAGCTCCTGGGAGGGGTGGGCGCCTTATGAGCCCCCTTCTCCAAAATGC
TTTCAAACGTGACCAGCTATATTTAATGTTTTTATTATGCCTGTGTATC
CATGTGGGACAAGAAAGCTTGAGAGTATCATAGCATGCATGTGGAGGTCA
AAGAACAACGTGTAAAGTCAGATCTCACTTCCCACCTTCACATGGGCTC
TGGCACTGAACTCATGTGAGTGACCTGAGAGGCACTTTATCCTCTAACAC

FIG.3D(57)

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GCACCCTGTGCCCAGCCTAAAATTTGACCTTTGCAAGGTTTAGTGTGTGT
TATCTGACTGTCTGAGTAAGGATGACAAAATGAAACCAAACCTTATGGGAT
AAAGCTTGGTGGTTGTATCAGTACATTTTTATTGTTGTGATAAACATTA
TGACCAAGACAGCTTATAGAAGAGTTTATTTGGGTGTATAGTTCCAGAGA
GGTAAGAGTCTGTCCTGACAAGGAAGCTGTGGCAGCAAGTGGCAGGTATG
GCTACAGGAGCAGGAAGCAGAAAGAGCAAACCTAGAAACAGTTGAGGTTTT
TTAATAGGAAAGCCCACTCCCCTAATGATGTCCTTCCCCTAGCAGACCAC
AAGTCCTAACCTCCCTACACAGCACCACCAGCTGGGGAGTTCAAATGTC
TGGGACTGCAGGGGACATCTCATTGAGCCACCTCAGTGGGAGAATGCTT
GCCTTCATAGTATGTGCAAGGCCCTAGGTTCAATTCTAGCCAAGAAAAGA
GAACATGAGGAAAGAAAAGAAGGTGGGAGAGAGTAGAGAAAGAAGAGAAG
AAGAGGAAAAAGGAAGGGGAAGGGGGAGACAGAGGAAAGCAGGGAAGCAGA
GGAGAGGAGAAGAGAAAGAAAAGATTAACCAGCCTGGTTTTTAATAGCAC
CCCTCCCCTCTCAGTAGTTCCCAATTTGAGCATTAGTTCAAGACTGAT
AGATATTTCTGGGTGGGTGACCAGTGTGGTCATAAACATGGTGACTTTTG
CTCTCCGTACAACCTGTGATTATGAACTTGTTAGATGATCAGCTTCAACA
GGAGAGGGCCTCCTTTAGTCTCAGGTGCCCCCTCCAGCCACCCTGGGACT
CGCAGCCTCTCTGTGATGAGACACAGGACATTAACCTGGTATGGTTCTGCT
TTGCCAAAACGTCAGTCCATGGTTGAACTCTCCACAATGAGAAAGAAGCT
TTGAGAATCATTACATGGCATCAGGCAAGCCAGGACTGATGGAGCCTGAG
AAAGGGCCAGGAGCATCGGCAGGTTTTGGCACCCAGTACTAACTAGTAAA

FIG.3D(58)

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AGCACCTCATAGGTTTCTTTAAAATGCAAACACTAAGGAAAATCTAACTT
TTTTTTATTTATTAAGGCCATTCATTTTATTTTATAAGTATTTTGCCTGT
ATACATATGTACCACATGCATACAAGGTCAAAGATAGTATTGGGTCTTC
GAACTGGAGGTACAGATGATTGTGAGCTGCCATGTGGATCCTCGAAATTG
AACCTAGGTCGTCTACAAGAGCAGGAAGTGCTCTTAACTTCTGAGCCATC
TCTCCAGCTCCAGAAAAGCTACTCATAAAAGTCAAATCTAAGCCATGTGT
CTGGTGATGTACACCTTTAATTGTAGCACATGGAAGGCGGAAGTAGGCGG
ATTGTTATTCATCCAAGGCCAGTCTTCTCTTAACAGTGACAAAAACAAAA
CCAAACCCGAAACCTGTTACTTTGCACTTTAGAGTATAAGTGATAGAGAA
AAGACACAGAAATTTTAGAATCTATACCTTAAAATACCTTATGGCTTATA
TGATACTGTTGGGACCATATTTACTTATGGAATGCAAAAAAAAAAAAAA
AAAAAAGATGGGGGGGAGCTGAAGGTCTCCTTTCTATTCTGTTGTAAA
TCTAGCTATAAAAAGAGTAAGAGGCATGAGTGTGTCTCAGTGGTAGAGCA
CCTGCTTAGCTTGTGTGGGATTGAATGATCCTCAGCACACAGAAGAAGG
GTGGGGCAATAAATTTAGGAAAATAAGATGCTAATCATTGACTTTCTTGA
TTTTTTTAAAAAAGTTATTATTTTATGTTTATTGTATATGTTTATATTT
TCTATGTGTGTTTTTGATGTGTGCTGGAGGGATGGGGGCCACTTGCTGAA
CTTCCCAATTGTTATCATAACTACCATCTTTAGTGAAACAGTTACCATCT
ACTTAGTAATTGTTTCATTGCAATAGATACTGAACACTCTTAATCTGAAA
CTAATGCTCAGAAAGTTCCACTTTGCCAAGCAAGCAGGATAATGTAAGCC
TATAATTTTAGCACTGGGAGGGTGAGGCAGAATTGTGAGCTCAAGGGCAC

FIG.3D(59)

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[illegible]

FIG.3D(60)

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GGTTTACTTGCAAACCTCCTGGGGTTCTCCTTTTTTTATAGTTTTCTTATT
AGTAGGGTTTTTTTTTTTTTTGAGAATACTATGCAGAAATGATTGAAAAG
AACAAATTAGTCATTGCATATTGGTAAGAGAAGCAGCAAGAGCCACCTCA
CCTCCCTCTGCTCTCCCCAAATAGAACTGCTCTGCTGTGCTGCTTCTCT
ACCTTCACACCAATGCTCGGCCTGCCAACTCAGTTATCTTTCCTTTCCTT
TTAAGATAGGGTCTCTCCTTATAGTAGTTATGACTGTCCTGGAATTCTAA
ATAGAAGAGGTTGGCTTTCAAATCACAGATCCTCCTGCCTCTGCCTTCTG
AGTACTGGAAGTATGGTGTATGCCACCGTGCCACAGCTAACTCAGTTATT
TTTTGGTGTTCTATAACTGCCTTACATACATACAGACCAGGTACACACAA
AATTCCTTTCATTAATTTAATAGTTATATCACAATGCATTGACCAACTA
AAAAATCCTAAATTGACTTATGATTCTACTTGCTCATGTTTTAAAGGAAA
GGTACTCTTTGCTTATCTTAAATGTAATATTTTTCCTTTGCAGTTGCTG
TTTAAATTTTCCCTATAAGTCGACCCCAAATTTACATCTATAATCTGGCA
AAACAAAAAGACCTCTAGTGATGGTTGTCTCTTAGCTTTAGTCTCTCTTG
GACTCCATTCCCTCCACCCATAATGTTCCATCCTCTGTCCTTAAGTGTAC
TAGTCTCCAAGGCCTGCTATGTGGTTGTCATTGTTGTAGTTACTTTTCTA
TGTTGTGACAAAGCACCTTGACAGTGGCAATTTAGAAAGCATATAATTTG
AGGATCACAGTTCCTGGTTAGAATCCATGACCATCTTAGCAAAGGCAGAC
AGGCAGGCCTGGCACTGAACAAGTAGCTGAGATCGTCCATCTGGTCCACA
AGCATAAGGCAGAGAAGCTAATTGGGAATGGCATGGGCTTTGGAAACCTC
AGAGTCCACTCTTAGTGATACCTCCTTATCCTTCCAAACAGTATTACACA

FIG.3D(61)

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TTCAAAC TTCAAATGTGTGAGCCTCTGGGGACCACTCTCATTTAAACCAC
CACAGTGATCTTGGCAACTTCTTTTGTGTTCTGTCATGCCACAGTCTTT
CCATGTATTTCTCCTTTTGCTGGAAC TTTTCCCTCGAAGGTTCTGAGG
AAAGAAACATAGATAACTTTTGTATGTACTTCTACAAC TGAAAGTATCTT
AATTTTTGCCCTAACAAATTTTTGTTTGCTTACTTGCTTGCTTACTTGAT
TCTGCGTGCATGCATTTATTTGTTTGTTTGTTTGTTTGTTTGTTTGAGAC
AAGATCTCTCTTTGTAGTTCTGGCTGCCTCAAAC TCAGAGAGATTCATCT
GCCTCTGCCTCCAGAATGCTGGGATAAAGGCATGCTCCACCATACCTAAT
CCAACCTCACAATTTTTTAAGTGTGTATTTATATGTGTGTGTGGTATATG
TAAAGGTGTGTGTGTTT CATGCACACATGTGCAGAGATCAGAGGAGTCAGG
TTTTCTCATCTATCACTCTCTGCCTTATTATTTTGAGACAGGGTCTCTTG
TTCGATATTACATATACTAGGTGAGATAGCCAGGAGCTTG TAGGAATTC
TCTCCATTTCTACCTTCAAATGTGTGCTACTGCATCTGGCTTTAAGCA
AGTTCTGGGAATCTGAGGTCAGGTCCTTACACCTATGTAGCAACTCTGCC
TACTGAGTCATCTTACTAGTATTCACAAGGTCAAAGGTTGGGACCAACAG
CCAAGGTTGTCCTCAGATCTCCACACAGATGTACCCACAATTATACAAAC
ACTCAACATAAACCTATTTACACACCCACATCACACGCACACACATACAT
GCACATACAAAAAATGCTTTTTGAAAGAAGTAGAGAATGCTAGATATGG
TATTACACGTATATAATCCAAGCCACTCTGGAAGCTGAGGCAGGAGGATT
TCAAGTTTGAAACCAGCTTGACCACATAATTATACCATGCCTCAAAAATT
GTATAGAGAATAAGAATGAATATGAATGAGACTAAAGTCATATCTCAGTT

FIG.3D(62)

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ACTTTTCTATTGCTGTGGCAAAACACCATGACAAAGGTAATTTACAGAAG
AGATTATTGGGGCATATAGTTTCAGAGGGTGAGTCCATGACAATTATGAT
ATGGCACTGAAGTAATAGCTGAGAGCTTAAATCTGGTCCACAACATTAGG
CAGACAGAGAGCTAACTGGAAATAGCCATGAGATTTTGAAACCTCAAGCC
CCACTCCTAGTGATGTCCCACACCTCCTAATCCTTCCCAAACAGTTCCAT
CAGCTGGGAACAAGATATTCAACATATAAGCCTATGGGGGTCATTCTCAT
TCAAACCACCAGTAGTAATTATTAGAGCCCAGCAAAGAAGGAAGGGATAG
AAAGAAATGATTGATGGGAACTGGGGTGAAGTCTGATACAGAGAGATCTT
TATGTACTGCAGCGTAGCTCAGGAAGATAACTATGGTTAAGGACAATTAG
CTAAGTGATTAGTAGAGAGGATTTTAATATTTCCAATACAAAGAAATGCT
GCAGGCCTGAAATAGGGTACGTTTCAGTGACCCAGATCTGATTATTACAA
CTCATACACTTGTACCAACCACATAAATATGTACAATAATTGTGTCAGTT
TTATATTAAATAAAAAATGTGGAGCAAGTTAAAAAATGCCTGTTTTAACT
GATCACAGTTATATGCCAGCTTTTCTTTGCTGTGACAAAATACCATAGGG
AGTAGTTTATAAGGAAAGAGATTTCTCCAGCTCATAATTCCAGAATTTT
CAGTCTAGAGTCAGTTAGTTCTATCATATTGGGCCCACAGCTAGACCAA
TACAATGATGGGGAGAATGTGGTAAAGAAAAGTATTTACCTCAGAGTGGT
CAGGAGGAACACAAGACAAAATATACATTTTCAGTCCCATACCTCCAGTGA
CTTGCTTCATCCAAACAGACGCCACCATCCAATAGCCATTAAATACAAG
TCAACCAGTTGATTGACATCCATTGATCTTAGTCATATCCCTAAATTCAA
CCTCTAAGCTCTGATGCTCTGGGGCCAAGCCTCTATTGCATAAATCTCT

FIG.3D(63)

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GGAGCATATTTTCATAATATGAAATATTA AACAGGTCTCTCAGGAGCTGTT
TGGTAGACTTAGTTGTTTTTTTTTTTTTTTGTAAAGGTTTTTTGGTT
GGGTTTTGTTTTGTTTTGTTTTGTTTTGTTTTGTTTGTGTTGTTTTT
TTCGAGACCGGGTTTCTCTGTATAGCCCTGGCGGTCTTGGAACCTCACTTG
TAGACCAGGCTGGCCTCGGACTCAGAAATTTACCTGCCTCCTCCTCCCAA
GTGCTGGGATTAAAGGTGTGCGACACCACTGCCTGGCCTAGACTTATTTT
TTAATCAGATTTGAGTCTTTGCCTCTGGAATCACAGTAGCTTTTCCCAT
TCAACACCTAGTTTACAGAAGAAAGAAAACCCAATTTTTTTTTTTATAAT
CATTAGACAACCTAGAAGTTTTCCCTCCTATTAAGAAAACATATTAACGGG
CTGGCGAGATGGCTCAGTGGGTAAGAGCACCCGACTGCTCTTCCCAAGGT
CCAGAGTTCAAATCCCAGCAACCACATGGTGGCTCACAACCATCCGTAAC
GAGATCTGACTCCCTCTTCTGGAGTGTCTGAAGACAGCTACAGTGTACTT
ACATATAATCAATAAATAAATCTTTTTAAAAAAAAAAAAAAAAAGAAAAAGA
AAAAGAAAACATATTAACAGTATTGAGAAAACCTGTTGGCTTAAATTGAT
GATTTGAATTTTATTTTACTAATAAATGCATGTATTGCTGGGCATGGCAG
CACATCCCAGCACTCAGGATTCGAGATAAGAGATCATAAGTCCACGCTA
GCTGGAATAGCAAAATAAATCTTTTTTTAAAAAATATACATACATACAT
ACATACATACATACATACATACATACACACACACACACTTTTCTCAGT
AGTACGGCCAATTAGTTGACTTGTCTAAGGGAGGGAGGAAGAGGAGGCAG
AGAGCATGCTGTTTCTGATCACGTTCTCTTTTGCATTGAGTCTGGGACCCC
AGCCCATAGTGTGGTGCTGCCCACATTGATTATTGGTATTCAGTTAACCC

FIG.3D(64)

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AGTGTAGAACTCTCTCAGAGACATGCCAGATGCTTGCCTCATAACCAC
TGTGTATGTATATATGCTTACAGAAAATATACTCATCATTACACATAAAT
TTCATCCACTTACCTCTTATGAAAAGTTGATTATTTACTGAGATTTTTCT
CATTCTGAAAATCCATAAAGTCTACCACATTGATTAAATTACTTGTTTTT
TACCTGTTATTGCTCATGTTAGAATTGCTTTCCTTATTTGGGGTAAGCTG
TCGTTGGCCACTGTGAGGGGCTTATCAAGAAGTCAGAAATGGGAACACCT
TCTAGGAAGTCAGGACTGGAAGCTTAGCTGAGCCAGCAAGTGTTCCTCAC
ACTGCACTTCCTGTGAGCCTACCTGTGCGGCATCAGGAACTGGAGTTGGG
ACCTTGAGGATTGTTCCCTGGAGGCAGGGGTGGAGTCAGGCAGGGGTGAA
GCTGACTCACAAGATGGTCTTGCCTTTCAGTTGTTTCCTCTCGCTGCTTC
TGGTGGCTGCAGTGGTCTGGAAGATCAAGCAGAGCTGTTGGGCATCCAGG
CGGAGAGAGGTAAGCCCAAGTAGACAAACTCCACATAAAACTCATTTTTT
TCCTTCTTTCTAGGCAGATCACTTTTACCTGTTGAGTGATGACTAATATT
CATATGAGAAGCATGCTGTTTAACCTGCATTCTGTGGTTCCACTATGTGC
CATCAGTAGATTTTAATTATTCTTGCATAAAGTGTCATTAGTTTTGCCAC
TGCTTGATTCAAGTCTTCCTAAGAGTCTTTCCTAAGAATATGAGTGTAGA
GACAAGTTCAGCTCAGTGACAGAGCACTTGCCTGGCATAAACTGAGTCCC
TGGATTCTAGTCTCAGCACCTCTAATAGCACAACTAGAGACAAAGCT
TCTAACCTGTGGGTCTTGGGCAGCAGGTAGGGGAGGGGGATTTAAAAAAC
AAAAACAAACCTCTAGCTGTAGCCTGTGTCATTTGTTATGACTAAGCACT
AGAGTGGGTACTAGTAGACATGCCATGTGGACATTGAGCACCTCTCCATC

FIG.3D(65)

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CCAGGCACTGATCCAGGTGGTTCTGCTTTATCTTCATCTCCACCCTAGGA
TATAAGGGAGGCTACGTAAC TACCATCACCACACAGATGCTGAGGTACA
GAACTGAGGGGTAAC TAGTGCCTCTGCCTTCACAGCACAGGTTCTAAAC
ACGTTTTCTACAAACACTTCATTTGTTCTAGTCTGTTTCAATTAAGAATCT
CATGTTCTGACTGAATGAGCTAGACAAC TACCCTAGACTATACATTCTA
AAGAAGGGCAACAAGGCAGTTTTGTTACTGTTGAGAAGAAAACAAAGTTA
TTTCCGTATGAGTTATTGAGATAGAATAGTAGAGATTTGTCTGAATACAA
AATAGAAAGTATATAAAAGTATATAAGTGGATCATAAAGAAAGCAACAAT
CAACTGGAAAATATTTGCAGTATCATGAGAGAGAGAAAAC TAGAAGATGA
ACCCCTCAAAAAAGGATTTTTAAAATATGCTTAGACTGTATTCAGTCAG
CTAATAAACTTTTTTTACCTTTATTTGGAATTTACGAATAGCACTGAACC
TGACCATTGTAAATGCACGAGGTCAGGCATGACTTGTTCCCAGTAGGAAG
TTGTTTTTAGTTCTTGCTGTGGCCTGGGTCCTGATGGAAGTTCTTTACCC
ACCTTATCTCCTGTCCTCTTGGCAGAGGTTCTAGAATAGTGCTGTGATGG
GGTAGCAACTGTCTTCCTGTGACCCTGCACCTAGATTATTACAGAACCCA
GACTGGGTTTGCTGAGTTAATGGAAATTCCTTCTAGGTTTCAGTAGAGAGA
TGTGCTGACACATACTAGGCCATCTAGTTTTTCAGTAATGCTCAGAGACC
GCAATAGGATATGTAACAGCAACAAAATTTTTAACATAAAATTTCCCTTC
TAAACAGAGTGATGATTTATGTAGCTTCAGGATCCTGCCTCCTAGAAGA
TGGTTTGAAGCAAGGCCAGTTTGTCTTCCCTAGCATAACCTCAGAAGACC
TCTCATATTATTGATGGTATAGGAATGAATGCCACATTCTGTATTTGAG

FIG.3D(66)

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ATGTGTGCTATAGTATCTCATCTGACCCAACATGAAAACATTTCAAGCCA
TGTGTGCTTGGGTAAGGTAGGAGTTCAAAGTCATCCAGTGAGTTCAAGGC
CAGCCTGGGCTGCATGAGACACTGTCTCATAAACAGACACTTGAATCTCA
TTTAAAGAAGACATTGAAGACTTGATACTTTGAACACCTATCCTAACGTA
TCCACCCCCAAATCCAGAGTCCTTCATGTTCTTGTCCTCTGCAGTTCAC
TTTCATTGTGTTCTCAGCAGCAGCTCTCTCCGAGGAGAGTTGTCTCCCAT
CCTATCAGCCATCTTTTTTATTGTTGTTGCTCTGACAATGTCTGGTTCAG
GTTTTAACACAAAGCAAGCTAGAGTGATTTTAATCTAGCAACAAAAATAT
AAAAAGGTAAGTTTTTGCCCTTTTATATATTCAATCAACAGATATCATAG
CATTATATCCTCCACTTTAACTTTTATTTCTTACTGGTAAGGGCTTTTTA
TAAAAATATAATAGTGTTACCACATGTAACAAAATTTGATACCTTGTGCT
ACCTAGCACCTTGTGATGTCCAGTTTTCTCAGCTGTCACAGAAGCGACA
CTGCATCTGATCAGTTTGAATCAGAGAGAGTGTAGCATGTCTAATATCTA
GTATTCATAATAAAATCTCAGTACTAAGCATATTAATAATACTATATTA
TTCATTAGCAACTTCTTCGGGAGATGCAACAGATGGCCAGCCGCCCTTT
GCTTCTGTAAACGTTGCCTTGGAACAGATGAAGAACCTCCTGATCTCAT
TGGGGGAAGTATAAAGGTGAGAAGTGGCTCAAAGGTCCATATAGCTTTTC
AGAACTCAGGCCTCAGTTTGCTAGGCTACAGACAGCAAGCGCTCTGTGTG
TCACTCCTGTCTCCTCTCTAACAGTTAGTCAGCAGAAGCAACCCCGAGCG
ACCGTAAGGGGCTCTGTGTGTGGCTTTACTTTTCGAGTTGTTGCATGTCA
GATTTTAACATGCAAATTAAGCTTGTTATTCTTACTTTGTGGCATAATAC

FIG.3D(67)

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TTTATAGTTTTTATTTGGAAATATCTAATCTGGGCTAGGTGTGATGGTGC
ACATCTTTAATCTCAGTTCAGAGGAGGCAGAGACAGAGGCAGGCAGGATC
TCCTTGAGTTCTAGAACAGCTGGTCTACATAATGAGACCCTATATGTTAG
AAAAAAGAAAGAGGGGGTGGGGGAAGGCAGCTAACTTTAACCATTAAATT
GAACCAACACACACACATTTTGTTCAGAGCCCCAGTACTCAATTAAAAGC
CAGGCAGGCATGGTAACAGTACTTAGGGAGTCAGAAACAGGATTCCCAGA
GTAAGCAGTCTGACTAGGCTAGCAGGAAATGGTGAGTTTCAGGTTCAGCA
AGAGGCCCTGCCTCAGTAAGTAAATTGAAGAACAACCTGAGGGAGACTTGC
ATGTGCACTTGTGCATGCACCCACACATGCACTTGCACACATACCATATG
TCACCATGCTTAGACTATAAAATGTAGTCACTACTGGCAGCACATGCCTA
CAATACAGATGCAGGAGAATCACTGCAAATTTGAGATCAGCCTGGGCTAC
TGGACAAGATTTTGTCTCAAGAAAACATAAACAATACAAAAGTGTACTGG
GGGGGTTATTCTAATGCCAGTGTTTATGACAGCACATTCAGAACTGACAG
TAAAGGCAATCAAGGACTGTCAGTGGTGGGTATATACATAGGCAGAGGAG
CAACTGCTACTAGAACTGTTTATCCTTTAAAGACTAATGTATGCTGCA
GCATAGACAAACGTTAAGTTGTGTTAAGTAAAGATGCTGTATCATTCCA
CTTACCCATCGAGAATAATCAAATACAAGACAGAGTAAATAGTGACTGC
TAGAGGCTTAAAGAAAAGACCAGGGGGTGGGGAAAGGGAGGGAAGGAAG
TGGGAGAGGGAGGAAGGGAGAGAGGGAGGGAGGGAGCCAGACTTTGTGGC
TTACAGCATCAAGAGGCTGAGGCAGAAGGGTTACAAATTCAAGGCCCTAC
TGGGCTACATAGTGAGAAGTAGGATTTCTTGAGCTGTCTTCTAGGTCA

FIG.3D(68)

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TAATCTCTCATTGGGGGAAGTCAGGGCAGGGACTTGAGGCAGAAACCATG
GGGAATGCTATTTGCTGGCTCCTTCCCAGGCTCCTCTCTAGCTTTGTTTT
CTCATTTTGTTTTTACTGTCTATGGGTGTTTTACCTGCTTGTTTTCTGT
GTACCATATACATGCCTGCTACCCACAGAGGCACTGATGCCTGGAACCTGG
AGTTACAGATGGTTGCAGGCTGCCCTGTGAGTGCTGGGAACATAAAGTCGG
GTCCTCTACATGAGCAAGTGTTCTTAACCATTGAGCCATCTCTCCAGCCT
ATAAAATTCTTTTTTAAAAATAAAGTCTGCAACAGAAAATGAATATTTTC
TAGAGCTGAAGCATTCAATGAGTGGATAAAGAATCCATTTGATGAGCTAT
CTACCTTTCACAAGCTCTTAACCCCTACAGACTCAGGACTTAGTGGCTGG
AAGATGAATGTAAACAGGTAGCTCTCTCCATAATATCTGGTCTGTTTGT
GCCAGGTGTGCAGAACTGTGCAACAGGTCACCATACAAACCGGCGTGGGC
CTTTCCTGACACTCACACAGCTCTCGGGACAGTGCCCGTGGGGACCTCTT
ATTGACCTTATAAGCACCTGACTGTGCAGTGTAGCAGGGAGTTAAGGTGC
TTCTGTTTTCTTCTCCAGACCGTTCTAAGCCCATTGCCCTGGAGCCCT
GCTTTGGTAACAAAGCCGCAGTCCTCTCTGTATTCGTGAGGCTCCCTCGA
GGACTGGGAGGAATCCCTCCTCCTGGTCAGTCAGGTGAGTAGACAGGAGA
CAATGACAGATATTGGTCTGTGAAGGACTGAGTCTTAGACACTTCTTCTG
GTATAGAACCTGGGTCTGGGCACAGTGCTTAGTGGTACAGAGCTTTGGTG
GAACAATTCTATAGTCCCCAACTGTGTTCTGAGCACTGACATTCCTGTC
CTGGGGTGGAAGTTCAGGACCTTCTCACGGTGCACAGCGTCCTCAGACA
TTCATGCTCTGGTCCCCTTGACTCTATTGATCCCTGCTTCTTTTTTTTTT

FIG.3D(69)

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TTAACCCCTTGTTCTTATCTCAAATTTAGGCTTTTTCTTCCTTGATACAA
GCTCCTATTCATCTCCATGCCTCTGGCTTCCAGCCATGTCCTCAAAGCTT
GTGTTGCCAAGTACAGAGTTCTAGTCATGCTCCACATCTTCTTAAGGTCT
TGCTATGCAGCCTTAGCTGGACGAGTGCTCGTTATAGGCCAGGCAGTGGT
GGTACACGCCTTATGTCCTAGCACTGAGGAGGCAGAGGCAGGCAGATCTC
TGAGTTCAAGACCACCCTGGTCTACAGAGTAAATTCCAGGACAACCAGAG
CTACATAGGGAAACCCTGTCTCAAAAAAATAAAAAACAACAGGAACAA
CCCCAAAACCTCATTATATTGCCAGGCTGGCTTCAAACCTCATAGTTATC
CTCCTACTTCAGCCTCCAAAGTGCTGGGATTATGGGTGTGACCCTTCATG
CCCAGATTGTCTTAAATATGAGGCATGAAGAAGTATTATGAAAACATAAA
GGATATTTTGAAAATTATAATTCTACTGGGTAAATGCAGATCCATTTTCA
TTTCATTGAAATAATGATACAGCCTTTGGAGGTTAGGGGAGCCTCTCCTG
TTTTCAAACCTGACTTTGAACTTCTGATCATCCCGCCACCACCGCCACCTC
CTCCTCCTCCTCCTCCTCCCCAGTGCTGAGATACATCACTACTCCTGGTT
TATGTGGCACAGAGGCTCAAACCCAGGGCCTCATGCATGCTAGGCAGACA
CTCTACCAGCCAACCTACCCACAGCTCCTAGATGTGCACCGTATTACAAA
CATTTATTCTTCAGCATGTTTTTTTTTTTTTTTCTTAAAAATCATCTCTA
CAGGAAACAAGTACCAGTGGTGTTTTAGGGCAGGAATAGGAAGAAAATAT
TTTTACTATATACTCTTTTTTTTTTAATCATTTTTTAGATTTTATTTATTT
TAAATTTATTTACTATTATTAATAAGTACACTGTAGCTGTCTTCAGACA
ACCCAGCAGAGGGCATCAGATCTCATTACGGATGGTTGTGAGCCACCAGG

FIG.3D(70)

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TAGTTGCTGGGATTTGAACTCAGGACCTTTGGAAGAGCAGTCAGTGCTCT
TAACTGGTGAGCCATCTCTCCAGCCCCTACTATATACTCTTTTAAATGAC
TTATTTGCTTTTATTTTTATGTGCATTGGTAATCTGCCTGCATGTATGTC
TCTGAGAGAGGATCAGATTCCTTGAATTTGAGTTACCTTGTGGGTGCTG
GGAATTGAACCCAGGTCCTCTGGAAGAACAGCCAGTGCTCATAACTGCTG
AGCCGTCTCTGCAGCCCCTACTATATACTTTTTTTATAGTTTTGAATTTT
TTTTTCTTTTTGGGTATTGCTAAGGATCAAATATAGATCTACTATTTATT
TTTTATAACATCCATTAGTATTTTTATAACTTACTACATAGTTTGCCAAT
TCTTTTATACATGTCCATCAAACATGTAAGTCATAATTTATATAAACCTT
GTGTTAAAGCTGGAGGCACAGAAGGAAGATTGCTACAGAGTGAAGTCTAG
ACTAGCCAGGGCTATATAGTGGGACCCTGTTGCAAAGAAAAAGTTCTCTC
TTTAAACACAAAGGCAGTATGAAAAGACATACCTTGATTCTGAAGCTGTG
CATAGGAATGCCTCACACAGTGTTCTGCTCAGGACTATACTCAGATGCAG
TGGTCTGAGGGACTTGGTGGTGTCTCAGCCAAAATAACCTGGAGTTTAGT
AGGAAAGTCTCCTTTATCCGTGTCCAGTCCTGAAGGGAAGCCTTATTTAT
GTATGATGAGTCAGGACCCATTGTCTTCATCTTACTTGGCATCCCCCAG
CACTGAGTCTCTGAGTTAGCCTTACTTGGACAGAGTGACTCTCTGGGCAC
TCTGGACAGCATCTCCTGCTTCAAAGGGCAAGATCTTTAGAAGACACAG
AGATGGAGCAGGTCTTACATGGAGATATAGCAGCTTTTCCTTCCTGACCC
TTGACCCAATGCTTCTTTGGAAATCCTCATGAAACCCTGCTCCTTTCTGG
AGACCCACCCACAGCAGGGTTATCCATGCCAAGCTTCCTGTACTTTCTC

FIG.3D(71)

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TTTTTGAGGAAGCACATACACACAAAGTTTTAGTAGCTCGCACATCTCAC
TGTGAAGTAGTGATACTTTCATTGCTATCTTCTGGAAACAGGCAGGAGTA
GGCACACGCTCAGAGCATAGCTGCACTCTCATTCACTTGCCACCCTGAGG
CAGAGCACACGACTTTGTGATCTGCTATGGAGGAGAGAGAAATGAGTAGT
TAGGTGTGTATAAATAAGCTAACACCATCACCCCTTTATCTTTCACTAGG
GAAATGTAAAAAGAAATCTGAAATTATTTGTAAAAAGTAAGCTGCTTC
ATGACACATGTCCCCTCTTGTGGGTTCTTCCAAGGTCTCGCTGTGGCCAG
TGCCCTGGTGGACATTTCTCAGCAGATGCCAATAGTGTACAAGGAGAAGT
CAGGAGCTGTAAAGAAACCGGAAGCAGCAGCGCCTGCACAGCCTGGAACC
TGCATTTGATACTGGGGCAGGAATTCGCCCTCACAGAGGGCGTGTGGTCC
ACGAAGCTGTCTACAGGGGAGGCTGCAGGCAGGAAGCAGGGGTGGGGCAG
AAGACTGGGGACCCTTGAAGCGTCCAACCTCATGTGCATGATCATGCAAGC
TGTTTTCATGGCTCACCCCTCTGTGTCCAGCATCTAACCTTTTACTTCTG
TGTAGGAAATAATTTAATTACAAGTCCAGGAATGGTCTGCTCTACTCATG
GGTGGAGGAGACCAGTGCCGACCCCGTGAGAGCTGAAGGTGATGCTGAGG
TCCCTTGTGGAAGCCTCTCTTGGGAATCTCAACTGCAGAGGAGCTGCCCT
CTGTCAGCAGCTCTCCAGCATGGTCCTCTGACACTCCTCAGATGAACGTG
TCTCATCGGAAGCTTGCTGTCTTTTTACAAGATGAGCTTTTACTCTCTTC
CAGGAAGTAGCTTTTTTCTAGCTGAGAATTAATAATGGTCTTCTCTTT
GGAAGTCATATCAAAGTATAATTGATGGGGGCCTTGTTTTGTTTTGTTTT
GGTTTTTGGAGACAGGGTCTCACTGTGTAGTCCTAGCTGGCCTGGAACCTC

FIG.3D(72)

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ACTATGTAGATCAGGCTGGACTGAACTCACAAAGATCCACCTGCCTCTGC
CTCACAAATGCTGGGATAAAAAGCATGAACCACCAGGCCAGCAAAGAGG
GCTATTCTAAATGTCAAGGTCAATGGAGTTAGAATATATATAAAAAATG
CAATTGATAATTCTCTATAGAACTTGATTAATTTTAATCCATTCTTTCC
TTCTCTTTCTCTCACTCTGTCTTACACACATGCACACATACACACACT
AAGTGCCTAGACTTTGAATAGATCTAGCAATTGGACATTAGTAAGCCTAA
GTTTTTACATGATTGCATTCTACATTCTTGTAACCTTTAAGTAACTACC
ATTGCAGTTTGTTCTTTTTTTAAAGTCTAATTTGCAGCCAAGAACGAGTA
ATTCTCACCCCAAGCAACATCTAATAGGGACTGAGTGACCCAGCCAGC
CTAGTGTCACTTTAGGCCTGACGTTTGAGCAACCCTCGGCTCTTGCCAAG
GCACCACAGAATGCACTTGCTCATGCCCTGTGCCTCTTGAGCAGAAAAGA
GCACTGACAACTGGGACACCTGGCTCTGTCTTCCTACAGCTGCTCGCACT
GACCTGTGGGAACCTGTGGGTCATCCCCAGGCTGAATGGAGTACACACTA
GAAGAGGGATGATGCCTAGCATTGGGGCAGCATCTGCTCAGCACATGGAA
AGGGACCTGGTTCCATCTCCCCTGGGCAGGAGTTGGTCCAGCCTCCTCCC
AGACCCAGCTGGTGGCTGTGAGGAGGTGGGGAATGCTAATGAGAATGAAA
AGCACATGGGTTGATGGGAAGGGACAAGATTACCACGTTAGGAGGGTGAG
CAGCCCTCTGCTATGTGCCAGGACCCTGCCTGGACATTGCATTTCCCCA
TTTATGGTGCTCCGTATTCTGGCATTATGCAGCAGCCTCACACACCTGTC
CTCTCCTTCTTCATGTCCTACAGTTCTGCTATCACCTGACTAGAATAGCC
CTCTAGGCAACAGTGCTCAAATGTATGAGTTTGGAGAAGTTAACAATCAG

FIG.3D(73)

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AAGAACAAAACTGTAGTGTTTCACCTTTAAATGCAGTGTTGAAGAGGGA
GCCTTTCTCTAAGCCCTGCACTAACCCACTCCTCCCAAGACTCTTGTGGA
GTGACAGTTCCAAGCTGAACCATAAATCACTGATGCACAAAACACTGCTA
GAAGGCTCACCTCTCAAAACAGGACTCTTTGCATCACTATTAAAGAGCAG
AAAGTTCTAGAAATGATCCCAGCCTCATCCCCTATACAGTTAGGAGCTCC
CCACATCTCTACCAAAACCCAGCACATAAGTATCTGCGTGGTCTAGCCTT
TCATCTCCGTAACAAGCCAGGGGACTCTTGGCCAAAAGAAAGAAAGGGAA
GTTGCACTAGGGCTTGTCCTGTCATAAGGAATCCCCTCTGCTTTGCTCA
AAGGACCAAATTTCTTTGGCCAAAGAAGTTGCTTCTATGTTAGTCCCATA
CCCTGAAGTAATATGTACCATGGCTCCCACCTACCTGTTTATGCTCTCCC
TGCCCCCAGGGAAACTGTTTATTCTTTCAAAGAAGCAAACAGCGTTCAT
TTCTGCTCCTGTAATGGAGAAACAGCCAGCTCCCCTGCATCCCTTACAGC
CAACAGCTCCCTTCAGGCTTAGAGCAGGGGGAATGGCAGGGATTAAGAGC
TCAGCTCAGAGCCAGTTACCAAGATGGAATGGAGTTGTGACCCAGTAACT
GTGTCACGAGAGACCATGTATATAAAATAGTCATGACGACACTGACCTCT
TGCACTTGACATAACTATACTGTAGTGTCCAGAATGTTGAGACATTCAG
GGTGTACATAAACAGAAGAGTATCATAATGTATTTTATTAAACACTAAC
ATCTGAGTTTCACCTAATCTGTTTCTGTGCCATATACTGGGTATCCAAGC
TCTGGGAAGTTATCCTACCAGGCCCTGATCTGTTGATAAGGCACTATACA
CCATGCTGGTGTGTTCTGTAGCCTTGTCGCCATTAGGTAACGAACAATG
ATTCAGCTCTTAGAATACCTAGGAAGACAGCAAGCAGGGTGACACACGGC

FIG.3D(74)

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TGTGATCTAAGCATTGAGAAGACAGAGGCAGGAAGAAAATTCAAAAATGG
GGCTGGAGAGATGGCTCAGTGGTTAAAAGCACTGGCTGCTCTTGGTCAGG
ACACTAGTTCAGTTCCCAGTACCCACATGGTGGCTCACAACTTCTGTGA
CTACAGTTCCAGATAACCTGACACCCTCCTCTGGCCTCCTCGGGTGCCTG
TGGTGGTCCACCTGGTGCACAGACAAACACCCAATACACACAAAACAAAA
GTA ACTCAAGAATAGCCTGGGCTACATAGCAAGAGCCTGTCTCAAAACAA
ACGAACCTATGAAGAGCCAGGCAGTCTATCTATTTACATGGCAGTATACT
AGAGAACTCAGGAAGCAAGAGTGTTCACTGTTGTAATTTCAAATGC
TCCTTG TGATTTCTGGCATCTCTGTGGGGTGAGGTGTTCTGTTACTCTTC
ACATTCAAAGACTGTCACCCATGAACGTCAGACTTTGCAAAGGGGCTCTC
TAAGCTGCACTGTTGTGGCTTTGTCTAAAATTTTAATGACGTTTCTGAGA
ACCATGTTCTTTTTATACTAAAATCTGGGGATGGGAGGGCTCATTGTG
ATAAATAGCACTATTTTCCCACACCTCAGCCTCCTGTCCCCGTCTGGTC
TTCCCTACACAGTCTGGAGAGGGCTCTGAAAGGTCCACAGAGTTTGACAG
ACACGAAAGCAACCCATTGCCCCGTTGACCTGACCTGGAAGAAGACTGTC
AGCAAAAGGAAAATACCAGAATATCTGGAAAGCTTGAAGTGTAAGATGGG
ATCTCGTTGGGGAATTGGATGAAGAAAAGCAGAGCGCCTCTGGTAGGTGA
CTCTGCAGCCTGCCAGCGCCCGCCCTCTTTCTACACAGCAGAGTGTGCAT
GGCAAGGAAATGAGTCACCTCCTTGGGGGATGGTGCTGTTTTTATGAAAA
CCTCTGATCCTTGGTGTCTTTAATTGATCTGTTCAACAAATATTTACTA
AACACTTCTAAGCTAACATTAGGGCAGTGACTGAGGTGGAAACCCAGCTC

FIG.3D(75)

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TTTAGACAGCTGTCATCCTAGGATAGCTTCCTGGAAGCAGAACCAAGAAG
CCAGAAGGTTCTTCCTAGGGTGGCCTTGGCTCCCTGAAGGAATCTGAAAT
GCTGACCCTGTCACAACCTCCCAGCACAGCTTTGGAATGAGACATCAGCC
TGGCCTCCAGCAGAGCAGAGGCTCTGGAGCTCCACATCCTGCCTGCAGGG
AGCCCTCAGGGTGCCCTCCAGAGTACAGGGAGAACTAAAGGCAATAACA
GAAGCTGCTCTCAGAGCCTGACTGTGCACAAAACACTAGTGAAGCCTGCT
GAACTAATTCTGCCTCTGGAAATCTTTTCTGGTTCTTTACAGTTTGTTGT
TTTGTTTTGATCCAAGCTTAGTTTGTTACTATGTGTGATTTAGCATCTGT
CGCACTTGTTGTAATATGGAGTAAGTATTGTAACTATTTAATTGCTGCG
ATTGTTGGGTTATACATACATTTAGGACTGCAATTTTTTGGTATTTTTTG
TATTGTAAAATAACAGCTAATTTTCATCAGGAACAAGAGAATTAAGGGGGT
CTGCATTTTAAATGCAGATGTGAAGCACTTGTATATAAATAAAAGTAAAT
ACTATAATACAAAGTTCCTTCTGAAATAAAAGTAGATCTGGTAAAAATGT
GCGTGCGTTTCGTTCTGAATGTTCAATGCTAATTTTGTTTTATTTTATAT
TTACATTTTAGTCCTTATTTTAGCAGTGAGGAGACAGGCACAGCAGTGCA
TTCTCACCTTGGCAGCTGAGGAATCCCCTAGAGTAGACTGCAACTCAAGA
CTCTTGGCTTCCACACTGAAAAGAGTTTCAGTTTATGAAGCAGAGTTTAG
GAAGTTTAGTGAGGAATTTAAGGACTTCTTTTAATGTTTGTGTCTACATA
TGTGGGTACATATATGACACAGCATGCATGTGGAAGGCAAACAACACCTT
AATGGAAGTGGCCTGAAGAACAACCTCAGGACTTCAATCTTGGCAGCATA
AACCTTTACCTAATGAGTCATCTCCAGTCTATACGGGGTGTGTGTGTGAA

FIG.3D(76)

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CACATGTGCAACAGCACACAGTGGAGGTCAGCACAACTCTTGCGAGTCAA
TTCTCCCTTACCTTGTAAGACCTAGAATTCCACATTGCCCAGGCTCTGAA
AGTTAGGTTGGGTCCACACTGGGCCATGGCTGATGAAATGTTGGAAAAGT
GATAACACCAAACCTTTTGCACAGAAAATATTTTCATCTGGGGCCTTCCCT
GGAGTTCACAGGCTAAAGTGTTGGAAGGAACATGGGTCCCTGAGCCACCA
CTTTCACAAAACTACCTGATCAAGAAGAACTATTCTGGGTTTCTGTTGC
TAAAATTCCTTCCCAGAGAGAAATGTAAGCAATGTCTGCCCCTTCAAGGG
TCCCAGCAAGAAACCAAGGCACAATTCCACCAAAGTTCCTAGAAAACCA
GTGAGTTTATTGGGCTTCCGTGCAGAACATACATGAGGGGTTACTTAGAG
AAGTGTGGATACTCCTCCCCCTAACAATCCACACCCTGAAAAAGCCTTAC
CCAGCAGGGATGAGGGCTTCCCAGACCCACATTGATGGTGCTCCCATTC
CATTTTTCCCTGGCATGCAAAGAGATAGACAGAAAAATAGATTATATATA
ATATACACATAAATTAGAAAAATAGATTATATAATATACACATAAATTAT
ATATTATATATATAATATATAATACACAGATAGATTATATATGATATATA
AAACACACAGAAATAGGGTATATATAATATATAATACACAACTACTCAG
CTATTAAAAACAGTGGATTCATGAAATCTTAGGCAAATGGATGGAACATA
GAAAATATTCTGAGTGAGGTAACCCAATCACAAAAGAACACACATGGTAT
GCACTCACTGATAAGTGGATATTAGCCCAGAAGCTTGAATACCCAAGAT
ACCATTACAGACCACATGAAGCTCAAGAAAGGAAGATCAACGTGTGGGT
GCTTCTGTTCTTCTTAGAGGAACACCCTCATAAAGTAGTGGTGGGGGGTG
GGGGGAGACAGAATAGGTGGTTTCCAGGAGAGGAGGAAAACAGGAAAGGG

FIG.3D(77)

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AATAAATAACATTTGAAATGTAAATAAAGAAAATACCCAATAATAAAAGA
AAAAGAATTTTGAACAGAGGGTAAAAAATAATACACAAACCAGGTAGAT
AGATTATATATAATATATATAACACAGAGATAGATAGATAGATAGATA
TAGATAGATAGATAGATAGATAGATAGATAGATAGGTCAACTGCTC
GCCCCTCCACTAGGTAACATGCAGTTAAGGCAGAGCTGCATACAACAGAT
GTTAGGGATACTCAGGTGAGAATCTCAGGCTTTGCTCCATCCATCTATGC
TGGGGTGTAAGCTGTCAACAAGTTTAGCTGGGATGATGCTTTGCAAGAGG
GCACAGCTGAATGCCCTAAGATGGTAGATGCTTGGCTCAAAGGAGACACT
ACAGCTCTGCATCAAGGCAAACTAACTGAGATGAGGGCCTTTATTTTCCA
GATCTGTATCCTGGAGCATCATTACCTGTTACTACACTGAAAACATTG
GTGTTGGTTTCATGGCAGATGACAGGCAGTGAGAGAAGTACAGCAGCGGA
CTGCTAGAGGTGGGGTCTGTCTCAGGACGTGGGAGGCTGTTTGGTTAGTA
ACTTGGAAGCAACAAGTTTTTAGCTAGAGGGAGAAAAGCTGGAGATAAC
TGTA CTTGCTTGATTTCTTAAATATCAAATTTTATTTTATGCATATGGGT
ATTTTGCTTG CATGTATGGCTATACACTACATGCTTGTGGTGCCACAGA
GACCAGAGGAAGTAGTGTGAGCCTCTGAACTGAAGTTACAGACATTACG
ACTTGAGTGCCTGAACTGAACCTTGGTCCTCTGGAAGAACAGCCAGGGC
TCCTAACCCTGAGCTATCTCTCCAGCCCTGACAGAACATCATGTACTCC
AGGCTGGTCTCAAATTTGCTTTATAGCCAAGAAGGGTCTTAAATTCTGAT
CCTCCTGTTCTCTCAAGTAGTGGGGTTACAGGTCTACACTGCCGTTTTCT
TGAGCAAATCATTACAAATTGAGTTCTAAGCCAGGTGTAATAGTTCATGT

FIG.3D(78)

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AGTAACAATCTGGAATTTTGGTCTCTTAAAAAACAATATTATAAGAAT
GTATTTTCATTTTAATCCCAGGTGTATGGCATATATCGAACTGCTTTGGA
CTGACTACAGCAGCTATGATTTTTTCTTGTTCTAGCAGAGGTATGGTTTT
GCCAGCTACAGATAGTTTCTGTGATTGTGTGACATTTGGAATTCTGGAAA
CTTTTCAGATGGTATATAAATATTAGAGCCCCAATAGGCAGAGTTGATGA
TTGTTGGTCATTCAGGGGTATTGGTTGTGGTTAGTAGTCTTGCTTGAAGA
AGAAACAAGAACAATTAGATTCAGAGATCTCTATATCTCTCTCTATCTT
CCTTTCTGTCCTATCTAGTAATAGGGGGTAAAACCAGGATGATAAAGGGT
TGGGGGAACCCACAAAGTAACAAAGACTGGCTACAAGTGGCACCCAACTT
GGAACCTCAAATTTGCCATAGAGGAAGCAGCAGGGGATGAAGGAATGGATT
GTGGCTGTTGTTGCTGGGATATTCTCACTTTGCTCCCAGAGGGGATTTT
TCTGAGGTTTTGTTGTTTTGCTTTGCTTTGCTTTGGTTTTCTTCTACATA
TTCTGTTTTTTAAGTAAGTTGAAATAATAGCCGAGAAGCTGGAAAAGTTT
GGTGTGGAAATGGAGCAGCCTGAGAAACAAACAATGTATGAAATGGGAAA
ACTAAAGGGGCCACTCTTCTCTCTTTTCTGAAAGGCTTGCAGACTTGGTG
GTGCACCTGGAGAGTTTATGGATGGAGATGGAAGCTCTTAGGAGACAAGA
AGCATGGAAAAAGAGAACAAAGGCTCAGTCCCAGTGACTGAAGAGAGCAG
GAGTTTTCCAAAGAAGGTGCATGGGAGGGCCACTGGTCAGAAAAAAAAGG
CTGAAAAATACCAAAGGACAATGTGCTGAAATAGCCCATTTCAAGAGAAA
GGGTTCATCTCAAACCAGCATTCTGACAGAGTGGAAGGAGGGGTGGCTCA
GGGTTATGAGATCACCATCAGCTTTTCCAGTTTTCCCATATAGCATATGC

FIG.3D(79)

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CTGCTAATGGTATGGAACAAGAGTAAGGCAAAATAGGATGGTGTCTATA
GAAATGATAGCTCTAAGGTGTTTTTAAAAGGCCTTGATTTTCATATGGAAT
GCACTCTCCTTATGTGGAACGGATATTAATAACCGGGGTACACAACTA
GAATCCCTTCCCAAGATTGGAAGGGATTGGTAACAGCTGTACTAGAGACT
GTCAGCCGTTGCAATGGTTAACATGCTGGAGGAAAGAAGCTGTGAACATT
GAACAGTAAACAGAGCAAGGGGTATTAATATAGTGAACGAACAGCTGCT
AGGTGAAGGGCGGTACTCTAGTGTACAAGCACAGACTCGGTGTCATGAAA
CTACTATAGAACAAGGTTGCCTCAGTGGCTATAACACCTTGGGACAAAGG
AGGAGCCAGGAAAAAGTCCAGTTCATTTACAAAGATTATATAAGGCTCTG
GAGAAGCCTTCACTGATTTTTTTTTTTTACAAAGATTAGTCTCAGCTATGA
ACAAAGCCATATCAGACCCTGACACAAGGCAGGTGTTGATAGAGACCTTG
GTGTATGACAATGCAAATACCAAATATAAAAAATGTCATTAGACTTTTAAA
GGCACAAGTAATGCCTATGGATGAGTGGATAAGGGATAAGACCAATATTA
GTTCTAATGTGTACTGTGCTAATATCATTGATCAAGCTATAGCTAGAGAT
CTCTGATGTCAAATGCCTTGTGCTTCAGTTGCAGCAAATACAGTAATTT
GCAAGGAGTCATTGTGGCCAAAACCTAAAGGTCTCAGATCTCAAATGCCT
GATGCTTTGTGGGAAATAGGGTCATTTGCAACAAAATGTGAACAAGACA
TCTTTAAGGGCAATGGTTTTTCTAAATATAAACCAGAAAGACGGCCTAGG
CTTCCAAGGTTGTGCTGGCGATGTGGCCAGGGTTGCCACTGGACCAATGA
GTGTAGGTCCAAAAGAGATATTCAAGGTAACGTATTACCATCATGAAATG
GTCTTGGGGGCCTATCTTGAGGCCCTGCAGCAAAGAGTATGAGCCATTCC

FIG.3D(80)

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AACCAGAGAGTGGCATGGAGACTCAAAACCTTCACTGGGCACTGGAGATT
TAATGCACACTAGCTATTGCAGGCAGCATGGCTCTAGACTTGGCCACAGA
TAAACATCTTGCTCTATCCCCAAAATTCAAAGTTATAACATAGCTACTG
GAGTGTATGGTCTTTTTCCCTCAGGGACAGTAAGGATAATCTTGGAAGG
AGTGGATTGACTTCCTAAGAATTCAGTGTGCATCAGGAAGTATAGATGAA
TATTTCAAAGGAGAAATTAAAATTGTGGCATATGTAAAGGTAGAGCTGCA
ACTTAACACAGGCGATAGGGTTGCTCAGCTGCTGCTGTTTCCCTATATCA
AAGGCAAAGCAACTGCAGCAGAAAGAGGAGAGGCCTGAAAACCTTGGGCA
CTGACACAAAAATTGCTTATTTCAATTGAAAATGTCTGTTTATAACTTCCC
ACTATACAGCACAAACAGGAGGGGGCTTAAACATAATGGGGAAAATGTCA
CAATTCTGCAATTTTTGTTTCCTTAAAAAAACACACACACAGAATTTTA
ATAATGTGTTCTCATCTTAATCCCGGGTGTGGGAATTAGGGCTGCTTTGG
ACCATTCCCAGCAGCTGACTATGATTTGCCTCATGCTCTAGCAGAAGTAT
GATTTTTGCCACCTGCAGATAGTTTCTGGGATTGTGTGACATTTGGAATT
TTGGGAACTTTTCTGAAGGTATATAAATGCTAAGGCCCTGGTGGGGAGGG
TTGGTGGTTGGTGGTCATTCAAGGGGGTGGTTGTGGTTAGTGGTCTTGCT
CAAAGAACAACAAGAAAGTCATTTGATTCAGATGTATCTTCTTCCTTC
CCCCACTCTTCTCTCCTCCCCCGGCACCCTGCCCCCTGCCCCGACCTC
TACCCTTCTTTTTCTATCTAGTGACAAGGATGAAACCAGGGGGATAAAGG
GTGGGAAAAAGAAGAGCCACAAAGTAACTCAGGTTGGCTACAAGTTCAT
GCCAAGAATCCTAGGACCTTGTTGTTTAAAGGCTTGTTTTATTTTGTGAA

FIG.3D(81)

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CATGAATGTTAAATGTACATACATGTTAAGTGTATGTATGTACACCATAT
GCATGCATACAGAATCCAGAAGAAAGTACATTATACCCTGGAATGGAAC
TAGAGTTGTGAGACAGCATGAGGATGCTGGGAACTGAACCCAGTTTCTCC
ACAAGAGGAGTAGTTGCTCTTCACTGCTTAACCTTTCTCCAGCCCCAAT
CCTAGCATTTTGGAGGCTGATGTAGGAAGATTATCCCAAGTGTGAGGTCA
TCTTGGGCTCCATAATAAGTTTAAGACCAATCTCAGCTCCAGAGTAGGAC
CCTGCCTCAAAAACACACAGGTGGAAAGATGGGTCGGCAATGAAGAGCAC
ACACTGTGCCTCCAGGGGACCCAAGCTTGGGTCCAAGCACCTTGTTGGG
CAGCTCACAACCTGCCTGTAACCTCCACCTCCAGAGGATCCTAAGCCACCTT
CTGGCTTGGCTTCATGGAGGGAACAGGTATGTGGGTATCTGAGTGTGACG
AATGAGCAGCAAGTGAGTCTCGCTGTGGCTAGCACAAAGTATGGGCTGAA
GAGCAGGAGGACAGCTGAAAAGTGGCCTTTCTGGTGACTAAGTTGGTCT
GAGCAGCTGAGTCAGTTTCTTCTGCTGGCTTGGCTGGTCTCAGTGCTTA
TAAGCTGCTCACTTGTAAGTCTTTTCTAGGAGCCCAGCTTGTCTAGGGG
TTGTCTTTGCAACTGGCCTTGCTCTGACAGTGACTTTCAGCAGTCTTAGCT
GCTTATATACACAGTCTTAGGAAAGAAGGCTGGTGAATCTGATCCATTTC
AGGAACTTTCTGAAGCTATTCTGAATTTACTTTACAAGCTTACCTGCAGG
ATAGAGGATCTCAGCTCTTTATAAACATCCTGTCCCTAAAACACCCTGTTG
TTCTCTTCTCTTTTACATCCTGTGTCTTGAGAAGTTTGCCTCCAGGATG
GAAGTTGTTCAATTCAGAGGACACTGTTGCACAAGCTCCCAGCACCCACA
TGTGAGCTCAGTGCTCTCCTTGGCTCTAGCTCTGCCCTATGAGGTTTTTT

FIG.3D(82)

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ATTTTGTATCATAATCTTTTCCTATATCCTTCCTTGTCTGGGAACTCA
TCTGGTTCATTTTTTTGGCATTTCGAGAAAAGCTCTCACTATACAAATCA
GGCTGCCTCCAAATCATCTTTTTGCCTTAACCTCCTCAGTACCAAGATCA
CGAGTGGATCTTAACACTTGACTGACTCGTTTAAGTGTGAGGAAATGTGG
ACCAATAAGAGAGCCCAGGAAAGCCCAGGAGAATCTGTAGCCCCATGGCT
GTTGTGTCAGAACCCAGAGTTTTGTCAACAGAATTTGGTTCCTAATTTCT
CCACTTTATAAAAACGAGTGAGAGAAACAGGAACCTATTCAGATCTGGCG
TCTGAGCAATCAGTGGGTGAACATCTAGAGATCTGTTCTGCATCTCCTCG
CCAGCTGGCAGAGCATGCGTAAGGCGGGAGGGAACAAGGGCAATCACTCA
CTCTGGGGCTCAGGCTTGCCCCTTGGGTCAGGTGTTTCTGAGAGACGTGA
TGTCTGCTTCTCTTGTTACCATCCCTCATCCTCTCCCCTCCTTCTGTCCC
CTACTTACCAATTTCACTGGCCAGTGTCCATATTTCTGCAAAAGCGATT
TGGTTTAATGAGCTTGACTATGCCCCGACTCCTTTAGGGAGGGTGGGGAAA
GGGCAACGAGGGCAGTAAGTGGTTTCCACAACCACTTTGCACCCGGCTGC
TGGGCCCCAAGCCAGAGGAACGTGCATGAGCCATGAAGTTTCCACTGATA
AATCCACAGATGCTTCTAGCACCTGCCTTTCTGACTCAGCCTCACCGTGC
CGCCTGCCAGCTGTGAAATCAGTGCCAACAACAGGTAACCGAGACCCAGG
CGCAGGGCCAGGACAGCTGTCTGACACTTCCAGACAGGATGTGGAGGCTG
ACAGTTGTGATGGAGAGGAGATGGGGAGGACAGAGACGGGCTCAGCTTTA
AGACACCGAGCCACAGAGCACCAAAACAAAAGCCAGGGCCTTCTGAGGTAG
AAGTAACAGAAACCAACAGGCAATTCTACTAGTTTCCTGGGACTGTTTG

FIG.3D(83)

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CTGCATTTGCCAATCTTGGTAGTTTTAAAAACAAAAACAGTTTGTTCCTC
AGCACTGGCAGAGCTTTCCTCCTCTGGAGGCTCCAGGGGTCCAGACTCTC
CTCTGTGGTACACTGGCTTCAGACATATCTCTTGCCTATGGCTGCCTCAC
TCTAAACTCTGCCTGTCCTTGAATTACCTCTCTCTGCACTGGCTTTATAA
AGGAAACATGAGATTGTGTTTAGGGCCTGTTTGGGTGACCTCCTCAGGAT
CTATAACATAATCACATCTCTACCGTATGAAGTGACGTTCCGTCCCAGT
GTGTAATACATTTGCCGGCGCCTGTCCTTAGGACAGTGACCACCACCAAC
TGTGGAACCTTGACTATGTCCACGTCATCTTCTACTAGCTTTAGAAGGCT
TATACCCACACTTTCTATCCAGAATTGTATTTTATTTAGAATCATTCCT
ACTTTTAAAAAAGTCTCTGTGGTTAAAAGCATTGCAGAGGGCTTGGGTTT
TGGTCCCCAGGACCCACATCAAGTGGCTCACAGTGTCTTGGAACTCTTGT
TCCAATACCCTCTTCTGGTCTCCATAGGCACTACATACATATGGCACATA
TATGTATACTCAGGCACACGTGTAAATTTTAATGTCTACTTTTTATGCTA
AATATCAAAGTCACTCGAGCAGTGGAGTTGAGCACACTCACATAAGGAAA
TCATCAGACAGACACTTCATCCTGTGTTGGAGCCACTTTGTGGCTGGAGT
AAGCAGGGCAGAGTGATGTTTTCTTACTCTCTGGCCCCAGCACCCCCTG
CCTCTCCCCACCCATTTCGTCCATGCAGGTGGGAAGAGAATTCTCTTTGT
GAAATTGGAAGTTTGGACCCAGCTTCACTCTTACTCTGCCCAGTACCTCC
TGTGAGAAACCCTCCTATCCCAGGTGACCTGCTGGCTGTGACTCTCTCA
GCAAAAGGCCCGTGACCCACACTGCGCCACTAATGTATCATCCCAAATG
CTGAAAAGGAAGCGTGTCTTCTCTCTCTCTTTTTCTTTTGGTCTTTT

FIG.3D(84)

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TGAGACAGAGTTTCTCTGTATAGCCCTGGCTGTCTGGAAC TCACTTTGT
AGACCAGGCTGGCCTCGAACTCAGAACTCCGCCTGCCTCTGCCTCCGAG
TGCTGGGATTAAAGGCGTGCATCACCCTGCCCCGGCTGCGTGTCTTTCTC
TTAGCGGTCTCTGTGGAGATGCTGAGTATGAAGCTCATCCTACCCACCCT
TCAGTGGGGCCTTTTCTAGCTACTGAGCAGCTGTGTGAGGACTCGTGATC
ACAAGGTCCTTTGAACCCTTGAGACAGATGTGCCTGAGCCCAGTTTGACC
TGACAAAAGCCTAGAGCTCACTGATAATGCCAGCAAACACCATCTTTGAG
TTTGCAAAGGAATCGCAACACATGCATTTCAGTTTCCGTTGCTGGCTGCTG
CTCCAGAGATGGCTATATTTCATTCTCAGGTACTCAGACTCAAGAGTAGTT
CTGGCCACACAGGTCTCCACATTTTCGAGGTCAAATGACAGAAAACCAGGT
TGGTCTCAGTGACATGGGTTTATTGAGCCACTGCAGGTGCTGGGGAAAC
CATGGCAGGGAGATCCTGGGAAGCCAGTGGGGTGCTGAGCAGGAGGGACC
TCAGTCTCTCCTTAATGTCTACACACTGTGTTCATAGGTGACAAGCCACGT
CAGTGCTGTGACACGGGTAAGCTTAATGGTGAGTAATGGCTAACTGGGAG
GGTATTTAGGCAGCCTTGCTGTGTCAGCCTGTTTCATATGATCTCCTTAGTG
CCTTGTCATCTTGAAAAGGACAGTTCCAAATTCTAGGAGCGGGGGCTAG
TCTCTGTCCTGCTCTGTAAGCCCAGGGGACCCAATGAGGCCTCATCTATG
GGTGCTCAGCTCTAGGATGGGGAAGAAAATGGACAAGATGCCTACTGACG
GGAACACAGGCTTTTTCAGTCAGACCCTAGCCTCCAGCCCCCAATCCAGAG
GACAGCCACACAGGGGTCCAGGCCTGCAAAGGGCAGCAGACCTGAGGGCA
AGGGAGTTTCAGCTCAGTGAGCAGTCATCGGGAGACATGGCAGTCAGCTG

FIG.3D(85)

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TGTCGTCCACGGTTCATGTTCTAATCAGAGCAGGGCCTGGAGAGCCAGG
GCAGTGAGTGCATACAGCCAGGACACCTTGGGCGTTAGGACAAAACAAGG
ACTGTTTCTGCCTCCAGCTCTTCTCAGGCCACTCGTGCCTTGCCTAGGAA
GGGTAAGAGAGCACAGATGGGAAGGATTGGGAACTGTCAACTCCCTGTC
CTCTCCCCATACCTACCCGCGGGAAACAGCACCCAGCAGTCTGGTCCTGC
AGAACTGATGGCTGCAAGCTGTCAAAGGCTTGTATGGCACCATCTGCGGA
GTGCAGAGATCCAGAGAAGGCTTGGCCAGGAAACCCTAGAAACTACCCCA
CTCCCTTGGGACAAAAAATAAGACACCCTGGAACCTGCAAGGCATGGCCT
GAGATGGAAGGTCCTGTGCTAAGAATGACCCACAACTGCTAGTGAGGT
TGACAAGGGCTGCCCCCTCTCCCTTTACAGGTGAACACAATGGGGATTAA
TAAGAGTTTAACTCTCAGCTACTAAGTGGCAGAGACAGGCTTCAAACAGA
CCCCCAGAAATCTGGAACCTGAGCCATTCCACCCAGAGGCAAGAACAGCAG
AGGTAAGTTGGGCACACATGGAAGAAAGGGCCACCCCATTAGTGTCAAAA
GGGAGGCCAACTTCAGGCCATTGGACACGTTTTAAGGCTGACTTCCACCC
ATGTACCATGGCATGTGCACACTGTCCATCGCCACACCAAACATGATGC
GACGTAAATAAGACCCACGGGCCAGGCAGCTTGGATTGGGCCACAGACAT

FIG.3D(86)

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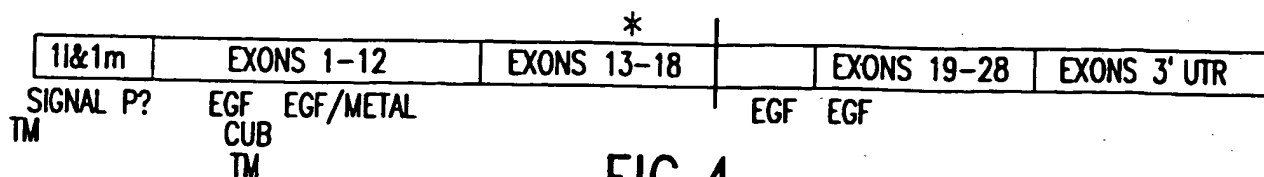


FIG.4

Exon 1	CelegE106	TCTCCTAGTTGTAGTACATGCTGTTG
	CelegE108	AGGTCCTGTCTCAAGAAATAGCAATAAC
Exon2	CelegE33	TTTGAAGGCCCTGAAGTCAGAG
	CelegE36	TTGAGTCCCATCATAAACATATAAATGG
	CelegE37	TTCTAGGCCAAATAGAATAATGAGACTTC
	CelegE40	AGAACTAATTCCATGAGATGAGTGTG
Exon 3	CelegE41	TGAAGTTGCTGTAATCTGGTCTGTG
	CelegE44	AAGGAGCCTGACTAGAAGCCTC
Exon4	CelegE69	TAAACTCCCTACAGTTCACTAACTCAG
	CelegE72	AGCGCTGTTGAGTGTGAATGTTCTG
	CelegE73	AAAGCCACAGTTGTCTGTACAGTGAG
	CelegE76	AGGTCTGCATTAGTTGCAATGTTGC
Exon5	CelegE77	TATACACCCCTTATATACACTCAG
	CelegE80	AGAGCCTCTCATAAAGCTGTGGTC
	CelegE81	TTGAACATATATCCGCCAACAACCC
	CelegE84	CTTGAATACTATAAACTTTTACGGCTGC
Exon6	CelegE101	TAAAGCAACAGGAAGAGTTGAACTTCTTG
	CelegE104	TGCACCCTGTGTGCACATGG
Exon7	CelegE109	TTACGGTGTCTTAATAATAAGGGCAG
	CelegE111	AATCATGGGTATTGTTAACTCCGAAAGC
	CelegE114	TGTAACAATGTGTGCCGAGTGTC
Exon8	CelegE116	TCTCTCTCCAGCCCTAGAGTTG
	CelegE86	AGAAGAGGAGCCTGCAACATTGAC
	CelegE88	TTTGTTGGCGCTGAAAGCCTTG
	CelegE89	TGGCCACAGTAGTGTTTATGATGAC
	CelegE91	TTAATCAATTGCCTCTGCAGATTCTAG

FIG.5(1)

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Exon9	CelegE93	TGGCTTACGTATAGGGGAAATCAAG
	CelegE95	TTGTGTGTGTTCCCTCCAAACACC
	CelegE98	GGACCATTCTTAAGGACAGCCGAT
	CelegE100	ACATAGTGATCTTTCCATCAGCAAAG
Exon10	CelegE117	TGAATGCACAGAGACCCTCCTG
	CelegE120	CCTCTTACCATTGAGATACTGTTAGG
Exon11	CelegE121	AGCAACAACCTCAAACCAGCCCTAC
	CelegE124	TTCTTCAGTTGCCAACTCCCAGG
	CelegE125	AAGCTGCTTGTGTGGCAGCAG
	CelegE128	AGTAAGGTGAACAGGAAAGTACAGAG
Exon12	CelegE130	TACATAAGAGAGGCTGCCGCATAG
	CelegE132	CCCTACACTCACACTCATCTAGC
<hr/>		
Exon13	CelegE30	CCCTGTGTTCCAGATCTCCATTG
	CelegE32	TTCTAGGTCCACCTTGATCTGAG
Exon14	CelegE14	AGCACCTGAATTCAAATCAGGATGAG
	CelegE15	AAACCAAAGTTCTGAACACATTAACAC
Exon15	CelegE17	CTGGTTGCATTCATAGCTGTGTTTC
	CelegE20	ACAGAAGCCAGCATCACTGGG
	CelegE21	TTACTGGTGCTGGGAGGATATGTC
	CelegE24	ATAAGTACTTCATCACCTCAGCGCTC
Exon16	CelegE1	TTGATCTTAGCTGACCAGTGCTTC
	CelegE4	TCTGCATGGACTTGAGCAGAAAGTC
Exon17	CelegE6	CAAATCTTGTGATAGTGAATTACAAGTTGG
	CelegE8	TTTATAGCTGCCCTCAATACATTTTCC
	CelegE9	TGTACCTGCAGCCATTGCTTGG
	CelegE12	GGATCTGGGCTCTAGTTTATGTAGG

FIG.5(2)

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Exon18	CelegE25 CelegE27	TTGAACTATAGGCACAGACAGCTG AACTTGACCTGTGTGACTTACGC
Exon19	CelegE193 CelegE194	TCACAGTCTATGGTAATCTGTCAAGC AAGGGCAACAATGCCCTGGCAA
Exon20	CelegE195 CelegE196	TTCCTGCAAATGGGATAGTCTCTCTG ATCCCCCAAGCATTTATCATTCTCAG
Exon21	CelegE197 CelegE198	TGTGTTTCCAGAAACCTGCTTTAGTTTG TAGTACTTTTGTCCAGGATGACCAAG
Exon22	CelegE199 CelegE200	TGACAAGAAATGTCATGTCTTAACATAAGC TTCAGAGCCTCCTTCCCCAACT
Exon23		
Exon24	CelegE203 CelegE204	TAGTCTGTAGCTGAGGCCATTTTGC AAGCAAGCTGCAGTTAAGGGACTGT
Exon25	CelegE205 CelegE206	TTGGGACCTTGAGGATTGTTCCC CACTCAACAGGTAAAAGTGATCTGCC
Exon26	CelegE207 CelegE208	TGCATCTGATCAGTTTGAATCAGAGAG AAACTGAGGCCTGAGTTCTGAAAAGC
Exon27	CelegE181 CelegE182	CACCAAAGCTCTGTACCACTAAGC TGACTGTGCAGTGATGCAGGG
Exon28 OUTR?	CelegE171 CelegE172	TTGACCTTGACATTTAGAATAGCCCTC GCTGAGAATTAATAATGGTCTTTCTCTTTG
	CelegE173 CelegE174	TACACAGTGAGACCCTGTCTCC TAGCTGAGGTCCCTTGTGGAAG
	CelegE175 C.elegE176	AGTGTGAGAGGACCATGCTGG CTTGAAGCGTCCAACATCATGTGC

FIG.5(3)

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CelegE161	AACTCATACATTTGAGCACTGTTGCC
CelegE162	TGAGGAGGTGGGGAATGCTAATG
CelegE163	ACATAGCAGAGGGCTGCTCAC
CelegE164	ACTGACCTGTGGGAACCTGTG
CelegE165	AATGCTAGGCATCATCCCTCTTCTAG
CelegE166	AACATCTAATAGGGAAGTGAAGTACCC
CelegE167	TTCTGTGGTGCCTTGGCAAGAG
CelegE168	CACACATACACACACTAAGTGCC
CelegE169	TGGTAGTTACTTAAAGTTTACAAGAATGTAGG
CelegE170	AAATGCTGGGATAAAAAGCATGAACCAC
C.elegE145	TTCAGTTACCTAATGGGCACAAGGC
CelegE148	ACGACACTGACCTCTTGCACTTG
CelegE150	TGTACACCCTGAATGTCTGAACATTG
CelegE152	GCGTTCATTTCTGCTCCTGTAATGG
CelegE153	TGAGCTCTTAATCCCTGCCATTCC
CelegE154	TAGGGCTTGTCCTGTCCTAAGG
CelegE157	TGTTACGGAGATGAAAGGCTAGACC
CelegE158	TAAGCCCTGCACTAACCCTC
CelegE159	TGTTTTGAGAGGTGAGCCTTCTAGC
CelegE160	CATGTCCTACAGTTCTGCTATCACC
CelegE141	CTTTTCTTCATCCAATTCCCCACGAG
CelegE144	TCTCTAAGCTGCACTGTTGTGGCT
C.elegE129	TGGAAGCCAAGAGTCTTGAGTTGC
CelegE132	GTCTGCATTTTAAATGCAGATGTGAAGC
CelegE134	CGAAACGCACGCACATTTTTTACCAG
CelegE136	GTGTGATTTAGCATCTGTGCACTTG
CelegE137	TGTATGTATAACCCAACAATCGCTGC
CelegE140	TCCAGAGTACAGGGAGAACTAAAGG

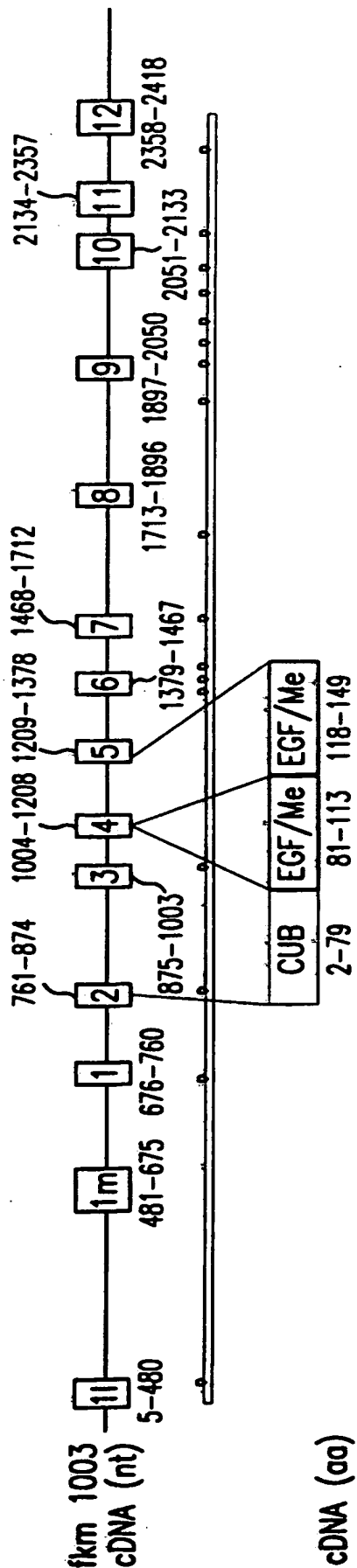
FIG.5(4)

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AGCGCTATTCAGCTGTGCCTCCTTTGCTGTCTTGGCTCCTCCTGGAGCACTAT
ATGCACCCATGTCCTTACCAGGCCTTTCACAGACGCTGCCATTGAGAGGGT
TGATGCAGGTTGCAGCCTTTAATCCCCGAGTACTAGGCTCTGACAAGATCCCA
CAGAAGCCAGCATCACTGGGCTCAGATGGCATCCACTGCAGCAAAC TATTTG
TGAATGGAGACATATCC

FIG.6

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386-402

TM

22-38

TM

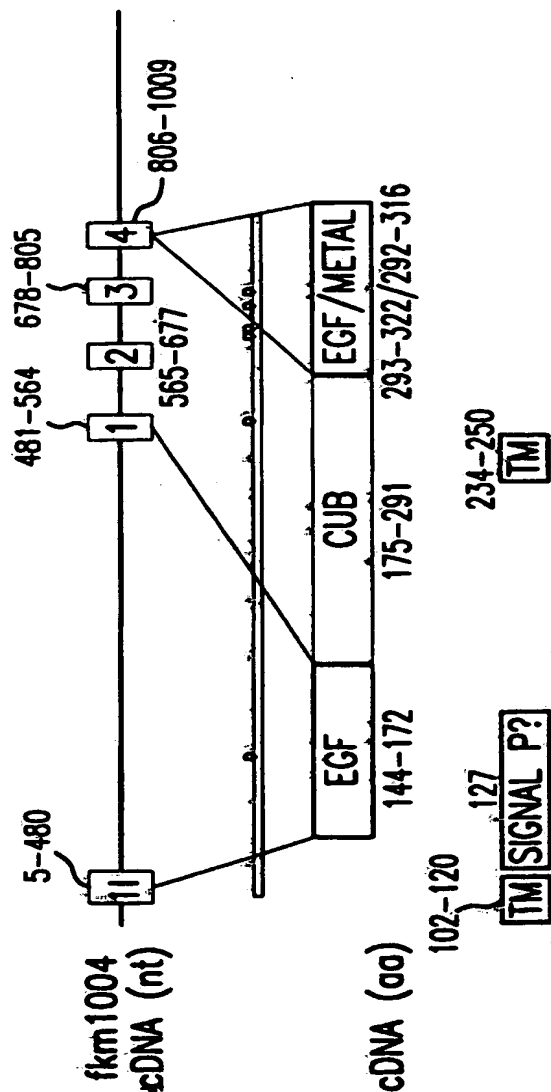


FIG. 7

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GAATTCGGGCGAAGGGAGCCGGCGTGCAGGGGTGTGTATGTGTTGGCTGGGCGCCGGCTCAGCCCCAGGAAGATGGTG
GCGGTGGCGGGCGGCGGCGGCGACTGAGGCGCGGCTGAGGGGGAGCACGAGGACGACAGCAGCGCCTGCGGGCAGGAAGG
GCAGGCAGCACCGACCCCTGCACCGCGACAGGGGCCCTGGAGGCCGGGACCGCGCGCCGGCTGTGTCTCCCGGGGTGCT
GTGCGGGGCGCTGCCCCCGCGCGGCTGCTGCCGCTGCTCTTTTCGCTGCTGCTGCCGCTGCCCGGGAGGCCGAG
GCCGCTGCGGTGGCGGGCGGCGGTGTCCGGCTCGGCCGCGAGCCGAGGCCAAGGAA GTGACCGGCCGTGTGTCAACGGCG
GCCGCTGCAACCCCTGGCACCGGCCAGTGGCTGTGCCCCACGGGCTGGGTGGGCGAGCAA TGCCAGCACTGCCGGGGGCGG
CTTCAGGACATCTGTCTCAGCCCTATAATCACAGCTGTTTCGGAAGGTGAGGCTGGAGGAACAGTTCGAGGCAAGCTTCG
GCTACAGAA TAAGTTCAAGAGTAACCTGGGGCACTTGGGCTTGCTCTCCAAAACCAAAATGAGCGAAAGGAGCAAGCT
AGAGTCTTTTGGGAAAATTTTAGCTGACTAA TTTTTCACCGAGAACTAACTGGCTCTTCTGGATTTGTACAGATGGAC
CTGGGAATTATAAATAAAGACGAAGTGCACATGGCTCATTGAAGGACAGCCAAATAGAAATAATGAGACTTCGCTTCAA
CCATTTTGCTACAGAA GTAGCTGGGACCATTATAATGTTTATGATGGGGACTCAATCTACGCACCTCTGATTGCTGCC
TTTAGTGGCCTCATTGTTCTGAAAGAGATGGCAATGAGACGGCTCCTGAGGTCACTGTCACTTCAGGTTATGCACTGC
TGCATTTTTTTCAGTGATGCTGCTTATAATCTGACTGGATTATAATATCACTTACAATTTTGACATGTGTCCGGAATAATTG

FIG.8A

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CTCAGGCCGAGGAGGTGAAGAGCAGTAACAGCAGCAGCGCTGTTGAGTGTGAATGTTCTGAAACTGGAAAGGGGAG
TCGTGTGACATTCCCTCACTGTACAGACAACGTGGCTTTCCCTCACCGAGGCATCTGTATGCAAGCGATACCAGAGGGT
GCTCCTGCTTTCCCTCACTGGCAGGGTCCCTGGATGTTCAATTCCCTGTGCCAGCTAACCCAGTCTTTTGGACTCGAGAAGA
ATAATTCGATTTAAAGCTTCCCAGAGCCTCTCATAAAGCTGTGGTCAATGGAAATATAATGTGGGTGTTGGCGGATAT
ATGTTCAACCAATTCAGATTACAGCATGGTTTTAGCGTATGACCTGACTTCTAGGGAAAGGCTTCCACTAAACCAATTCG
TGAACAGTGTGGTTGAAGATATGGTCATTCTTTGGCATTACATAAGGATAAAATCTACATGTATGGAGGAAAAATTGA
TTCAACAGGGAACGTGACCAATGAGCTGAGAGTATTTCATATTCAATGAATCATGGGTATTGTTAACTCCGAAAGCT
AAGGATCAGTATGCAGTGGTTGGACACTCAGCACACATTGTTACACTGGCATCTGGCCGTGTGGTCATGTTGGTCATCT
TCGGTCATTGCCCACTCTATGGATATATAAGCGTTGTGCAGGAATATGACTTGGAAAAGAACACATGGAGTATATTACA
TACTCAGGGTGCTCTTGTGCAAGGGGGTTATGGCCACAGTAGTGTTTATGATGACAGGACCAAGGCTCTGTACGTTTCAT
GGTGGCTACAAGGCTTTCAGCGCCAACAATAACCGGCTTGAGATGACCTCTACAGATACGATGTGGATCTCAGATGT
GGACCAATTCCTTAAGGACAGCCGATTTTCCGTTACTTGCATACAGCTGTGATAGTGAGTGGAAACCATGCTGGTGTGG
AGGGAACACACACAATGACACTTCCATGAGCCAGGTGCCAAATGCTTCTCCTCGGACTTCATGGCTTATGACATTGCT

FIG. 8B

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TGTGACCGATGGTCAGTGCTTCCCAGACCTGAGCTCCATCATGTGTCAACAGATTTGGCCATTTCAGCAGTCTTGTACA
ACAGCACCATGTATGTGTTCCGGCGGCTTCAACAGCCTCCTCCTCAGTGACGTCTTGGTCTTTACCTCGGAGCAGTGCGA
TGCACACCGCAGTGAAGCTGCTTGTGTGGCAGCAGGACCTGGTATCCGGTGTCTGTGGGACACACAGTGTCTCGATGT
ACCTCCTGGGAGTTGGCAACTGAAGAACAAGCAGAAAGTTAAATCAGAGTGTCTTCTAAAGAACCCCTTGACCATG
ACAGATGTGACCGACACACAGATTGTTACAGCTGCACAGCCAAATACCAA

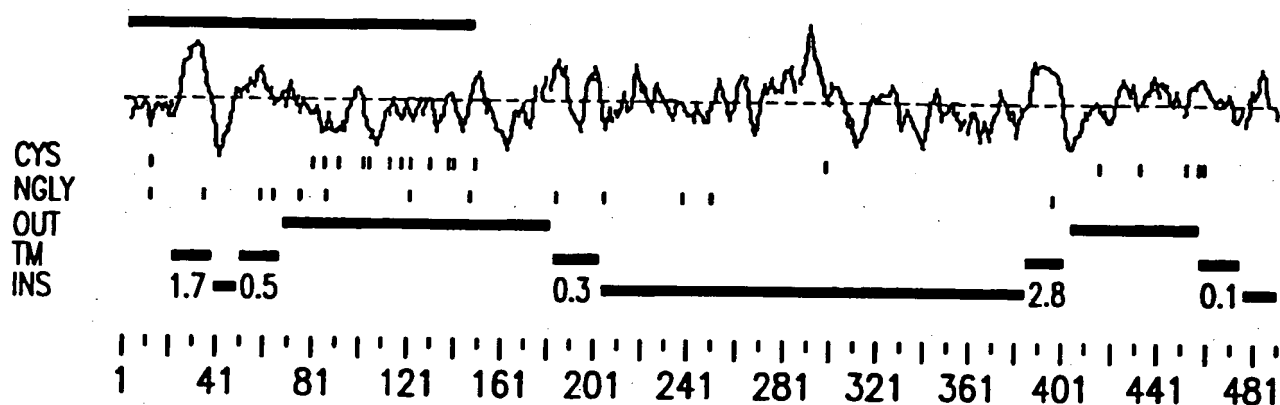
FIG.8C

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MRLRFNHFATECSWDHLYVYDGD SIYAPLIAAFSGLIVPERDGNETAPEVTVTSGYALLHFFSDAAYNL TGFNITYNFD
MCPNNGSGRGECKSSNSSSAVECECSENWKGESCDIPHCTDNCGFPHRGICNASDTRGCSCFPHWQGPCCIPVPANQS
FWTREEYSOLKLPRASHKAVVNGNIMWVGGYMFNHSYSMWLAYDLTSREWLP LNHSVNSVWVRYGHSALHKKDIYM
YGGKIDSTGNVTNELRVFIHNESWLLTPKAKDQYAVVGHSAHIVTLASGRVWMLVIFGHCPLYGYISVWQEYDLEKN
TWSILHTQGALVQGGYGHSSVYDDRTKALYVHGGYKAFSANKYRLADDLYRYVDVDTQMWTILKDSRFFRYLHTAVIVSG
TMLVFGGNTHNDTSMHGAKECFSSDFMAYDIACDRWSVLPPELHHDVNRFGHSAVLYNSTMYVFGGFNSLLLSDVLVF
TSEQCDHRSEAAACVAAGPGIRCLWDTQSSRCTSWELATEEQAEKLEKSECFSKRTLHDHRCDDQHTDCYSC TANTX

FIG. 8D

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TRANSMEMBRANE SEGMENTS PREDICTED BY MEMSAT

START	END	ORIENT	SCORE
22	38	OUT-->INS	1.7
50	67	INS-->OUT	0.5
183	203	OUT-->INS	0.3
386	402	INS-->OUT	2.8
458	474	OUT-->INS	0.1

SIGNAL PEPTIDE PREDICTIONS

METHOD	PREDICT	SCORE	Mat@
SignalP (eukaryote)	NO		

FIG.8E

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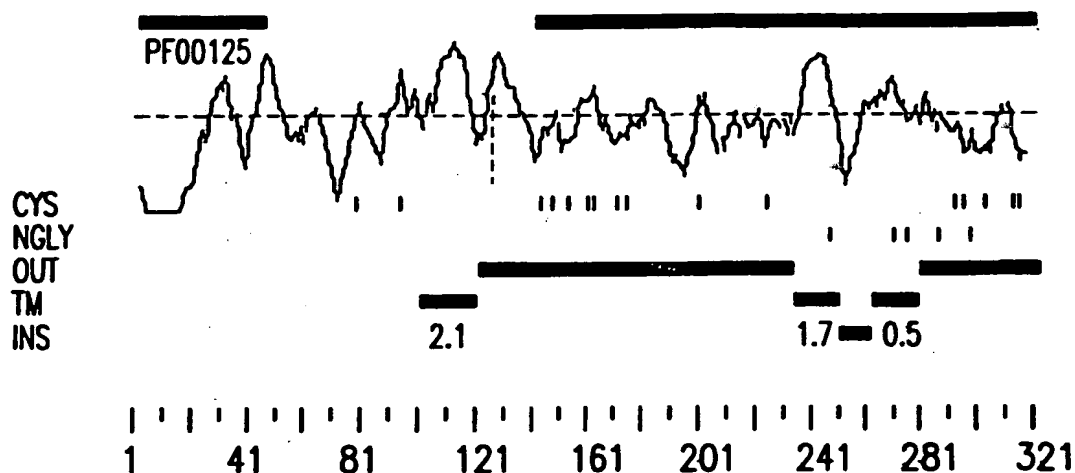
GAATTCGGAAAAA
AAAAA
CGTGGGGGTGTATGTGTTGGGCGCCGGCTCAGCCCCAGGAAGATGGTGGCGGTGGCGGGCGGGCGGCGACT
GAGGCGGGCTGAGGGGAGCACGACGACAGCGCCTGCGGGCAGGAAGGCAGGCACCGACCCCTGCACCG
CGACAGGGGCTGGAGGCGGGACCGCGCGCCGGCTGTGTCTCCCGGGGTGCTGTCGGGGCGCTGCCCGCGCGCC
GCTGCTGCCGCTGCTCTTTTCGCTGCTGCTGCCGCTGCCCGGGAGGCCGAGGCCGCTGCGGTGGCGGGCGGGTG
TCCGGCTCGGCGCAGCCGAGGCCAAGGAATGTGACCGGCCGTGTGTCAACGGCGGCCGCTGCAACCCCTGGCACCGGCC
AGTGGCTGCCCCACGGGCTGGGTGGCGAGCAATGCCAGCACTGCGGGGGCCGCTTCAGACTAACTGGCTCTTCTGG
ATTTGTACAGATGGACCTGGGAATTATAATATAAGACGAAGTGCACATGGCTCATTGAAGGACAGCCAAATAGAATA
ATGAGACTTCGCTTCAACCAATTTGCTACAGAATGTAGCTGGGACCAATTTATATGTTTATGATGGGACTCAATCTACG
CACCTCTGATTGCTGCCTTTAGTGGCTCATTTGTTCTGAAAGAGATGGCAATGAGACGGCTCCTGAGGTCACTGTCAC
TTCAGGTTATGCACTGCTGCATTTTTCAGTGATGCTGCTTATAATCTGACTGGATTTAATATCACTTACAATTTTGAC
ATGTGTCCGAATAATTGCTCAGGCCGAGGAGAGTGTAAAGACAGTAACAGCAGCAGCGCTGTTGAGTGTGAATGTTCTG
AAACTGGAAAGGGGCGGGAATTC

FIG.9A

[illegible]

FIG. 9B

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SIGNAL PEPTIDE PREDICTIONS

METHOD	PREDICT	SCORE	Mat@
SignalP (eukaryote)	MAYBE		127

TRANSMEMBRANE SEGMENTS PREDICTED BY MEMSAT

START	END	ORIENT	SCORE
102	120	INS-->OUT	2.1
234	250	OUT-->INS	1.7
262	279	INS-->OUT	0.5

FIG.9C

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ATGTACTACTGTAAAGAAGACCAGCTGCAGGAGCTGTGCCCTGGACCAGAACTGCCAGTGGGAGCCCCGGAATCAGG
AGTGCAATTGCCCTGCCCGAAAAATATCTGTGGCAATTGGCTGGCAATTTGGTTGGAACTCATGTTTGAAAAATTACTACTGC
CAAGGAGAAATTATGACAATGCTAAATTGTTCTGTAGGAACCAACAATGCCCTTTTGGCTTCTCTTACAACCCAGAAGAAG
GTAGAAATTTGTCTTAAGCAGCTGCCGAATAATGCAGTCATCTCAGAGCATGTCCAAGCTCACCTTAAACCCCATGGGTGC
GGCCTTCGGGAAGGTCAATGTGTCTACTKGGTGTGGGGAAGGATATGKTCCCATTTTACAAATAGTTTTACTACA
GTGGGATGCCCGTCTTGAGGCCCCAGTGTGCTTGGRAATCTGTGGGAATTTT:ATTACAGGAACCCAGTTACTTCGGGGA
CTGAAGGCTGCAACCTGCATTCAACCCACTYMAATGGTAGTGCTGTGAAAGGCTGCAAAACACAGTGTCTAAGGCAGT
GCCGGACACCATGTGCCTTGAGGACAGCATGTGGAGATTGCACCAGCGGAGCTCTGAGTG:CATGTGGTGCAGCAACA
TGAAG:CAGTGTGGGACTCCAATGCCTATGTGGCCTCCTTCCCTTTTGG:CCAGTGTATGGAATGGTATACGATGAGC
ACCTGCCCCCCCTGAAAAATTGTTACGGCTACTGTACCTGTAGTCAATTGCTTGAGCAACCAAGGCTGTGGCTGGTGTACTG
ATCCCAGCAATACTGGCAAGGGGAAATGCATAGAGGGTTCTATAAAGGACCAGTGAAGATGCCCTTCGCAAGCCCCCTAC
AGGAAATTTCTATCCACAGCCCCCTGCTCAATTCAGCATGTGTCTAGAGGACAGCAGATACAACCTGGTCTTTTCATTAC
TGTCCAGCTTGCCCAATGCAACGGCCACAGTAAATGCATCAATCAGAGCATCTGTGAGAAGTGTGAGAACCCTGACCCACAG

FIG.10A(1)

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GCAAGCACTGCGAGACCTGCATATCTGGCTTCTACGGTGATCCCAACCAATGGAGGAAATGTCAGCCATGCAAGTGCAA
TGGGCACGGCTCTCTGTGCAACACCAACACGGGCAAGTGCTTCTGCACCACCAAGGGCGTCAAGGGGGACGAGTGCCAG
CTATGTGAGGTAGAAAATCGATACCAAGGAAACCCCTCTCAGAGGAACATGTTATTACTCTTCTTATTGACTATCAGT
TCACCTTTAGTCTATCCCAGGAAGATGATCGCTATTACACAGCTATCAATTTTGTGGCTACTCTGACGAACAAACAG
GGATTGGACATGTTTCATCAATGCCCTCCAAGAAATTTCAACCTCAACATCACCTGGGCTGCCAGTTTCTCAGCTGGAACC
CAGGCTGGAGAAGAGATGCCGTGTGTTTCAAAAACCAACATTAAAGGAGTACAAAGATAGTTTCTCTAATGAGAAGTTTG
ATTTTCGCAACCAACCAATATCACTTTCTTGTGTTATGTAGTAATTTACCTGGCCCATCAAAATTCAGATTGCCTT
CTCTCAGCACAGCAATTTTATGGACCTGGTACAGTCTCTCGTGACTTCTTCAGTTGTTCCTCTCTCTTGTCTCCTGGTG
GCTGCTGTGGTTTGGAGATCAACAAAGTTGTGGGCTCCAGACGTAGAGAGCAACTTCTTCGAGAGATGCAACAGA
TGGCCAGCCGTCCTTGGCTCTGTAAATGTGGCTTGGAAACAGATGAGGAGCCTCCTGATCTTATTGGGGGGAGTAT
AAAGACTGTTCCCAACCCATTGCACCTGGAGCCGTGTTTGGCAACAAGCCGCTGTCTCTCTGTGTTTGTGAGGCTC
CCTCGAGGCCCTGGGTGGCATCCCTCCTCGGACGTACGGTCTTGCTGTGGCCAGCGCCCTGGTGGACATTTCTCAGC
AGATGCCGATAGTGTACAAGGAGAAGTCAGGAGCCGTGAGAAACCGGAAGCAGCAGCCCCCTGCACAGCCTGGGACCTG

FIG. 10A(2)

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CATCTGATGCTGGGGCCAGGGACTCTCCACGCACGAGCTAGTGAGTGGCACACCAGAGCCATCTGCAGGGAAGGGCGT
GGCGGGAAATGGCTGTGCGGTGCGGGACGGAAGACTGGAACCCCTCAAAGCATCTGACTCACCTGCGATGATCACAAAGC
TTTTCTTGACGGTTTCTCCCATCCGTGTTCCAGCATCTAACCTTTTACTTTTTTGCATAGGAAATACTTTGATTTAATTACA
GGTCCAGGGATGAGCTGATGGTTGCTGGAGGAGGCCAGTGTAGAGCCAGTGAGAGAACTAGGAATGACACTCAGGTTCA
CTGTGGAAACTGTTCTTGGGACTGTCTCAACTGTGCAAAAAACAAAAGATGGAGTGTTTACAAGTAGACATTCGTCAT
CAGTTGTTCTTGAACATGGTCTTTTTAAAACTAGTCAGATGAATTAACCTTGTTTTCATCTGAAGCCTGCATCTTTTTT
AAAAGATGTCATTTTATTTCTTGACGATTTAGGCAATTATCTCTCTCCAGGAGTACCTTTTTTCTAGTTGAGAAT
TAATAATGGTCCATCTCTTTTGATCATATCAAGCTAGGATAGAGGGGGCTATTTTAAATGTCAAGGTACGAGTGTT
ACTTTGAATGTAACTGGTATAATAGGTAGTTTCTATAGTAACCTTGATTAAATTTAGTCTTAATCCATTTGAAACTCTC
TCTTCCTTTCTCTCTGCGCTGCGCTCTCCTCTCCATCTCACCCCTCCCTCTCTCACACATACACACAACACATACA
CACAACTAAGTGCCTAGACTTTAAATAGATCTAGCAATTGGAAAGTTAGTAAGCCTAAGTTTTACATAATTGCATT
CCTACATCTTGTAATAATTTAAATAGCTACCATTGGCAATCTGCTTTTTTCTTAAATCTGATTTGCAGCCAGGAAAGA
ATTTCTCACCCCAAGGAACATTTGATCTAGCAGAGGGATGAGAGGAAAGCAGAAATGAATGAAGTGTGAAAGCTCCTG

FIG. 10A(3)

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TTTTATTATCAAAAGGACACTGTCAAGAGGGGCCCTTGGCCCCACCCCGTGTACCCCTAGGCCTGATAAGCGAT
CAGAGGAAGGACTCATTATGTCACGCTTCCCTTGAGCAGAAAAGAGCACTGAGAGCACTTGGGACCCCTGGATCAGAG
AGCATCTGTGTCTGCAGCCTCCTCTGAACCTTGTTGGTTTCATTCTCAGGCTGGGGTGGACTCAGATGCCAGGAAAGGG
ACAGCCTCCCATTTGTCAGGCAGAGCTGCCAAAGCCTGGAGAAGGACTTGTTCGCCCTCTTCCCCAGGAGGGGCTC
GACCCACCCACCCCTCCCTCTCAGACCAGGTGGTGGCTGTGAGGAGGGCAGCAAAATGCTGACAAGGATGAAAAGCACAT
GGAAAAAATGGACGAGGAGGGGAAAACCTCTGCCAAATGGAAAATGACCAAAATTAAGAGGGTGGACAGTCCCCCTGCTC
CTCTCCAGAGGGCACTGCTTGGAATTTGTGTTTCCCCATTTATGGTGCTCTGTATTCTGGCAATTATGCAGCAGCCTC
CCAGAACTCTCTCTGCTTCAAAACCTGGGATCTCTGGCATTACCCCTATTGGGATGGACCGCTGGACAGCAATGCTCG
AGTTGTGAATTTGGAGAGATACTCAAAGAGCTAAACTGCAGCATTTTACCTTTAAATGCAGTGCCTAGAGAGAGAG
TATTGTCTCTTCCCCAACACTAACCCCACTCCCATGAAGAATTGCCTGGAAAGATGTTTTCAGGAAATTTGAACCATAA
AACACTATCTGATGCACAGAACCTCTACTTTGAGACTCACCTCTCATAAAGCTTCTTTTTCACATTACTGTTAAAGA
CCAGAGTTCTAGAAAAGACCCCTCCTCTCATGAGCTCCCCCATCCCTGCTACAGAACACAGCACCCCATGGCGCCTGCA
GTGGACTGGCCCCCTTAATTCCCAAGGCCCCCCCCAGCAAGGCCAAAGGGAGGCCCTGGGTATTGTCTCTCTACAAGGA

FIG. 10A(4)

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AGATCCTCTTTGTTTCAAGGACCAGTTTTCCTAGGCCAAAGAAGTCTCTTCCCCATGTTAGTCCTATGCCTTGAA
ATATCATGCACCATGACCCACAGCCATCTGGTTATGCTTATTTTTTCTTAAAGATAATGTTTATTTTTTAAAGGA
AGGAAGAAGCAAGTGAAGTTTCATTCTGCTCCAGCGGTGGGGAAGCCGCTGAATCCACCTGCTTCTCCTTTGCAACCGA
CAGCAAACAGCTTTCCTCGGCCCTCAGGGCAGAAAAGGGAATGGCAGGGAGTAAGAGGCGCTGGGCTCGGAGCCTGTTT
CCAAGAAGGAATTGGTTGTCATCTGGCAGTGTGGCGGTCAAGAAGAGAGCCTGTATATAAAATTAAATAGTCAAGACAA
CACTGACCTTGCACTTGTACATAACTATACAGTAGTGTCCAGAAATGTTCAAGACATTCGGAGGTACATAAAACAGAAAA
AATCTTCATGTTTTTATTAAATATAACAATGTCTGAGTTTCACCTAAGATGTTTTTGTGCCATATGCTGGATATCCA
GGTTCTGCCAGGCCCGATACATGAATAACAACCCCAAGAAACGCATCCCCATTGTGTGATGTGTTTCAGATGCATCTG
GCACCAATTAGGTATTTCTTAAACAGGACTCATCTGTCAAGTGCACATGAAAAATCAGGCAGGGAATCGAAACGACA
GCGCTGGAGGAGACTCAGGAAGCAGAGGCGTCCCTGCCGCTGCCCTTGGCCCTGCAAGCACATCATGACCCCTTTCTGGC
AGCCTCTGGTGCTCTGGGTAGTGAGGGATGACCAGTCTTGCTCCTGAGAAATGTTTCTCTTCTTAAAGTTCAAAGA
CTAACCTGTAGCAATCAGACTTTCCTCCAAAGGGGTTCTCCATTTTTTGTAGTTTTTGCTAAATTTTTTAATGACCATTTT
CTGGAATCAGTTTATTATCTGAAAACTGGGGGTGGGAGTAGGGAGCTAGTTTGTGATAAATAGTCCCATTTCCCGG

FIG. 10A(5)

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TGGAGAAATTTGACATACCCTGGACTCCTGTGTGCCCTCCCTGCCATCCCTGCACAGCCTGGGGAGAAGCCTGTGCCTCC
CCGTGTGGAGAGAAGGCAACCCAGATCCCCTGAGCTAACCCGGAGGAAAGGCAGTCCCTGGACAGAAGACTGTACGCAG
AAGGAAAGTACTGGACTACCCGTGGGTAAGTCCTGCCATTCAAGACTGGAGACACCTGGGAAATAAAAAGAGCAGGGCA
CTGCTGGTGGGAAGAGGCATTTTACCCTCCAGTGCAAATCCTGCTCCTTTGATTTAATGGGGGTGTACTGGGGCCAGGGG
CTGATTCACCTTCCCTGGGAGATGGTGGTGTTCATGAACAATCTTTGATCCTTCCATTTTCATTTATTCATCCATCCATT
CAACAAGTATTTGCTAAACACTAACTTAAGCTAATGCTAGGGTAGTGACTGAGATGTAAAAATAGATTTTAGAAATTAAA
ACAAAATCCAAGTCTCACACCCCTGTCAATCCCAGGAGATCTTTCCCTTGGTGGTTCTGTGAGAAATGGGCCATCCTG
AGGACACAGCCAGGACGGCAGAGGCCCTCCTGGCCTCAGGGCATGCCCTGCCCTACCTTCTGAAATGTTTACCCCAATTGAC
CAAACTTGGCTCCAGCCAATTGCGGTGGTTCTAGATAGCCAGGCCCCACCAAGAGATATTGCCCCCTTGATGAGAGTCAAA
CACCCTGCCTACAAGGAGATGTTTGTAAATGGAGAGGAAAAATTGGCACCTCATCTTTTAAAGGCAGTAATGGAAATTGAT
TTTCAGTAAC TGAAATTTGTGCACAAAACAATCTAAACACTAGTGAAGCCTGTTCGTGAACTAAATCTGGCTCTGGAA
ATGTTTGTGTTTATAGTTATTTACGATTTGTTGTTGGATTCAAGCTTAGTTGTTAAATGTAATTTAGCATC
TATTACACTCATGTAATATGGAGTAAGTATTGTAACTATTTCAATTGCGGGGATTGTGGGTGTTATACATACATTTAG

FIG. 10A(6)

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GACTGCAATTTTGGTATTTTGGTATTGTTGTAATAACAGCTAATTTAAGCAGGAACAAGAGAAC TAAGGAGGTCTG
TGCATTTTAAACACACAAATGTGAAGAAC TTGTATATAAACAAAAAGTAAATACTATAATACAAACTTCC TTCTGAAATAAA
AGTAGATCTGGTAAAAAAGAAAAAAGAAAAAAGAAAAAAGGGCGGCCGC

FIG. 10A(7)

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MYCNKKTSCRSALDQNCQWEPNQEIALPENICGIGWHLVGN SCLKITTAKENYDNAKLCFRNHNALLASLTTQKK
VEFVLKQLRIMQSSQSM SKLTLTPWVGPSGRXNVSYXVLGKDMXPILQIVLLQWDXRLEAQCCCLXFCGNFXSGTQLLRG
LKAATCIQPTXMYVSVKGLQTTVL RQCRTPCALRTACGDCTSGSSEXHV VQQHEXSVWTPMPMWPSSLXQCM EWYTMS
TCPENC SGYCTCSHCLEQPGCGWCTDPSNTGKGKCI EGSYKGPVKMPSQAPTGNFYQPQLLNSSMCLEDSRYNWSFIH
CPACQCNGH SKCINQSI CEKCENLTTGKH CETCISGFYGDPTNGGKCQPCCKCNGHASLCNTNTGKCFCTTKGVKGDECQ
LCEVENRYQGNPLRGTCYYTLLIDYQFTFSLSQEDDRYYTAINFVATPDEQNRDLDMFINASKNFNLNITWAASFAGT
QAGEEMPVVS KTN IKEYKDSFSNEKDFRNHPNITFFVYVSNFTWPIKIQIAFSQHSNFMDLVQFFVTFSCFLSLLL
AAVWVWIKQSCWASRRREQLLREMQQMASRPFASVNVVALETDEEPPDLIGGSIKTVPKPIALEPCFGNKA AVL SVFVRL
PRGLGGIPPPGQGLAVASALVDISQQMPIVYKEKSGAVNRKQQPPAQPGTCI

FIG. 10B

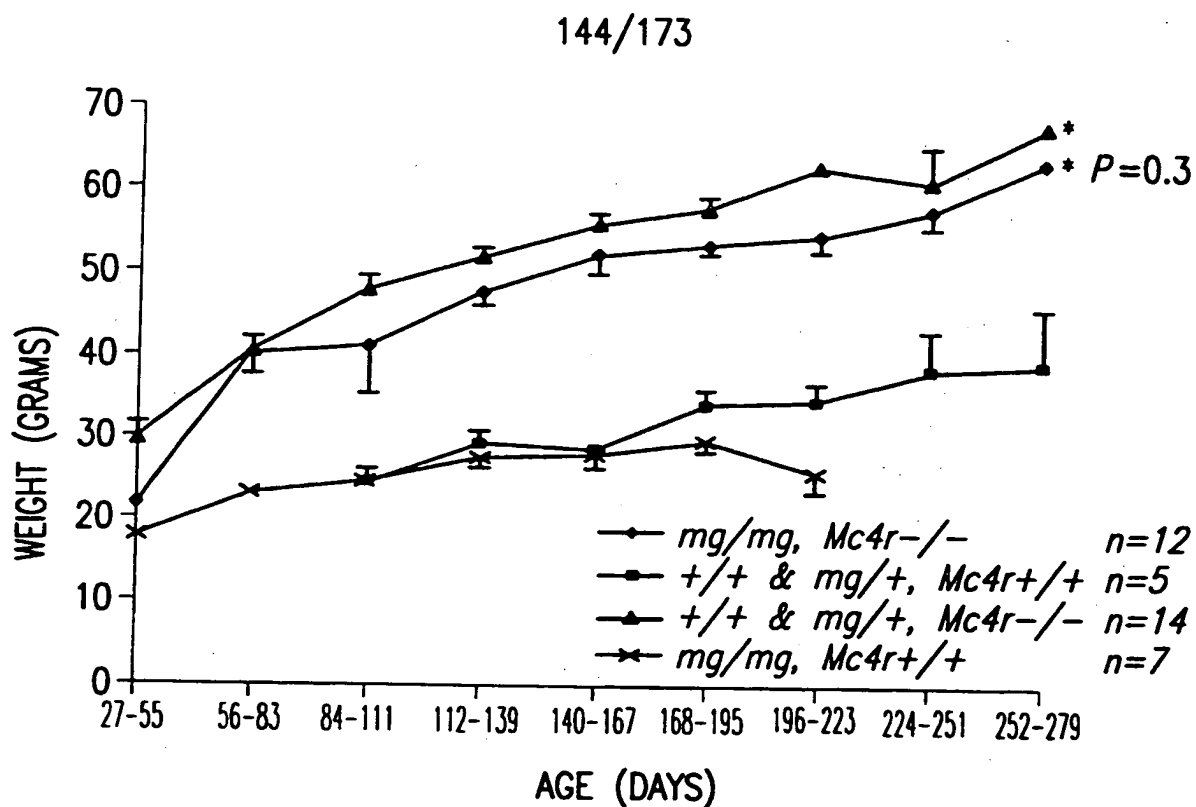


FIG.11A

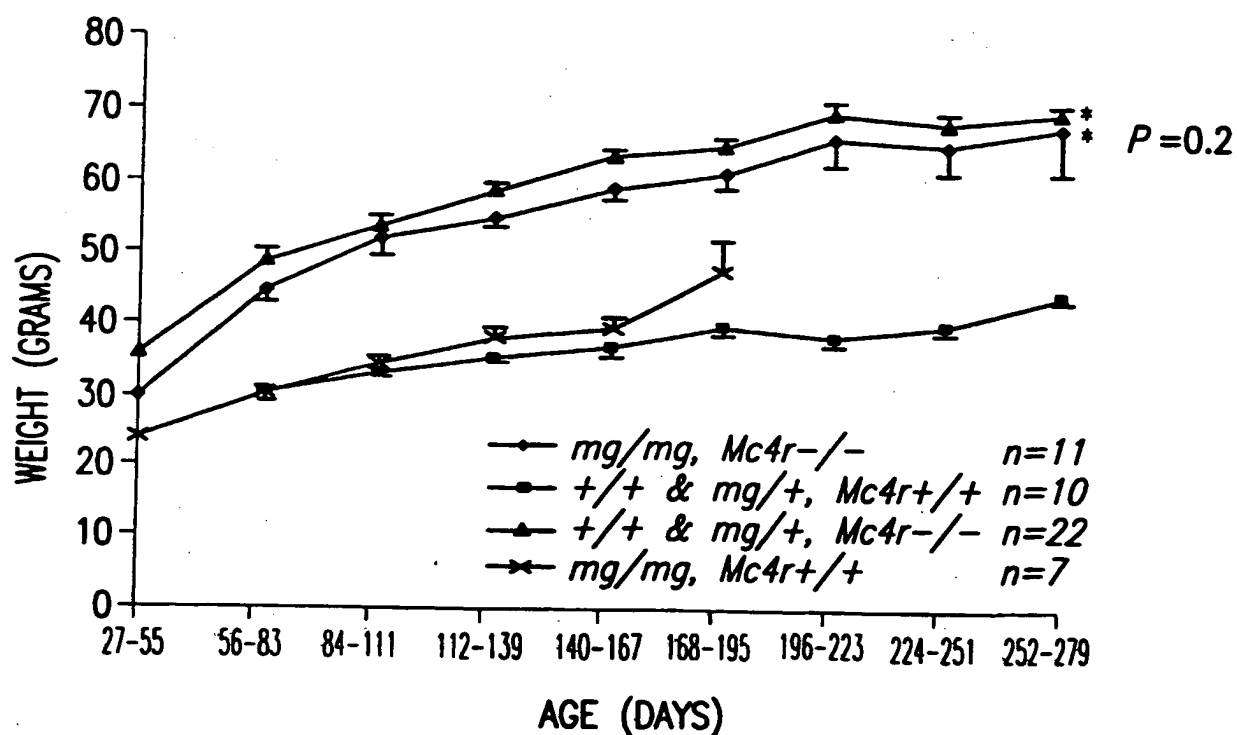


FIG.11B

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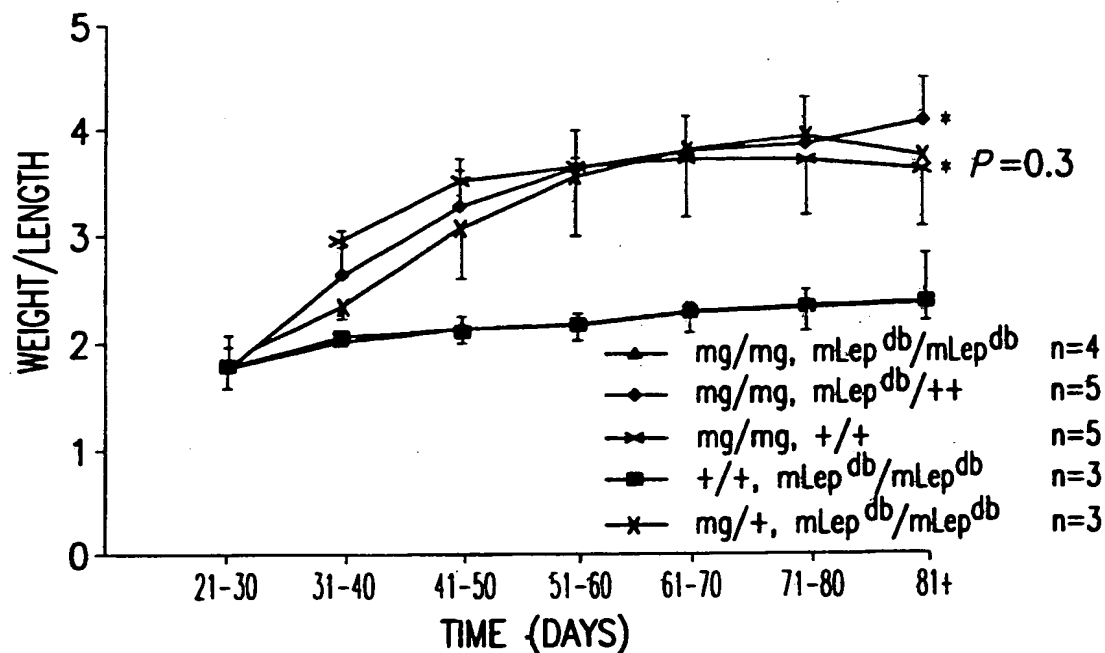


FIG. 12A

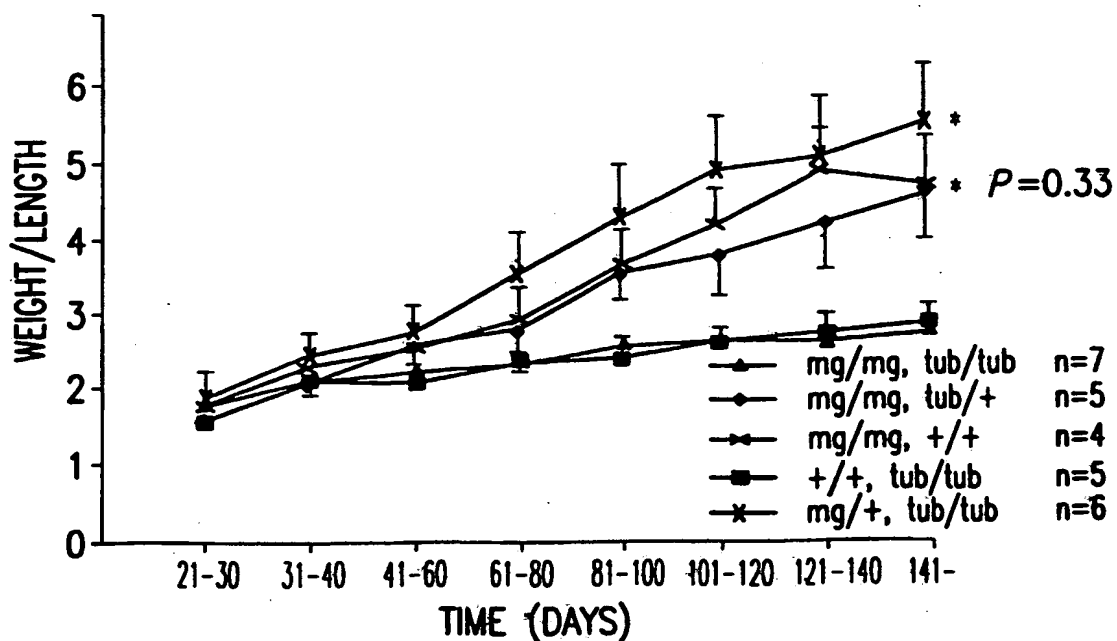


FIG. 12B

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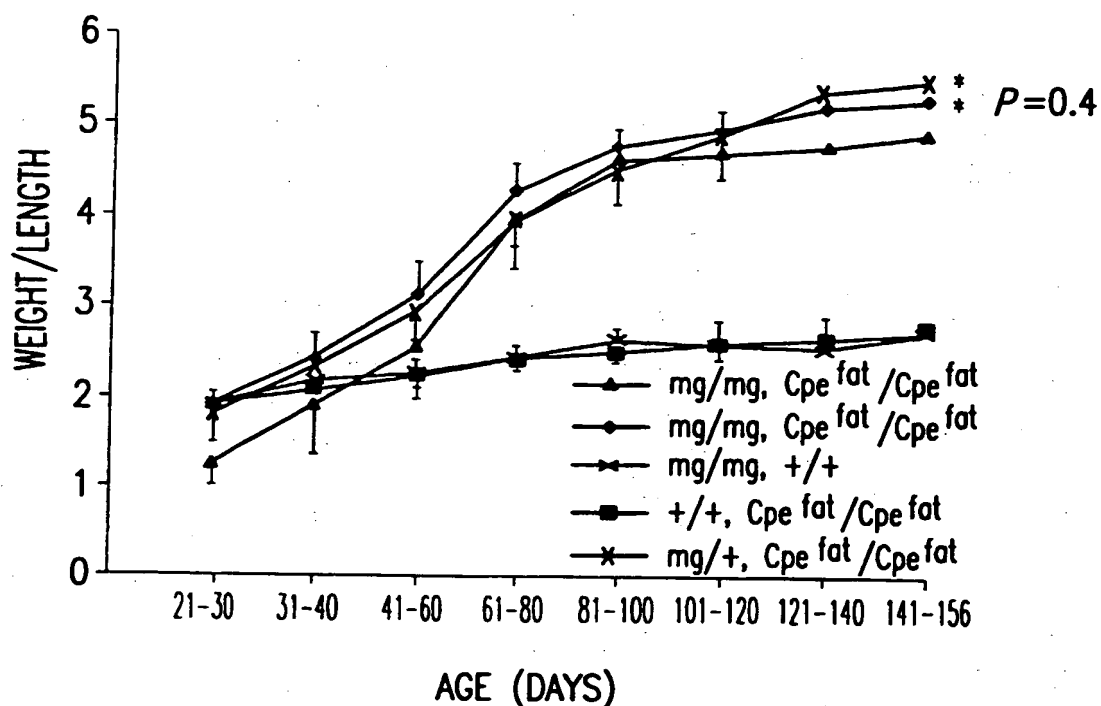


FIG.12C

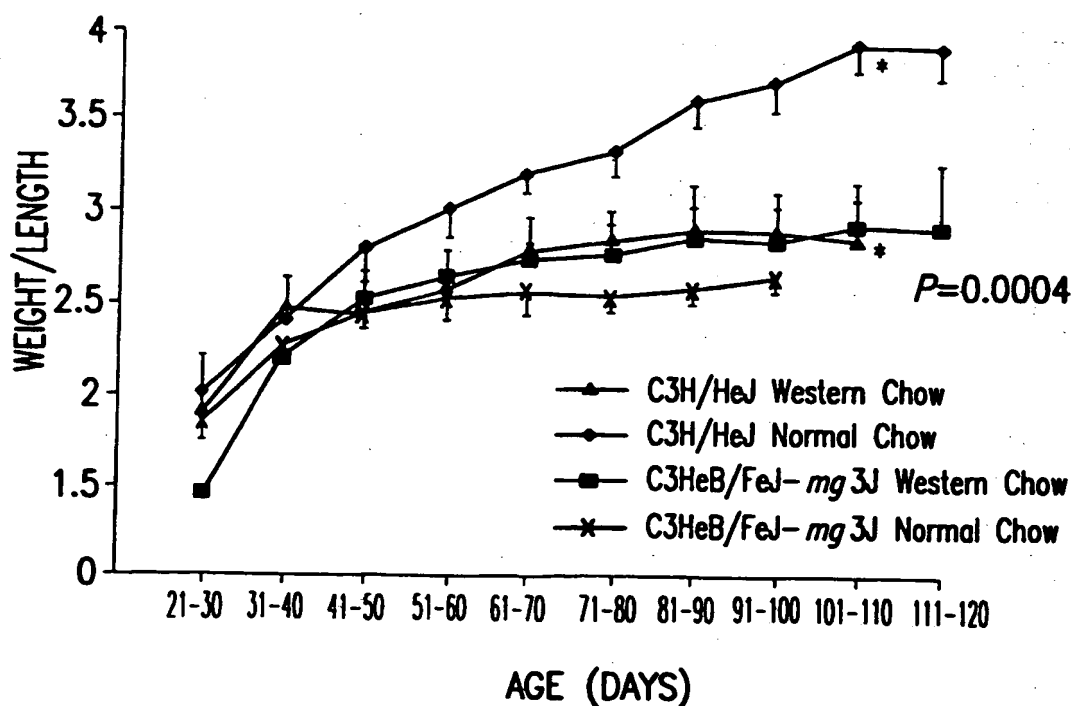


FIG.12D



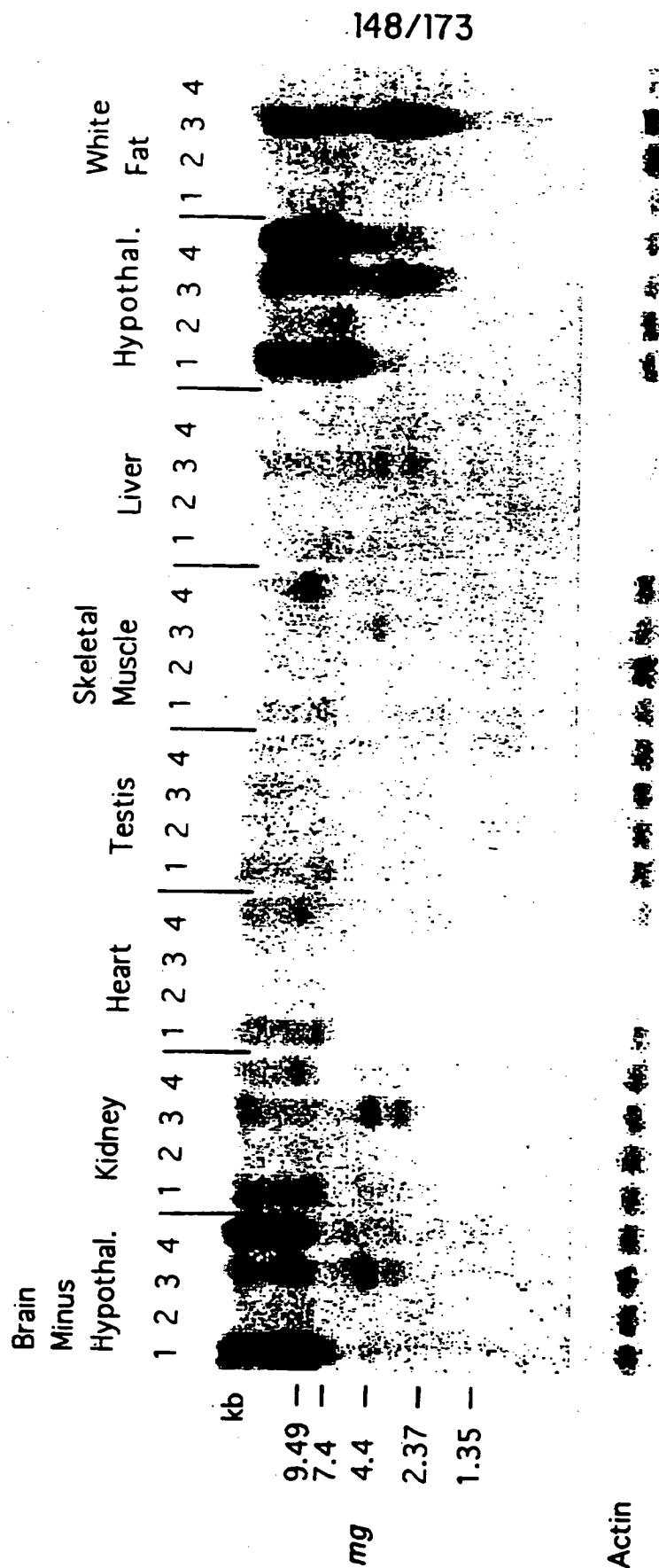


FIG.14

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FIG. 15B

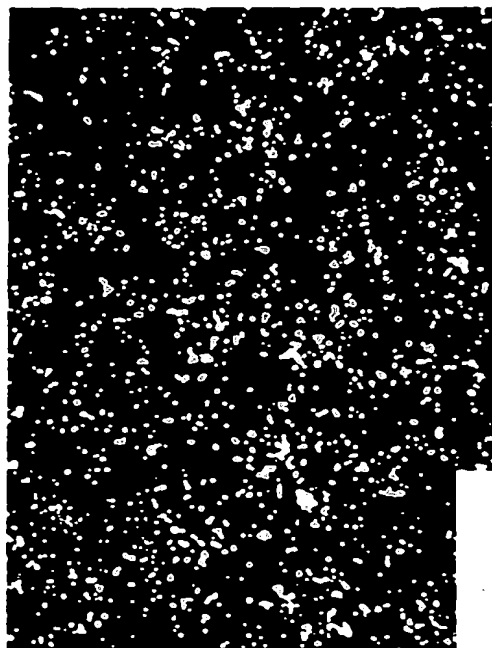


FIG. 15D



FIG. 15A



FIG. 15C



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obe2	FRNHPNITFFVYVSNTWP-----	[IKIQIAFSQHSNFM	MDLVQFFVTFFSCFLSLLVA	Transmembrane
K1AA0534	FRSNPNITFYVYVSNSWP-----		IKIQIAFSQHNTIM	DLVQFFVTFFSCFLSLLVA	
YC81_CAEEL	FGPDSNTTFFVRVYNFTP-----		VQIVVSFAQSPPI	N-WVLFVIFAACFIVLLVVA	
MEGF8	LKSSRFYLLLLGVGDPSGPGANGS		QGLLFFRQDQAH	IDLFFVFFSVFFSCFFLFLSLC	
		Site			
obe2	AVVWKIKQSCWASRRREQLLREMQ		MA SRPF	ASVETLPWNR-----	
K1AA0534	AVVWKIKQTCWASRRREQLLRERQ		MA SRPF	ASVDVALEVGAEQTEFLRGPLEGAPKPIA	
YC81_CAEEL	GLLWMIKVRTEAYRRNQRRIDEIE		HMA SRPF	ASTKMEL SML SQFSSAG-----	
MEGF8	VLLWKAKQALDQRQEQRRHLQEM		TKMA SRPF	AKVTVCFPDPPTAPASAWKP-AGLPPP-A	

FIG.16A

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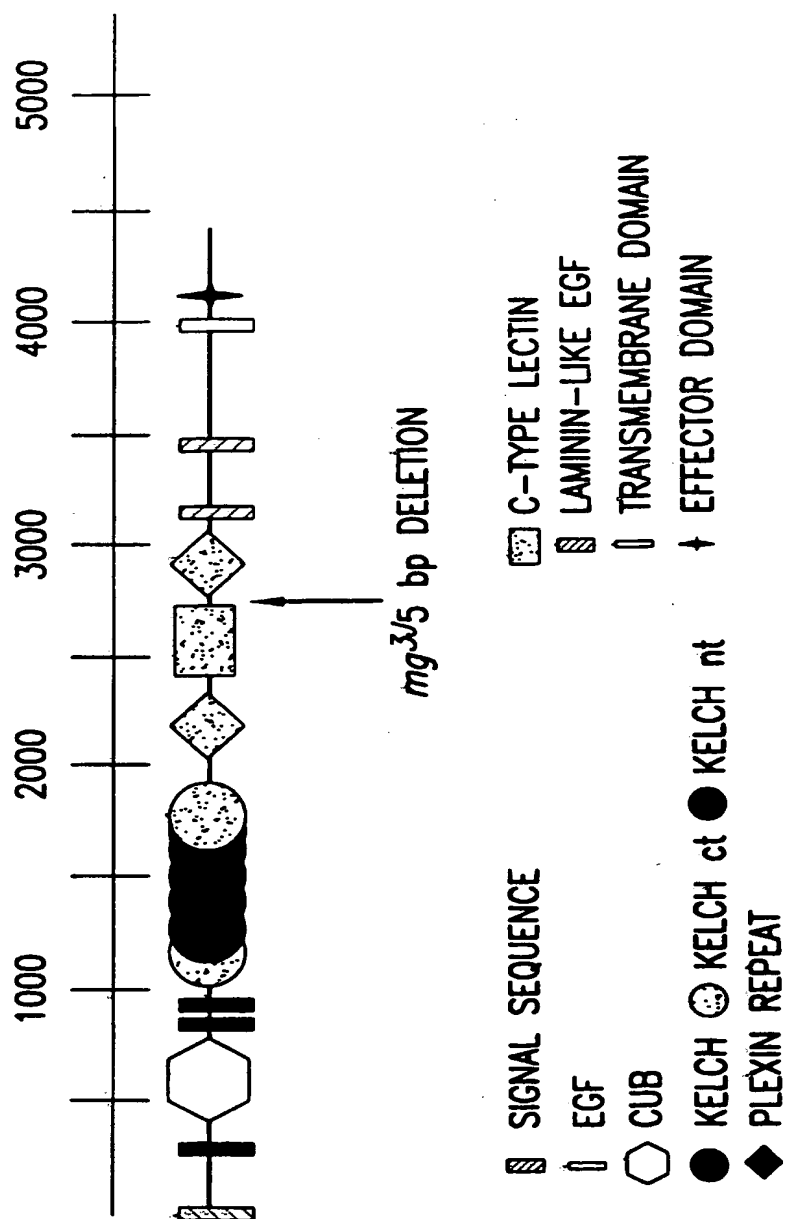
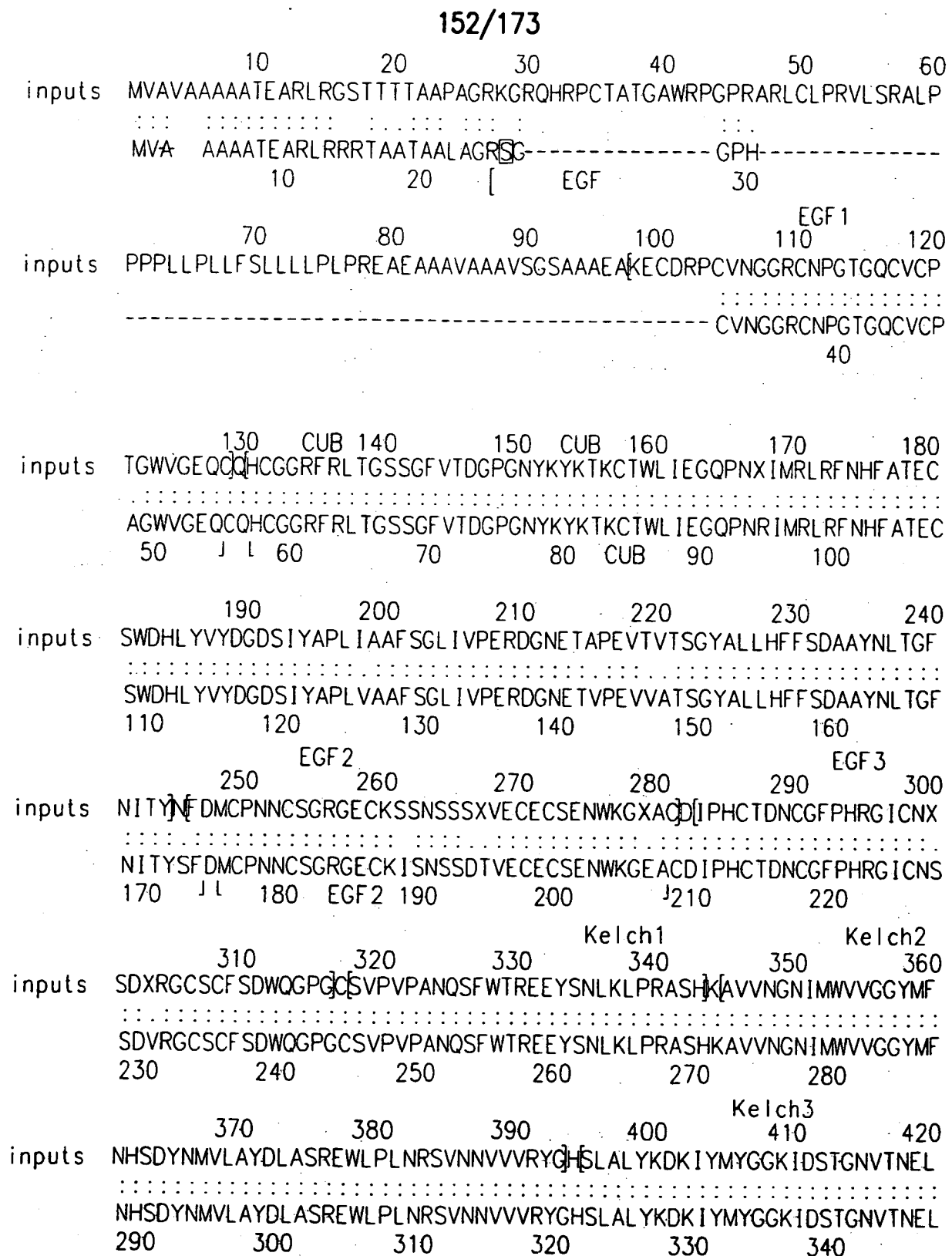


FIG.16B

**FIG.17A**

inputs

430 440 450 kelch4 460 470 480

RVFHIHNE SWVLLTPKAKEQYAVVGHS[SAHIVTLKNGRVVMLVIFGHCPLYGYISNVQEYD

.....

RVFHIHNE SWVLLTPKAKEQYAVVGHS[SAHIVTLKNGRVVMLVIFGHCPLYGYISNVQEYD

350 360 370 380 390 400

inputs

490 500 510 kelch5 520 530 540

LDKNTWSILHTQGALVQGGYGH[SSVYDHRTRALYVHGGYKAFSANKYRLADDLYRYDVD

.....

LDKNTWSILHTQGALVQGGYGH[SSVYDHRTRALYVHGGYKAFSANKYRLADDLYRYDVD

410 420 430 440 450 460

inputs

550 560 kelch 6nt 570 580 590 600

QMWTILKDSRFFRYL[HTAVIVSGTMLVFGGNT[HN[DTSM[SHGAKCFSSDFMAYD[ACDRWS

.....

QMWTILKDSRFFRYL[HTAVIVSGTMLVFGGNT[HN[DTSM[SHGAKCFSSDFMAYD[ACDRWS

470 480 490 500 510 520

inputs

610 620 kelch 1ct 630 640 650 660

VLPRPDLHHDVNRF[GH[SAVLHNSTMYVFGGFNSLLLSDILVF[TSE[QCD[HRSEAA[CLAAG

.....

VLPRPDSTMMSTD[LAIPAVLHNSTMYVFGGFNSLLLSDILVF[TSE[QCD[HRSEAA[CLAAG

530 540 550 560 570 580

inputs

670 680 plexin 1 690 700 710 720

PGIRCVWNTGSSQCI[SWALATDEQEEKLKSECF[SKRTL[DH[DRCDQHTDCYSCTANTNDCH

.....

PGIRCVWNTGSSQCI[SWALATDEQEEKLKSECF[SKRTL[DH[DRCDQHTDCYSCTANTNDCH

590 600 610 620 630 640

inputs

730 740 ligand-binding cytokine chain 750 760 770 780

WCNDHCVPRNHSCSEGQISIFRYENC[PKDNPMYYCNKKT[SCRSCALDQNCOWE[PRNQECI

.....

WCNDHCVPRNHSCSEGQISIFRYENC[PKDNPMYYCNKKT[SCRSCALDQNCOWE[PRNQECI

650 660 670 680 690 700

inputs

790 800 c-type lectin 810 820 830 840

AL[PENI[CGIGWHLVGN[SLCKIT[TAKENYD[NAKLFCRNHNALLASLT[TQKKVEFVLKQLRI

.....

AL[PENI[CGIGWHLVGN[SLCKIT[TAKENYD[NAKLFCRNHNALLASLT[TQKKVEFVLKQLRI

710 720 730 740 750 760

FIG. 17B

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	850	860	870	880	890	900
inputs	MQSSQSMSKL TL TPWVGLRK INVSYWCWEDMSPF TNSLLQWMPSEPSDAGFCGILSEPST					
	MQSSQSMSKL TL TPWVGLRK INVSYWCWEDMSPF TNSLLQWMPSEPSDAGFCGILSEPST					
	770	780	790	800	810	820
	plexin repeat 2					
	910	920	930	940	950	960
inputs	RGLKAATCINPLNGSVCEIPANHSIAKQCRTPCALRTACGDCTSGSSECMWCSNMKQCVDS					
	RGLKAATCINPLNGSVCEIPANHSIAKQCRTPCALRTACGDCTSGSSECMWCSNMKQCVDS					
	830	840	850	860	870	880
	970	980	990	1000	1010	1020
inputs	NAYVASFPFGQCMEWYTMSTCPPENC SGYCTCSHCLEQPGCGWCTDPSNTGKGKCIEGSY					
	NAYVASFPFGQCMEWYTMSTCPPENC SGYCTCSHCLEQPGCGWCTDPSNTGKGKCIEGSY					
	890	900	910	920	930	940
	lamin-like EGF-1					
	1030	1040	1050	1060	1070	1080
inputs	KGPVKMPSQAPTGNFYPOPLLNSSMCLEDSRYNWSFIHCPACQCNGHSKCINQSICEKCE					
	KGPVKMPSQAPTGNFYPOPLLNSSMCLEDSRYNWSFIHCPACQCNGHSKCINQSICEKCE					
	950	960	970	980	990	1000
	lamin-like EGF-2					
	1090	1100	1110	1120	1130	1140
inputs	NLTTGKHCE TCISGFYGDPTNGGKCQPCCKNGHASLCNTNTGKCFCTTKGVKGDECQLCE					
	NLTTGKHCE TCISGFYGDPTNGGKCQPCCKNGHASLCNTNTGKCFCTTKGVKGDECQLCE					
	1010	1020	1030	1040	1050	1060
	1150	1160	1170	1180	1190	1200
inputs	VENRYQGNPLRGTCYYTLLIDYQFTFSLSQEDDRYYTAINFVATPDEQNRDLDMFINASK					
	VENRYQGNPLRGTCYYTLLIDYQFTFSLSQEDDRYYTAINFVATPDEQNRDLDMFINASK					
	1070	1080	1090	1100	1110	1120
	1210	1220	1230	1240	1250	1260
inputs	NFNLNITWAASF SAGTQAGEEMPVVSKTNIKEYKDSFSNEKFDFRNHPNITFFVYVSNT					
	NFNLNITWAASF SAGTQAGEEMPVVSKTNIKEYKDSFSNEKFDFRNHPNITFFVYVSNT					
	1130	1140	1150	1160	1170	1180

FIG.17C

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	1270	1280	1290	1300	1310	1320
inputs	WPIKIQIAFSQHSNFM	DLVQFFVTFFSCFLS	LLVAAVVK	IJKQSCWASRRRE	QLL	REMQ
	
	WPIKIQV-----			QT		EQ-----
	1190					

	1330	1340	1350	1360	1370	1380
inputs	QMASRPFASVNVALE	TDEEPPDL	IGGSIKTVPKPI	ALEPCFGNKA	AVLSVFVRL	PRGLGG

	1390	1400	1410	1420
inputs	IPPPGQSGLA	VASALVDISQ	MPIVYKEK	SGAVRNRKQ
	PPPAQPGTCIN			

FIG.17D

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ATGTTGGCGGTGGCCGACGGCGGCAACTGAGGCAAGGCTGAGGAGGACGGCGGCAGCGCTCGCGGGCAGGAGCGCGGGCC
GCACCGACCCCTGCACCGCAGAGGGCCCTGGAGGCCGGGACCGCGGCCCGGCTGTGTCTCCCGGGGTGCTGTGCGGGCGCTGCCCCCGC
CGCCGCTGCTGCCGCTGCTCTTTTCGCTGCTGCTGCCGCTGCCCGGGAGGCCGAGGCCGCTGCGGTGGCGGCCGCGGTGTCCGGCTCG
GCCGAGCCGAGGCCAAGGAAITGTACCGGCCGTGTGTCAACGGCGGTGCTGCAACCCCTGGCACCGGCCAGTGGCTCTGCCCGCCGGCTG
GGTGGCGAGCAATGCCAGCACTGCGGGGGCGCTTCAGACTAACTGGATCTCTGGGTTTGTGACAGATGGACCTGGAAATTATAAATACA
AAACGAAGTGACGTGGCTCATTGAAGGACAGCCAAATAGAAATAGAGACTTCGTTTCAATCATTTTGTACAGAGTGTAGTTGGACCAT
TTATATGTTTATGATGGGGACTCAATTTATGCACCGCTAGTTGCTGCAATTTAGTGGCTCATTTGTTCTGAGAGAGATGGCAATGAGACTGT
CCCTGAGGTTGTTGCCACATCAGGTTATGCCCTTGCTGCAATTTTTTATGATGCTGCTTATAATTTGACTGGATTTAATATTACTTACAGTT
TTGATATGTGTCCAAATAACTGCTCAGGCCGAGGAGAGTGTAGATCAGTAATAGCAGCGATACTGTTGAATGTGAATGTTCTGAAAACCTGG
AAAGGTGAAGCATGTGACATTCTCTACTGTACAGACAACCTGTGGTTTTCTCTCATCGAGGCATCTGCAATTCAGTGATGTCAGAGGATGCTC
CTGCTTCTCAGACTGGCAGGGTCTGGATGTTTCAGTTCTGTACCAGCTAACCAGTCAATTTTGGACTCGAGAGGAAATATTTCTAACTTAAAGC
TCCCCAGAGCATCTCATAAAGCTGTGGTCAATGGAACAATTATGTGGGTTGTTGGAGGATATATGTTCAACCACCTCAGATTATAACATGGTT
CTAGCGTATGACCTTCTCTAGGGAGTGGCTTCCACTAAACCGTTCTGTGAACAATGTGGTTGTTAGATATGGTCATTTCTTTGGCATTATA

FIG. 18A(1)

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CAAGGATAAAATTTACATGTATGGAGGAAAAATTGATTCAACTGGGAATGTGACCAATGAGTTGAGAGTTTTTCACATTCATAATGAGTCAT
GGGTGTTGTTGACCCCTAAGGCAAGGAGCAGTATGCAGTGGTTGGGCACCTCTGCACACATTGTTACACTGAAGAATGGCCGAGTGGTCATG
CTGGTCATCTTTGGTCAC TGCCCTCTCTATGGATATATAAGCAATGTGCAGGAATATGATTTGGATAAGAACACATGGAGTATATTACACAC
CCAGGGTGCCCTTGTGCAAGGGGGTTACGGCCATAGCAGTGTTTACGACCATTAGGACCAGGGCCCTATACGTTTCATGGTGGCTACAAGGCTT
TCAGTGCCAAATAAGTACCGGCTTGCCAGATGATCTCTACCGATATGATGTGGATACCCAGATGTGGACCATTCTTAAGGACAGCCGATTTTTC
CGTTACTTGCCACACAGCTGTGATAGTGAGTGGAAACCATGCTGGTGTTTGGGGGAAACACACACAATGACACATCTATGAGCCATGGCGCCAA
ATGCTTCTCTTCAGATTTTCATGGCCTATGACATTGCCTGTGACCGCTGGTCAGTGCCTCCAGACCTGATCTCCACCATGATGTCAACAGAT
TTGGCCATTGAGCAGCTTTACACAACAGCACCATTGATGTGTTGGTGGTTTCAATAGTCTCCTCCTCAGCGACATCCTGGTATTCACCTCG
GAACAGTGTGATGCGCATCGGAGTGAAGCCGCTTGTTAGCAGCAGGACCTGGTATTCGGTGTGTGTGGAAACAGGGTCTGCTCAGTGTAT
CTCGTGGGCGCTGGCAACTGATGAACAAGAAGAAAAGTTAAAAATCAGAAATGTTTTTCCAAAAGAACTCTTGACCATTGACAGATGTGACCAGC
ACACAGATTGTTACAGCTGCACAGCCAAACACCAATGACTGCCACTGGTGCAATGACCATTGTGTCCCCAGGAACACACAGCTGCTCAGAAGGC
CAGATCTCCATTTTAGGTATGAGNAATTGCCCCAAGGATAACCCCTATGTACTACTGTAAACAAGAAGACCAGCTGCAGGAGCTGTGCCCCCTGGA
CCAGAAGTCCAGTGGGAGCCCCGGGAATCAGGAGTGCATTGCCCTGCCCGAAAAATATCTGTGGCATTGGCTGGCATTGGTTGGAAACTCAT

FIG. 18A(2)

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GTTTGAAAATTACTACTGCCAAGGAGAAATTATGACAAATGCTAAATTGTTCTCTAGGAACCAACAATGCCCTTTTGGCTTCTCTTACAACCCAG
AAGAAGGTAGAAATTTGTCTTAAGCAGCTGCCGAATAATGCAGTCATCTCAGAGCATGTCCAAGCTACCTTAACCCCATGGGTGGCCTTCG
GAAGATCAATGTGTCTCTACTGGTGTCTGGGAAGATATGTCCCATTTACAAATAGTTTACTACAGTGGATGCCGTCTGAGCCCAGTGATGCTG
GATTCTGTGGAAATTTTATCAGAACCCAGTACTCGGGGACTGAAGCTGCAACCTGCATCAACCCACTCAATGGTAGTGTCTGTGAAAGGCCT
GCAAAACCACAGTGCTAAGCAGTGGCCGGACACCATGTGCCTTGAGGACAGCATGTGGAGATTGCACCAGCGGCAGCTCTGAGTGCAATGTGGTG
CAGCAACATGAAGCAGTGTGTGGACTCCAATGCCTATGTGGCCCTCTCCCTTTTGGCCAGTGTATGGAATGGTATACGATGAGCACCTGGCC
CCCCTGAAAATTGTTCAGGCTACTGTACCTGTAGTCATTGCTTGGAGCAACCAGGCTGTGGCTGGTGTACTGATCCAGCAATACTGGCAAA
GGGAAATGCATAGAGGGTTCCTATAAAGGACCAGTGAAGATGCCTTCGCAAGCCCTACAGGAAATTTCTATCCACAGCCCTGTCTCAATTC
CAGCATGTGTCTAGAGGACAGCAGATACAACTGGTCTTTTCATCTGTCAGCTTGCCAAATGCAACGGCCACAGTAAATGCATCAATCAGA
GCATCTGTGAGAAGTGTGAGAACCTTGACCACAGGCAAGCACTGCGAGACCTGCATATCTGGCTTCTACGGTGTATCCCACTGAGGGGAAA
TGTCAGCCATGCAAGTGCATTTGGGCACGCGTCTCTGTGCAACACCAACACGGGGCAAGTGTCTTGCAACCACCAAGGGCGTCAAGGGGGACGA
GTGCCAGCTATGTGAGGTAGAAAAATCGATACCAAGGAACCCCTCTCAGAGGAACATGTTATTATCTCTTCTTATTGACTATCAGTTCACCT
TTAGTCTATCCCAGGAAGATGATCGCTATTACACAGCTATCAATTTTGTGGCTACTCCTGACGACAAACAGGGATTTGGACATGTTTCATC

FIG. 18A(3)

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AATGCCTCCAAGAAATTTCAACCTCAACATCACCTGGGCTGCCAGTTTCTCAGCTGGAACCCAGGCTGGAGAGAAGAGATGCCTGTTGTTTCAAA
AACCAACATTAGGAGTACAAAGATAGTTTCTCTAATGAGAAGTTTGATTTTCGAACACCACCCAAAATATCACATTTCTTTGTTTATGTCAGTA
ATTCACCTGGCCCATCAAAATTCAGATTGCCCTTCTCTCAGCACAGCAATTTTATGGACCCTGGTACAGTTCTTCGTGACTTCTTCAGTTGT
TTCTCTCTTTGCTCCTGGTGGCTGCTGTGGTTTGGGAAGATCAAAACAAGTTGTGTTGGGCTCCAGACGTAGAGAGCAACTTCTTCGAGAGAT
GCAACAGATGGCCAGCCGTCCCTTTGCCCTCTGTAAATGTGCGCTTGGAAACAGATGAGGAGCCCTCCTGATCTTATTGGGGGGAGTATAAAGA
CTGTTCCAAACCCATTGCACTGGAGCCGTGTTTGGCAACAAAGCCGCTGCTCTCTGTGTTTGTGAGGCTCCCTCGAGGCCCTGGGTGGC
ATCCCTCCTCCTGGGCAGTCAGGCTTGCTGTGGCCAGCGCCCTGGTGGACATTTCTCAGCAGATGCCGATAGTGTACAAGGAGAAGTCAGG
AGCCGTGAGAAACCGGAAGCAGAGCCCTTGCACAGCCTGGGACCTGCACTCTGATGCTGGGGCCAGGGACTCTCCCACGCACGAGCTAGTG
AGTGGCACACCAGAGCCATCTGCAGGGAAGGGCGTGGCGGGGAAATGGCTGTGCGGTGCGGGACGGAAGACTGGAAACCCCTCAAAGCATCTG
ACTACCTGCATGATCACAAAGCTTTCTTTGACGGTTTCTCCCATCCGTGTTCCAGCATCTAACCTTTTACTTTTGCATAGGAAATACTTGAT
TTAATTACAGGTCCAGGGATGAGCTGATGGTTGCTGGAGGAGGCCAGTGTAGAGCCAGTGAGAGAAGTACAGGATGACACTCAGGTTCACTGT
GGAAACTGTTCTTGGGACTGTCTCAACTGTGCAAAAACAAAGATGGAGTGTTTACAAGTAGACATTCGTGTCATCAGTTGTTCTTTGAACAT
GGTCTTTTAAAACCTAGTCAGATGAATTAACCTGTTTTCATCTGAGCCGTGCTATCTTTTAAAAGATGTGCTATTTATTCTTTGACCGATT

FIG. 18A(4)

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TAGGCAATTATCTCTCTCCAGGGAGTACCTTTTTTCTAGTTGAGAAATTAATAATGGTCCATCTCTCTTTTGATCATATCAAGCTAGGATAGA
AGGGGGCTATTTTAAATGTC AAGGTCAGCAGTGTACTTTGAATGTAAACTGGTATAATAGGTAGTTTTTCTATAGTAAC TTGATTAAATTTA
GTCTTAATCCATTTGAAACTCTCTCTCTCTCTGCTGCTCCCTCTCTCTCCATCTCACCCCTCCCTCTCTCACACATACACACACA
AACACATACACACAACACTAAGTGCCTAGACTTTTAAATAGATCTAGCAATTGGAAAGTTAGTAAGCCTAAGTTTTTACATAATTGCATTCTT
ACATTCTTGTAATAATTTAAATAGCTACCATTTGGCAATCTGCTTTTTTCTAAAATCTGATTTTGCAGCCAGGAAAGAAATTTTCTCACCCAAGG
AACATTTGATCTAGCAGCAGGGATGAGAGGAAAGCAGAAATGAATGAAC TGTGAAGCTCCTGTTTTTATTATCAAAAAGGACACTGTCAAG
AAGGGCCCCCTGCCCCACCCCGTGTACCCCTAGGCCGTGTAAGCGATCAGAGGAAAGGACTCATTCATGTCACGCTTCTTGAGCAGAA
AAGAGCACTGAGAGCAC TTGGGACCCCTGGATCAGAGAGCATCTGTGTCTCTGCAGCCTCCTCTGAAC TTGTGGTTCA TTCTCAGGCTGGG
GTGGACTCAGATGCCAGGAAAGGGACAGCCTCCCATTTGT CAGGCAGAAGCTGCCCAAAGCCTGGAGAAGGACTTGT TTGGCCCTCTTTCCCCC
AGGAGGGGCTCGACCCACCCCTCCTCTCAGACCAAGGTGGCTGTGAGGAGGGCAGCAAAATGCTGACAAGGATGAAAAGCACATGG
AAAAAATGGACGAGGAGGAAAAC TCTGCCAAATGGAAAATGACC AAAATTAAGAGGGTGGGACAGTCCCTGCTCTCTCCAGAGGGCA
CTGCTTGGAATGTGTTTTCCCAATTTATGGTGTCTGTATTTCTGGCATTATGCAGCAGCCTCC CAGAAGCTCTCTCTCTGCTTCAAAACCT
GGGATCTCTGGCATTACCCATTGGGATGGACCGCTGGACAGCAATGCTCGAGTTTGTGAATTTGGAGAGATACTCAAAAGAGCTAAAAC TGT

FIG. 18A(5)

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CAGCATTTTACCTTTAAATGCAGTGCCTAGAGAGAGAGTATTGTCTCTTCCCCAACACTAACCCCTACTCCCATGAAGAAATTGCCTGGAAAAGA
TGTTTTCAAGGAATTTGAACCATAAAACACTATCTGATGCACAGAACACCTCTACTTTGAGACTCACCTCTCATAAAGCTTCTTTTTTCACAT
TACTGTTAAAGACCAGACGTTCTAGAAAAGACCCCTCCTCTCATGAGCTCCCCCATCCCTGCTACAGAACACAGCACCCCATGGCGCCTGCAG
TGGACTGGCCCCCTTAATTCACAGGCCCCCCCCAGCAAGGCCAAAGGAGGCCCTTGGGTATTGTCTCCTACAAGGAAGATCCTCTTTTGT
TGTTCAAGGACCAGTTTCTTAGGCCAAAGAGTCTCTTCCCCATGTTAGTCCCTATGCCTTGAAATATCATGCACCATGACCCACAGCCAT
CTGTTATGTCTTATTTTTTCTTAAAGATAATGTTTATTTTTTAAAGGAAGGAAGCAAGTGAAGTTTCAATTCGTCCAGCGGTGG
GGAAGCGCTGAATCCACCTGCTTCTCCTTTGCAACCGACAGCAACAGCTTTCTCCGGCTCAGGGCAGAAAAAGGGAATGGCAGGGAGTA
AGAGGCGCTGGGCTGGAGCTGTTTCCAAGGAAGGAATTGGTTGTCTATCTGGCAGTGTTCGCGGTACAAGAGAGCCCTGTATATAAAATTAAA
ATAGTCAAGACAACACTGACCTTGCACCTGTACATAACTATACAGTAGTGTCCAGAATGTTCAGACATTCGGAGTGATACATAAAACAGAAAA
AATCTTCATGTATTTTATTAATAATAACAAATGCTGTAGTTTCACCTAAGATGTTTTGTGCCATATGCTGGAATCCAGGTTCTCGCCAGG
CCCCGATACATGAATAACAACCCCAAGAAACGCATCCCCATTGTGTGATGTGTTCAGATGCATCTGGCACCATAATTAGGTATTTCTTAAACA
GGACTCATCTGTACAGTGCACATGAAAAATCAGGCAGGGGAATCGAAACACAGCGCTGGAGGAGACTCAGGAAGCAGAGGCGTCCCTGCGCG
CTGCCCCTGGCCCTGCAAGCACATCATGACCCCTTCTTGGCAGCCTCTTGGTGCTCTGGGTAGTGAGGGATGACCAGTCTTGCTCTGAGAAAT

FIG. 18A(6)

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GTTCCTTAGTCCTTAAGTTCAAAGACTAACCTGTAGCAATCAGACTTTCCAAAGGGGTCTCCATTTTGTAGTTTTGTCTAAATTT
TTAATGACCATTTCCTGGAATCAGTTTATTATACTGAAAACTGGGGGTGGAGTAGGGAGCTAGTTTGTGATAAATAGTTCCCATTTTCCCC
GTGGAGAAATTGACATACCCCTGGACTCCTGTGTGCTCTCTGCCATCCCTGCACACAGCCTGGGGGAGAAGCCTGTGCCCTCCCCGTGTGGAGAG
AAGGCAACCCAGATCCCTGAGCTAACCCGGAGGAAGGCAGTCTCGACAGAAGACTGTCAGCAGAAGGAAAGTACTGGACTACCCCGTGG
GTAAGTCCTGCCATTCAAGACTGGAGACACCTGGGAAATAAAAGAGCAGGGCAGTCTGCTGGGGAAGAGGCATTTTACCTTCCAGTGCAAA
TCCTGCTCTTTGATTTAATGGGGGTGACTGGGGCCAGGGGCTGATTCACCTTCCTTGGGAGATGGTGGTGTTCATGAAACATCTTTTGATCC
TTCCATTTTCATTTATTCATCCATCCATTCAACAAGTATTTGCTAAACACTAACTTAAGCTAACTGCTAGGGTAGTGACTGAGATGTAAAAATA
GATTTTAGAATTAACACAAAATCCAAGTCTCACACCCCTGTATCCAGGAGATCTTTCCTTGTGGTGGTTTCTGTGAGAAATTGGCCATCC
TGAGGACACAGCCAGGACGGCAGAGGCCCTCCTGGCCTCAGGGCATGCCCTGCTTCTGAAATGTTTACCCCATTTGACCAAACCTTGCGT
CCAGCCATTGCGGTGGTTCTAGATAGCCAGGCCCCACCAAGAGATATTGCCCTTGTATGAGAGTCAAAACACCCCTGCCCTACAAGGAGATGTTT
TGAAATGGAGAGGAAAATTGGCACCTCATCTTTTAAAGGCAGTAATGGAATTGATTTTCAGTAACAGTAAATTTGTGCACAAAAACATTTCTAAAC
ACTAGTGAAGCCTGTTTCGTTGAACTAATCTGGCTCTGGAAATGTTTTGTTTTATAGTTATTTACGATTCGTTTGTGGATTCAAGCT
TAGTTTGTATATGATAATTTAGCATCTATTACACTCATGTAAATATGGAGTAAGTATTGTAAACTATTTCATTGCGGGGATTGTGGGTG

FIG. 18A(7)

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TTATACATACATTTAGGACTGCAATTTTGGTATTTTGGTATTGTGTAATAACAGCTAATTTAAGCAGGAACAAGAGAACTAAGGGAGGT
CTGTGCAATTTAAACACAAAATGTGAAGAAGTTGTATATAAACAAAAGTAAATACTATATAACAACTTCCTTCTGAAATAAAAGTAGATCTG
GTAAAAAAAAAGAAAAAAAAAAAA

FIG. 18A(8)

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MVAVAAAAATEARLRRRTAATAAGRSGGPHRPTATGAWRPGPRARLCLPRVLSRALPPPPLPLLSLPLPREAEEAAVAAVSGS
 AAEEAKECDRPCVNGRCNPGTGQCVCAPGWGEQCQCGRFRLTGSSGFVTDGPGNYKYKTKTWLIEGQPNRIMRLRFNFATECSWDH
 LYVYDGDSIYAPLVAAFSGLIVPERDNETVPEVWATSGYALLHFFSDAAAYNL TGFNITYSFDMPNCSGRGECKISNSSDTVECECSENW
 KGEACDIPHCTDNCGFPHRGICNSSDVRGSCFSDWQPGCSVPVPANQSFWTREEYSNLKLPRASHKAVVNGNIMWVVGGMFNHSDYNMV
 LAYDLASREWLPNRSVNNVVRYGHSALYKDKIYMYGGKIDSTGNVTNELRVFHIHNEVWLLTPKAKEQYAVVGHSAHIVTLKNGRVVM
 LVIFGHCPLYGYISNVQEYDLKNTWSILHTQALVQGGYGHSSVYDHRTRALYVHGGYKAFSANKYRLADDL YRYDVTQMWTLKDSRFF
 RYLHTAVIVSGTMLVFGGNTHTDTSMSGHAKCFSSDFMAYDIACDRWSVLPRPDLHHDVNRFGHSVAVLNSTMYVFGGNSLLSDILVFTS
 EQCDAHRSEAACLAAGPGIPCVMWNTGSSQCSWALATDEQEEKLKSECFSKRTL DHDRCDDQHTDCYSCTANTNDCHWCNDHCVPRNHSCSEG
 QISIFRYENCPCNPMYYCNKKTSCRSCALDQNCQWEPNQECIALPENICGIGWHLVGNISCLKIT TAKENTDNAKLFCRNHNALLASLTTQ
 KKVEFVLKQLRIMQSSQSMKSLTLTPWVGLRKINVSYWCHWEDMSPFTNSLLQWMPSEPSDAGFCGILSEPSTRGLKAAATCINPLNGSV CERP
 ANHSAKQCRTPCALRTACGDCTSGSSECMWCSNMKQCVDSNAYVASFPFGQCMWYTMSTCPPENC SGYCTCSHCLEQPGCGWCTDPSNTGK
 GKCIEGSYKGPVKMPSQAPTGNFYPQPLLNSSMCLDSRYNWSFIHCPACQCNGHSCINQSIKECENLTTGKHCECTCISGFYGDPTNGGK
 CQPCCKNGHASL CNTNTGKCFCTTKGVKGDECCQLCEVENRYQGNPLRGTCYYTLL IDYQFTFSLSQEDDRYYTAINFVATPDEQNRDLDMFI

FIG. 18B

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NASKNFNLNITWAASFAGTQAGEEMPVSKTNIKEYKDSFNEKDFRNHPNITFFVYVSNFTWPIKIQIAFSQHSNFMDLVQFFVTFSC
FLSLLLVAUVVWIKQSCWASRRREQLREMQMASRPFASVNVVALETDEEPPDLIGGSIKTVPKPIALEPCFGNKAVALSVFVRLPRGLGG
IPPPGQGLAVASALVDISQQMPIVYKEKSGAVNRKQPPAQPATCICWGQGLSHARASEHTRAICREGRGGEMAVRCGTEDWKPSKHLT
HLHDHKLSTVSPIRVPASNLLLLHRKYLILQVQGADGCWRRPVSQENHSGSLWKTVLGTVSTVQKTKDGVFTSRHSSSVWLEHGLLKTSQ
MNLVFISSLFLKOVLFILARFRQLSLFQGVPPFLLVENWSISFDHIKLGKGYFKCQGGQCYFECKLVVWFYSNLINLVL IHLKLSLPFSLP
VPLLLHLTLPLSHIHTQHTNTKCLDFKIQLESVFTLHSYILVKFLPLAICFFSKIFAARKEFSHPNIISSRDERKAEMNELKLLFLL
SKRTLRRRRPLPPPPCHPRDPKRSEERTHSCHASLSRKEHEHLPLDQRASVCPAASSELVHWSQAGVSDARKGTASHCQAEAAQSLEKDL
FALFPPGGARPTHPPSQTKVVAVRRAANADKDEKHEKNGRGGKTL PNGKPNLRGWDSPLLL SQRALLGNCVFP IYGAL YSGIMQPPRSSL
LLQNLGSLALPYWDGPLDSNARVCEFGEILKRAKTAIFYLMQCLEREYCLFPNTNPTPMKNCLERCFCQGITIKHYLMHRTPLLDSPLIKLLF
HITVKQQTFKRPLLSAPPSLLQNTAPMAVDWPLNSHRPPQQGQREAPGYCPPTRKILFVCSKQFSAKEVSSPCSYALKYHAPPTAIWLC
L IFFLKONVYFKGRKKQVKFHSAPAVGKPLNPPASPLQPTANSFLRPQGRKREWGVRGAGLGACFQEGIGCHLAVLRVTREPVYKLSRQH
PCTCTLYSSVQNVQTFGVYIKQKSSCIFIKYNVWVSPKMFCHMLDIOVLARPRYMNPKKRIPIVCVQMH LAP IRYFLKQDSSVRVHMK
NQAGNRNDSAGDGSRGVPAALGPASTSPFLAASWCSGGMTSLVRNVSLSLVQRL TCSNQTFQKGVHLFCLNFPFPGISLLYKLGVG

FIG. 18C

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VGSFVDKFPFPRGEFDIPWTPVCLLPSLHTAWGEACASPGGEKATPDP LSPGGKAVLDRRLSAEGKYWTRGVLPFKTGD TWEIKRAGHCWW
EEAFYLPVQIILLFNGVYWGQGLIHFLGRWMC FHEHLSFHFYSSIHSTSICTLTANARVVTEMKILELKQNPSPHTPVIPGDLSLW FLEL
AILRTQPGRQPPGLRACPAYLLKCLPHPNLAPAIWVSRPGRPDIAPESNTLPTRRCFEMERKIGTSSFKGSNGIDFQNLCTKHSHSL
FRTNSGSGNVFVLLFTISFWIQAFVNMYNLASITLMIWSKYCKLFHCGDGCYTYIDCNFLVFFVLNNSFKQEQENG RSVHFKHKCEELVY
KQKILYKLPSEIKVDLVKKKKEKKKKK

FIG.18D

ATGTTGGCGTGGCCGACAGCGCGGCAACTGAGGCAAGGCTGAGGAGGACGGCGGCACGGCAGCGCTCGCGGGCAGGAGCGGGCGCACCGACCCCTGCACC
GCGACAGGGGCCCTGGAGGCCGGGACCGCGCGCCCGGCTGTGTCTCCCGGGGTGCTGTGCGGGGCGCTGCCCGCGCGCGCTGCTGCCGCTGCTCTTTTCGCTGCTG
CTGCTGCCGCTGCCCGGGAGGCCGAGGCCGCTGCGGTGGCGGGCGGCTGTCGGCTCGGCCGACGCCAGGCCAAGGAATGTGACCGGCCGTGTGTCAACGGCGGT
CGCTGCAACCCTGGCACCGGCCAGTGGCTGTGCCCGCGGGCTGGGTGGCGGAGCAATGCCAGCACTGCCGGGGCGCTTCAGACTAACTGGATCTTCTGGGTTTGTG
ACAGATGGACCTGGAAATTATAATACAAAACGAAGTGCACGTGGCTCATTTGAAGGACAGCCAAATAGAAATAATGAGACTTCGTTTCAATCATTTTGTACAGAGTGT
AGTTGGGACCATTATATGTTTATGATGGGACTCAATTTATGCACCGCTAGTTGCTGCAATTTAGTGGCCTCATTTGTTCTGAGAGAGATGGCAATGAGACTGTCCCT
GAGTTGTTGCCACATCAGTTATGCCTTGCTGCTATTTTATGATGCTGCTTATAATTTGACTGGAATTAATATTACTTACAGTTTGTATATGTTGCCAAATAAC
TGCTCAGGCCGAGGAGTGAAGATCAGTAAATAGCAGCGATACTGTTGAATGTGAATGTTCTGAAAACCTGGAAAGGTGAAGCATGTGACATTCCTCACTGTACAGAC
AACTGTGGTTTCCCTCATCGAGGCATCTGCAATTCAAGTGAATGCAGAGGATGCTCCTGCTTCTCAGACTGGCAGGGTCTGGATGTTCACTTCTGTACCAGCTAAC
CAGTCATTTTGGACTCGAGAGGAATAATCTAACTTAAAGCTCCCAGAGCATCTCATAAAGCTGTGGTCAATGGAAACAATTAATGTGGGTTGTTGGAGGATATATGTTT
AACCACTCAGATTATAACATGGTTCTAGCGTATGACCTTGCTTCTAGGGAGTGGCTTCCACTAAACCGTTCGTGGAACAATGTGGTTGTAGATATGGTCATTTCTTG
GCATTATACAAGGATAAAATTTACATGTATGGAGGAAAAATTTGATTCAACTGGGAATGTGACCAATGAGTTGAGAGTTTTTCACATTCATTAATGAGTCATGGGTGTG
TTGACCCCTAAGGCAAAGGAGCAGTATGCAGTGGTTGGGCACTCTGCACACATTGTTACACTGAAGAAATGGCCGAGTGGTCAATGCTGGTCACTCTTTGGTCACTGCCCT

FIG. 19A

CTCTATGGATATATAAGCAATGTGCAGGAATATGATTTGGATAAGAACACATGGAGTATATTACACACCCAGGGTGCCCTTGTGCAAGGGGGTTACGGCCATAGCAGT
GTTTACGACCATAGGACCAGGGCCCTATACGTTTCATGGTGGCTACAAGGCTTTCAGTGCCTAAAGTACCGGCTTGACAGATGATCTCTACCGATATGATGTGGATACC
CAGATGTGGACCATCTTAAGGACAGCCGATTTTCCGTTACTTGCACACAGCTGTGATAGTGAAGCAACCATGCTGGTGTGTTGGGGGAAACACACACAATGACACA
TCTATGAGCCATGGCGCCAAATGCTTCTTCAGATTTTCATGGCCTATGACATTGCCGTGACCGCTGGTCAGTGCTTCCAGACCTGATCTCCACCATGATGTCAAC
AGATTTGGCCATTCAGCAGTCTTACACAACAGCACCATGTATGTGTTCCGGTGGTTTCAATAGTCTCCTCAGCGACATCCTGGTATTCACCTCGGAACAGTGTGAT
GGCATCGGAGTGAAGCCGCTTGTTTAGCAGCAGGACCTGGTATTCGGTGTGTGTGGAAACACAGGGTCGTCTCAGTGTATCTCGTGGGCGCTGGCAACTGATGAACAA
GAAGAAAAGTTAAAATCAGAAATGTTTTCCAAAAGAACTCTTGACCATGACAGATGTGACCAGCACACAGATTGTTACAGCTGCACAGCCAACACCAATGACTGCCAC
TGGTGCAATGACCATTGTGTCCCCAGGAACACAGCTGCTCAGAAGGCCAGATCTCCATTTTAGGTATGAGAAATTGCCCCAAGGATAACCCCTATGTACTACTGTAAAC
AAGAAGACCAGCTGCAGGAGCTGTGCCCTGGACCAGAACTGCCAGTGGGAGCCCCGGAAATCAGGAGTGCATTGCCCTGCCCGAAATAATCTGTGGCATTTGGCTGGCAT
TTGGTTGGAAACTCATGTGTAATAATTACTACTGCCAAGGAGAAATTATGACAAATGCTAAATTGTTCTGTAGGAACCAACAATGCCCTTTTGGCTTCTCTTACAACCCAG
AAGAAGGTAGAAATTTGTCTTAAGCAGCTGCCGAATAATGCAGTCATCTCAGAGCATGTCCAAGCTCACCTTAACCCCATGGGTGGCCCTTCGGGAAGATCAATGTGTCC
TACTGGTGTGGGAAGATATGTCCCCATTACAAAATAGTTTACTACAGTGGATGCCGTCTGAGCCCCAGTGATGCTGGAAATTTTATCAGAACCCAGTACT
CGGGGACTGAAGGCTGCAACCTGCATCAACCCACTCAATGGTAGTGTCTGTGAAAGGCCCTGCAAAACCACAGTGCTAAGCAGTGCCGGACACCAATGTGCCCTTGAGGACA

FIG. 19B

[illegible]

FIG. 19C

MVAVAAAAEARLRRRTAAALAGRSGGPHRPTATGAWRPGPRARCLPRVLSRALPPPPPLPLFSLLLLPLPREAEAAAAVSGSAAAEAKECDRPCVNGG
RCNP GTGCVC PAGVGEQCCHGGRFRLTGSSGVTDPGPNYKTKCTMLIEGQPNRIMRLRFNFHAFATECSWDHLVYDGD SYAPLVAAFSGLIVPERDGNETVP
EWWATSGYALLHFFSDAAYNLTGFENITYSFDMPNCSGRGECKISNSSDTVECECSENWKGEACDIPHCTDNCGFPHRGICNSSDVRGCSCFSDWQPGGCSVPVPPAN
QSFWTREEYSNLKLPRASHKAVVNGNIMWVVGGMFNHSDYNNMVLAYDLASREWLPNRSVNNVVRYGHSALAYDKIYMYGGKIDSTGNVTNELRVFHIHNESWVL
LTPKAKEQYAVVGHSAHIVTLKNGRVVMLVIFGHCPLYGYISNVQEYDLDKNTWSILHTQGALVQGGYGHSSVYDHRTRALYVHGGYKAFSANKYRLADDLYRYDVT
QMWTILKDSRFFRYLHTAVIVSGTMLVFGGNTHNDTSMHGAKECFSSDFMAYDIACDRWSVLPRPDLHHDVNRFGHSAVLHNSTMYVFGGFNSLLLLSDILVFTSEQCD
AHRSEAAACLAAGPIRCVWNTGSSQCSWALATDEQEEKLKSECFSKRTL DHRCDQHTDCYCTANTNDCHWCNDHCVRNHCSCSEQSIFRYENC PKDNP MYCN
KKTSCRSALDQNCQWEPNQEIALPENICGIGWHLVGN SCLKIT TAKENYDNAKLCFRNHALLASLTTQKKVEFVLKQLRIMQSSQSMSKLTLPWVGLRKINVS
YWCWEDMSPFTNSLLQWMPSEPSDAGFCGILSEPSTRGLKAATCINPLNGSVCPANHSKQCRTPCALRTACGDCTSGSSECMWCSNMKQCVDSNAYVASFPFGQC
MEWYTMSTCPPENC SGYCTCSHCL EQPGCGWCTDPSNTGKGKIEG SYKGPVKMPSQAPTGNFYQPPLNSSMCLED SRYNWFSF I HCPACQCNGH SKCINQSICEKCE
NLTTGKHICETCISGFYGDPTNGGKCQPKCKNGHASLCNTNTGKCFCTTKGWKGDECQLCEVENRYQGNPLRGTCYYTLLIDYQFTFSLSQEDDRYYTAINFVATPDEQ
NRDLDMFINASKNFNLNITWAASFAGTQAGEEMPVSKTNIKEYKDSFNEKFDNRNHPNITFFVYVSNFTWPIKIQVQTEQGRMDTGRGTSHTRACCGVGGRGRDS
IRGYTCMTSWVQHTNMAYVYICNPACCAHVPNLKYNKKKKKKKKKKKKKKKKKK

FIG. 19D

FIG. 20A

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CTCTATGGATATAAGCAATGTGCAGGAATATGATTTGGATAAGAACACATGGAGTATATTACACACCCAGGGTGCCCTTGTGCAAGGGGTTACGGCCATAGCAGT
GTTTACGACCATAGGACCAGGGCCCTATACGTTTCATGGTGGCTACAAGGCTTTCAGTGCCAAATAAGTACCGGCTTGCGAGATGATCTCTACCGATATGATGTGGATACC
CAGATGTGGACCATTCCTTAAGGACAGCCGATTTTCCGTTACTTGCCACACAGCTGTGATAGTGAGTGGAAACCATGCTGGTGTGGGGGAAACACACACAATGACACA
TCTATGAGCCATGGGCGCCAAATGCTTCTTCAGATTTTCATGGCCTATGACATTGGCTGTGACCGCTGGTCAGTGTCTCCAGACCTGATCTCCACCATGATGTCAAC
AGATTTGGCCATTCAGCAGTCTTACACAACAGCACCATGTATGTGTTCCGGTGGTTTCAATAGTCTCCTCCTCAGCGACATCCTGGTATTCACCTCGGAACAGTGTGAT
GCGCATCGGAGTGAAGCCGCTTGTTAGCAGCAGGACCCTGGTATTCGGTGTGTGTGGAAACACAGGGTGGTCTCAGTGTATCTCGTGGGCGCTGGCAACTGATGAACAA
GAAGAAAGTTAAATCAGAATGTTTTTCCAAAAGAATCTTTGACCATGACAGATGTGACCAGCACACAGATTGTTACAGCTGCACAGCCCAACACCAATGACTGCCAC
TGGTGCAATGACCATTGTGTCCCAGGAACACAGCTGCTCAGAAGGCCAGATCTCCATTTTAGGTATGAGAAATGGCCCCAAGGATAACCCCTATGTACTACTGTAAC
AAGAAGACCAGCTGCAGGAGCTGTGCCCCTGGACCAGAACTGCCAGTGGGAGCCCCGGGAATCAGGAGTGCAATGGCCCTGCCCCGGTAGGCCCTTGCAGGGTCATCTTGGTG
TGTGTGGGTCCATTACTCAGCCTGCTTCCCCCAACACTGTGCAGCCTAAGTTGAACCTAGCAGAGGGGAAGAGCTAATCTGTCCATTATCCCCCACACGAGTATT
ATGGGCTTTTGTGTTTAACTAAATACAGTTCCTTAAGTATTTGTCTCTACTGTCTCTTGAATAAAGTGAAACATCCTTTGCTGCTCTGTAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

FIG. 20B

MVAVAAAAATEARLRRRTAATAALAGRSGGPHRPTATGAWRPGPRARLCLPRVLSRALPPPPLPLLSLPLPREAEAAVAAAVSGSAAAEAKECDRPCVNGG
RCNPGTGQCVCPAGWGEQCQHCGRFRLTGSSGFVTDGPGNYKYKTKCTLIEGQPNRIMRLRFNHFATECSWDHLVYVDGDSIYAPLVAAFSGLIVPERDGNETVP
EVAATSGYALLHFFSDAAYNL TGFNITYSFDMPNCSGRGECKISNSSDTVECECSENWKEACDIPHCTDNCGFPHRGICNSSDVRGCSCFSDWQGPCCSVPVPAN
QSFITREEYSNLKLPRASHKAVVNGNIMWVGGYMFNHSYNMVLAYDLASREWLPNRSVNNVVRYGHSALYKDKIYMYGGKIDSTGNVTNELRVFHIHNESWVL
LTPKAKEQYAVVGHSAHIVTLKNGRVVWMLVIFGHCPLYGYISNVQYOLDKNTWSILHTQGVGGYGHSSVYDHRTRALYVHGGYKAFSANKYRLADDLYRYDVDY
QMWITILKDSRFFRYLHTAVIVSGTMLVFGGNTHTDTSMSHGAKCFSSDFMAYDIACDRWSVLPRPDLHHDVNRFGHSAVLHNSTMYVFGGFNSLLSDILVFTSEQCD
AHRSEAAACLAAGPGIRCVWNTGSSQCSWALATDEQEEKLKSECFSKRTLHDHRCDDQHTDCYSTANTNDCHWCNDHCVPRNHSCSEGQISIFRYENCCKDNPMYYCN
KKTSCRSCLDQNCQWEPNQEICIALPGRPCRVILVCVGPLLQPASPNVQPKNLAEKSFPCFIPHTSIMGFFVFNNTVLKYLLSFEIKNIIILCCSVKKKKKKKK
KKKKKKKK

FIG. 20C

INTERNATIONAL SEARCH REPORT

Inter al Application No
PCT/US 99/16484

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C07K14/705 A61K38/17 G01N33/68 C07K16/28

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C07K C12N A61K G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	NAGASE ET AL.: "Prediction of the coding sequences of unidentified human genes IX: the complete sequences of 100 new clones from brain which can code for large proteins in vitro" DNA RESEARCH, vol. 5, 1998, pages 31-39, XP000884356 table 2	1,2,5,11
X	DATABASE GENBAN 'Online! Accession no. AB11120, 10 April 1998 (1998-04-10) NAGASE ET AL.: "Prediction of the coding sequences of unidentified human genes" XP002135391 abstract	1,2,5,11



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

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"P" document published prior to the international filing date but later than the priority date claimed

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"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"Z" document member of the same patent family

Date of the actual completion of the international search

11 April 2000

Date of mailing of the international search report

27/04/2000

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Skelly, J

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 99/16484

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	NAGLE ET AL.: "The mahogany protein is a receptor involved in suppression of obesity" NATURE, vol. 398, 11 March 1999 (1999-03-11), pages 148-152, XP002135389 the whole document ----	1-28
P,X	GUNN ET AL.: "The mouse mahogany locus encodes a transmembrane form of attractin" NATURE, vol. 398, 11 March 1999 (1999-03-11), pages 152-156, XP002135390 the whole document ----	1-28
X	DUKE-COHAN ET AL.: "A novel form of dipeptidylpeptidase IV found in human serum" J. BIOL. CHEM., vol. 270, no. 23, 9 June 1995 (1995-06-09), pages 14107-14114, XP000579864 page 14109 -page 14111 -----	16-18

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 99/16484

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claims 26-28 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

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